

416 Rec'd PCT/PTO 12 JUN 2000

WO 99/29870

PCT/AU98/01023

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## (2) INFORMATION FOR SEQ ID NO:1

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25 TTCTGTGTCA TGGCAAAAGT TATAAAAACA AAAAAAGGCC TTGCACTTAA TCTGAAAGGA 60  
AAACCGCTGC CCGAGATGCT GGCCGAACCG GCCCAAAGTC CTAATTACGC GGTGCTGCCG 120  
GACGATTTTG AAGGTGTTAT CCCCAAGGTG ACGGCTCGTC CGGGGATAA GGTGCTGCCG 180  
GGCTCAGCAC TGATGCACCA CAAGGCATAT CCGGAGATGA AGTTTACAAG TCCGGTTAGC 240  
GGCGAAGTGA TCGCGGTGAA TCGCGGTGCC AAGCGCAAGG TGTTGAGCAT CGAGGTGAAA 300  
CCGGACGGAC TGAACGAATA CGAGTCATTC CCTGTGGGGG ATCGGTCTGC CCTCTCTGCC 360  
30 GAACAGATCA AGGAGCTTTT ACTGTCGAGC GGTATGTGGG GTTTTATTAA GCAACGTCCT 420  
TAGCACATAG TGGCTACACC GGATATAGCT CCACGCGACA TTTATATTAC TGCCAACTTT 480  
ACTGCACCAT TGGCTCCGGA CTTCGATTTT ATCGTTCGAG GAGAAGAAGC CGCCCTGCAG 540  
ACTGCCATCG ATGCCCTGGC CAACTCACG ACAGGAAAGG TGATGTGGG CCTGAAGCCG 600  
GGTTCATCTC TGGGCTTGCA CAATGCAGAA ATCGTAGAAG TACACGGACC TCATCCGGCA 660  
35 GGTAACGTGG GCGTGTGAT CAATCATACG AAGCCAATCA ATCGGGGCGA AACGGTGTGG 720  
ACGCTCAAGG CTACCGACCT GATCGTGATC GGACGTTTCC TGCTTACGGG CAAAGCCGAT 780  
TTTACCAGAA TGATTGCCAT GACCGGCTCA GACGCTGAG CTCACGGATA CGTCGGTATT 840  
ATGCGGGGTT GCAATGTCTT TGCTTCTTC CCGGCGGAC TCACATAAAA GGAATCTCAC 900  
GAGCGTGTGA TCGATGGCAA TGTGCTGACC GGTAGAAGC TCTGCGAGAA GGASCCTTTC 960  
40 CTGTGAGCCC GGTGTGACCA GATCAGGTTG ATCCCGAAG GCGACGATGT GGACGAACTC 1020  
TTCGGGTGGG CTCACCCCG TCTCGATCAG TACAGCATGA GCAGAGCTTA TTTCTCTTGG 1080  
TTGACGGGGA AAAACAAAGA GTACGTACTC GATGCCCGGA TCAAGGGTGG CGAACGTGCT 1140  
ATGATCATGA GCAACGAGTA TGACCGCGTT TTCCTGATGG ACATCTATCC GGAGTATTTG 1200  
CTCAAGGCTT TTATAGCATT CGACATCGAC AAGATGGAGG ACTTAGGCAT ATATGAAGTG 1260  
45 GCTCCGGAGG ACTTTGCCAC TTGCGAATTT GTGGATACAT CCAAGATCGA GCTGCAGCGT 1320  
ATCGTTCCCG AGGGCTTGGA TATGCTCTAT AAGGAATGA AT 1362

## (2) INFORMATION FOR SEQ ID NO:2

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

75 GAATAAGCA AGTGTTACAT GGATAAAGTG AGCTATGCTC TGGGATTGAG CATCGGTAAT 60  
AATTTCAAGT CTTCGGGCAT CGACAGCGTC GTTATGGATG ATTTATGCA AGGTCTGTCT 120  
GATGTACTGG AAGAAAAAGC CCCTCAGCTC TCGTATGAGC AGGCCAAGCG CGAAATAGAG 180  
GGGTATTTC TGGATTGCA GCAGAAGGCT GTCAACTGA ACAAGAGGC CGGAGAAGAA 240

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5 TTCTCAAGA TAAATGCACA CAAGGAAGGT GTGACGACCT TACCGAGGG CTTGCAATAC 300  
 GAAGTCATTA AGATGGGAGA GGGCCCGAAA CCCACCCTTT CGGACACGGT AACCTGTCAT 360  
 TATCAGGGTA CGCTCATCAA CGGTATCGTT TTGATAGCT CTATGGACAG GGGAGAACCG 420  
 GCCAGTTTCC CTCTAAGAGG AGTTATAGCC GGCTGGACGG AGATTCTTCA ATTAATGCCCT 480  
 GTAGGATCCA AGTGAAAGT AACTATAACG AGCGATCTGG CGTATGGAGA TCGTGGTGCC 540  
 GCGGAACATA TCAAACCGGG TAGTACGCTC ATTTTATAA TCGAATTATT GAGTATCAAC 600  
 AAA 603

10 (2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 837 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...837

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

35 CAAAAAACA AACGAAGAT GAAAAAAGCA TTAATTATG GTGCTGCTCT TTGGGAGCA 60  
 GTGCTTTTG CAAGTGCTCA GTCTTTGAGC ACAATCAAAG TACAGAACA TTCAGTACAG 120  
 CAACCTCGTG AGGAAGCCAC TATTCAGGTT TGTGGAGAAT TGGCAGAGCA AGTTGACTGC 180  
 ATTGGGACAG GTAATTCTGC AATCATAGCC GCTGCAGCGA AATTGAAAG CGATGATCTC 240  
 GAAAGCTATG TTGGCTGGGA GATCATGAGT GTTGATTTCT TCCTGGATA TAAAGCGTGC 300  
 AAGTACACAT CTGCAGTCTG GGCTGATGAT ATGACCATTT TGGGCCAATC AGAAGATAGT 360  
 GATCCCGAAA TGCAGACTAT CAACAATCTT GCTCTCAAGA CTAGTGTCAA GATTGAAGCC 420  
 GGCAAGAATT ACATAGTTGG TTATATTGCT AATACCGCAG GTGGACATCC TATCGGATGT 480  
 GATCAGGGCC CTGCCGTTGA TGGTTATGGA GATTGGTTT CTATATCAGA AGATGGTGGT 540  
 GCTACTTTCC CTCCGTTGCA ATCTCTTCAT CAAGCAGTTC CTACCTTAA TTACAACATC 600  
 TATGTCGTTG TTCATTTGAA GAAGGGTGAA GGTGTTGAGG CTGTTCTTAC CAACGACAAG 660  
 GCTAATGCTT ATGTTTCAGAA TGGCGTTATC TATGTAGCCG GAGCTAATGG TCGTCAGGTA 720  
 TCTCTGTTG ACATGAACGG TAAGGTTGTT TATACCGCGG TTAGCGAAAC GATTGCAGCT 780  
 CCTCAGAAGG GCATGTATAT CCTCCGTGTA GGTGCTAAGA GCATCAAGCT GGCTATC 837

50 (2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...471

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

75 CGTGAATTCC TGCCGGAGAA AGCTCTCTAT ATCGGCTGJC GCGTGGAGAC GCAAGAGGGG 60  
 CATGCCGTAG GTTTCGGAAT GGATGACGGC CTGCGGATGA AAGGCAAGGG CGATCTGGTC 120  
 GGGAGCTATC TTCCCGGTGC TGCTCCGATG CCTTTGTCC CGCTTCTGA TATCCGGCT 180  
 CGTTCGATGG ATGCCAATTT TTATATCTAT TCTCGTATT CACTGGGTTC GGGCAGCGAT 240

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5 GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCCAACCCCTG CCACGACGGA GCTGCATGTG 300  
 GAAGCCCTGT CCGCATGGGT GGGCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTCGG 360  
 GTATCGGCTC GGACGGTGA TAGCGAGAAG CTGTGCATCG ACATTGCCTC ACTGCCCGTG 420  
 GGGCTCTATA TGCTGCGCAT CGGCAGCTAC TCGGCCAAGT TCGAGAAGAG A 471

## (2) INFORMATION FOR SEQ ID NO:5

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1686 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1686

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

30 ACAAGAAATG TTTCATCAT AAAAATGCCA AGAATTATGA AATTAATAAT TGCACTCAGA 60  
 CTGCTGCTGG CGACTTTTGC CATAGTTTGA TTTAGCCCTC TGGCCAAGGC CCAGATGGAT 120  
 ATTGGTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT 180  
 TTTTATTACA AGATGGCTGT GGCAGACAAAT GGATGGATCT ATGTGATGTT GGATTTCTCT 240  
 CGTATTATT TTGATGATGT CAGGCTGTAT CGTTCCAAAG ACGGTGGTGC TACTTACCAA 300  
 AAGTTAGGGT CTTTGGGGTC TTTGGTGCTT TATGACTTCG ATGTCTCGCA TTGCGATTTT 360  
 ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGA CAGTCATGAC AGCATTGCAA 420  
 TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATCGCCATGA TGCAGATATC 480  
 AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGTGTAGCC 540  
 ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGTCTC 600  
 GCTGTCCCGG TTAGTGGCTC CGGAAGCGAT CACAGCTTCT TGGACTATAT TTTTTCGTTA 660  
 GATGGTGGAG TACACTTTGA GCAAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC 720  
 AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTAA TACTTGGCCA 780  
 CTATGGGAG TCGTATTGTA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT 840  
 TCCAACCTTG TGGACTATGA TCCCGCTAT GCGTGGTCTG AACCGATAAT AATAGAAGAA 900  
 45 TTGGATGACA ATTCCGATAA TACCGTGGGT GGAGCACTAA GTATAGAGAT CCAATGATG 960  
 TACCCGGGCC ATTACGTATA TCCGAAGCAA TCTTTCAATT ATTCTCCCGG ACATACACCG 1020  
 ACAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG 1140  
 GAAGGCGATC GTTATCTGAC TACTTTTCAA GATCACAATC TAATGAGATA CAGATGGATC 1200  
 50 AAATACGATG ACATTAATCT TTTTATGGT TGGAGTTGCG CATATGTATA TGCAAAAGAA 1260  
 GCTAAAGATA AAAAGAGGCG CCGTCCGCAA GTAGCACTCA ATCCTACCAA TGGAAAGGCT 1320  
 TGTTGGGTAT GGCATACTCG CAAGAGCCCA TATGATGAAA CCAAACCA CA TCTACTCCT 1380  
 GTAATTATTA AACATTTCTT ATGGTCCGAT ACGGAGTGGG TACATGCTCT GGAGGTGGGG 1440  
 GACGTATTGC AGAAGGAGGG TAGCATGAAG CTCTACCCCA ATCCTGCCAA AGAATATGTT 1500  
 55 CTGATCAACC TACCCAAAGA AGGGGGGCAC GAGGCACTCG TATACGACAT GCAGGGCCGA 1560  
 ATCGTGGAGA AAGTTTCATT TTCAGGGAAG GAATATAAGC TGAATGTGCA GTATCTGTCC 1620  
 AAAGGTACGT ACATGCTGAA AGTTGTAGCG GATACGGAGT ATTTCTGTGA AAAAATCATT 1680  
 GTAGAG 1686

## (2) INFORMATION FOR SEQ ID NO:6

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 70 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

10 CAAATGAAC GATTACTCCC CTTTCTCCTT TTAGCAGGAC TCGTAGCCGT AGGAAACGTG 60  
 TCTGCTCAGT CACCCCGAAT CCCTCAAGTG GATGTACACA CTCGCATCGC AAGAAATGCC 120  
 CGTTATCGAC TGGACAAGAT CAGTGTCCCG GATTCTCGTC AGATATTGGA TTACTTCTAT 180  
 AAAGAAGAAA CGATACCCAC TAAATACAA ACGACCACAG GAGGTGCAAT TACAAGCATC 240  
 GATTCCGTTT TCTATGAAGA CGACAGGTG GTTCAGGTGC GCTATTTTGA CAATAACCTT 300  
 GAATTAAAC AAGCGGAGAA GTATGTATG GACGGTCTA AGCTGGTCTT TCGAGAAAT 360  
 15 CGCAAGTCGC CGACAGACGA AACGCCAATA AAGAAAGTTA GCTATCACTA TCTCTGTGGC 420  
 AGCGATATGC CTTTTGAGAT TACGACAGAG ATGAGCGATG GCTATTTTGA AAGCCATACG 480  
 CTTAACIATC TGAATGGAAA GATTGCCGGA ATAGATATCA TGACTCAACA GAACCCATCG 540  
 GCCGAATTGA TCGAAACGGG TAGAATGGTA TATGAGTTTG ATGCCAATAA TGATGCTGTA 600  
 CTGCTTCGTG ACAGTGTAT TCTTCTCCTT CAAAACAAGT GGGTAGAAAT GTTACTCAC 660  
 20 CGTTATACAT ACGACAATAA GCATTAATGT ATTCTGTTGG AACAGACGA ATTCCGCACC 720  
 CTCACCTTGG CCAACAACCT CGAATACGAC ACCACTATCC CTCTGTCGTC TGTATTGTTT 780  
 CCCACGCAAT AGGAGTTCTT CCGTCTCTT CTTCCTCAAT TTATGAAGCA TATGCGTACG 840  
 AAGCAACGCT ATTTCAATTA CTCGGGAGAA GGCTTGTCAG AGGTATGCGA TTACAACATC 900  
 TTCTATACCG ATATGCAGGG TAATGCACTG ACCGATGTTG CCGTGAACGA ATCGATCAAG 960  
 25 ATTTATCCCT GTCCCTGCCAC GGATTTTCTG CGTATAGAAC GTTCGCAACT GCTTCGCTT 1020  
 TCGCTATTGG ACATGAACGG GAACTCATC AGAGCTACCG AATTGACAGG CGATTGGGCC 1080  
 ATTATCGGAG TTGCATCTCT TCCGAGAGGC ACTTACATCG CAGAAATAAC TGCTGCAAAC 1140  
 AGCAAAACCA TACGTGCAAA AGTATCGCTC AGA 1173

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

55 AAGAGGAATC CTTACCTTT GACGGCATCA AATCGAAAGA TTTTATAAAA AATGAGACAG 60  
 CATTATCTC TATTTCTTT TATCTTGTG CTGCTTCTTG CCTTCTCTTA TGTCCGTTGC 120  
 AGAACAGTCC GACAAACACC TAAGCAGTCC GAACGGTACG TCGTAGTCTT GTCTTTGGAC 180  
 GGCTTCGGAC CGGACTATAC CGATCGGGCA CGTACACCGG CGTTGGATCG GATGGCACAG 240  
 GAGGGATTGA GCGGGTCGCT CCAACCATGC TTCCCTCCGC TTACATTTC CAATCATTAC 300  
 AGCATGGCTA CGGGGCTTTA CCCCGATCAT CACGGTATCG TAGCCAATGA GTTTGTGGAT 360  
 60 TCGCTACTGG GCATCTTTCG TATATCCGAC CGAAAAGCCG TGGAGACCCC CGGATTTTGG 420  
 GCGGGCGAGC CGTTTGGAA TACGGCCGCA CGCCAAGGCA TCCGTACCGG TGTCTACTTT 480  
 TGGGTAGGAT CCGAAACGGC TGTGAACGGA AATCGGCCGT GCGGTGGAA AAAATTCTCC 540  
 TCCACCGTTC CGTTTCGTGA CCGTGCCGAC TCCGTATCG CGTGGCTCGG ACTGCCCGAA 600  
 AAGAGCGCAG CGCGCTTGTG CATGTGGTAC ATCGAGGAGC CGGATATGAT CGGACACAGC 660  
 65 CAAACGCCCG AAAGCCCGCT GACACTGGCA ATGGTAGAGC GATTGGACAG TGTGCTCGGC 720  
 TATTTCCGCA AGCGGTTGGA CTCTCTGCCC ATAGCCGCAC AGACCGACTT CATCATAGTA 780  
 TCCGATCAGC GTATGGCCAC GTACGAAAAT GAGAAATGTG TCAATCTGTC GCATTATCTG 840  
 CCTGCGGACA GTTCTCTCTA CATGGCCACC GGGGCCCTTA CCCACTTGTA CCGAAGCCCC 900  
 TCCTATACCG AGCGAGCTTA TGAGATCTTG CCGGCCATTC CACATATATC GGTTTACCGC 960  
 70 AAGGCGGAGG TGCCCAAGCG TTTCGCTGT GGCACCAATC CTCGTTTGGG CGAACTGGTC 1020  
 GTGATTCCCG ACATAGGCTC CACCGTCTT TTCCGAATAA ATGAAGACGT TCGTCCGGGA 1080  
 GCGGCACATG GCTATGACAA CCAAGCACCG GAAATGCGGG CTTTACTCCG GGTGTCCGGA 1140  
 CCCGATTTCG GTCCGGGCG TAGGGTGGAA AACCTGCCGA ATATCACCAT CTATCCGCTC 1200  
 75 ATATCGAGGC GTTGGGTAT AGAGCCTGCA CCAACGATG CCGACGAAAC GTTGTGAAC 1260  
 GGCCTGATCC GAGACAAACG ACCA 1284

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## (2) INFORMATION FOR SEQ ID NO:8

- 5 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...846

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

25 CTTTCCCGTG GAGTTTTC CCTGATGAT GGCCGAAGAG GAAGCATTCG TGCCTCTTCA 60  
 GGGCATAGGG ACAAATTTT TAAGAATACA ATTATCAGAT TTATCACRAT GAAAGTAGGT 120  
 TTGTTTCATCC CCTGTTATGT CAATGCASTG TATCCGGAAG TGGGTATCGC CACGTACAAA 180  
 CTGCTGAAGA GTTTGGACAT AGATGTCGAC TACCCGATGG ATCAGACATG TTGGGGCCAG 240  
 30 CCTATGGCCA ATGCCGATG CGAACAGAAA GCTCAAAAGC TGGCTTTGCG ATTCGAAGAG 300  
 CTGTTTCGAGT CGTATGATGT AGTCGTAGGG CCATCGGCCA GTTGGCTTGC TTTCGTGAAA 360  
 GAAACTATG ATCATATCCT CAGACCGACA GGACATGTCT GCAAGTCGGC AGCCAAGGTT 420  
 CGGGATATAT GCGAGTTCTT GCACGATGAC CTGAAGATCA CCAGCCTCCC CTCCCGATTG 480  
 35 GCCCATAGAG TGAGCCTGCA CAACAGTTGC CACGGTGTGC GCGAAGTCCA TCTGTCCACC 540  
 CCCAGTGAAG TGCACCGACC GTACCACAAC AAGGTGCGCC GGCTATTGGA GATGGTGCAG 600  
 GGCATAGAGG TATTCGAGCC GAAGCGAATA GACGAATGCT GCGGTTTCGG CGGTATGTAC 660  
 TCGGTGGAGG AGCCGGAGGT ATCCACCTGT ATGGGGCATG ACAAGGTGCT GGATCACATA 720  
 TCCACAGGTG CCGAGTACAT CACAGGGCCG GACAGCTCGT GCCTCATGCA TATGCAGGGA 780  
 40 GTGATAGACA GAGAGAAATT GCCGATCAAG ACAATTCATG CAGTAGAART TTAGCAGCA 840  
 AACTTA 846

## (2) INFORMATION FOR SEQ ID NO:9

- 45 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

65 CCTCTGAAA AACGAATGGA TATTGTAAGT ATGGCCGATA AAGCTCTTGT ACTGGAGATG 60  
 AGAGATGTGA CGCTCTGTCA GGAGGAAAAC GTCAITTTTC AAAATTGAA TCTGACCCTT 120  
 TCCGCGGGAG ACTTCGTCTA TCTGATAGGC TCAGTGGGAT CCGGGAAGAG CACTTTGCTG 180  
 70 AAGGCTTTGT ATGCTGAGGT GCCTATCTCT GCCGGTTATG CCCCGTGAT AGATTATGAT 240  
 CTGGCAAAGT TGAACGGAA GCAGTTGUCC TATCTGCGCA GGAATTTGGG CATTTGTGTT 300  
 CAGGATTTCC AGTTGCTGAA CGGACGTACT GTTGGCGAGA ATTTGGATTG CGTTTTCGGA 360  
 GCTACGGACT GGAAAAACCG AGCCGATCGC GAGCAGCGTA TCGAGGAGGT TTTGACCCGT 420  
 GTGGGAATGT CTCGGAAGGC TTATTAAGAGA CCGCAGCAAC TGTCCGGAGG GGAGCAACAA 480  
 75 CGTGTGGGTA TAGCCAGAGC TTTGCTGGCG AAGCCTGCGT TGATCCTGGC CGACGAACCC 540  
 ACAGGCAACC TCGATTCGGT GACCGGATTG CAGATCGCTT CTCTGCTCTA CGAAATCAGT 600

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AAGCAGGGCA CTGCAGTACT TATGAGCAGC CACAACAGCA GCCTGCTGTC GCATCTGCCG 660  
 GCACGGACAT TGGCCGTTTC TAAGAATGGC GATGCCCTCT CTTTGGTCGA GCTGAGTGCA 720  
 GATGCTGTTT CAAGAAAAA TACGGAAATA GAT 753

5

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 714 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

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(A) NAME/KEY: misc feature  
(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

30 ACCAGGCAAT GTCCGGCTTG TCGCTCTTCC TTTCACCTCA TAAAAACAAG TAAACAATG 60  
 ATTGAAATCA GCAACCTCAC CAAGGTTTTC AGAACAGAG AAATAGAGAC GGTAGCCCTC 120  
 GATGGCGTAT CGCTCAAAGT GGACAAAGGC GAATTTATCG CCATAATGGG GCCTTCGGGA 180  
 TGGGTAAGT CCACTCTGCT CAATATCCTC GGCTTCTCG ACAATCCCAC TTCCGGTATC 240  
 TACAAGCTCG ATGGGGCAGA AGTGGGCAAC CTCGGGAAA AAGACAGGAC TGCCGTCCGT 300  
 AAGGGCAATA TCGGCTTCGT ATTCCAGAGC TTCAACCTCA TCGAAGAGAT GACGGAAGC 360  
 35 GAGAACGTGG AGTTGCCGCT CGTCTATCTG GGTGTGAAGG CCTCCGAGCG GAAAGAGCGA 420  
 GTGGAGGAGG CACTGCGCAA GATGAGCATC AGCCACCGGG CCGGCCACTT CCCCAATCAG 480  
 CTCTCCGGAG GACAAACAGCA GCGCGTGGCT ATCGCCCGTG CCGTGGTGGC CAATCCGAAG 540  
 CTCATCCTCG CCGATGAACC CACGGGTAAC CTCGACTCCA AAAACGGAGC CGATGTCATG 600  
 40 GAACTGCTCA GAGGTCTCAA TCGCGAAGGT GCAACCATCG TCATGGTGAC GCACCTCCGAG 660  
 CACGATGCAC GTAGTGCCGG CCGCATCATC AATCTGTTTC ACGGTAAGAT TCGC 714

(2) INFORMATION FOR SEQ ID NO:11

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1812 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...1812

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

AGCAGAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTGGCCTCG 60  
 ATCCTCGGGG TTATAACGGC AGGAATCATC TTGTTCTGTA TCTTTCTATT TATCTTTTTC 120  
 GGCATCGTAG CCGGTATTGC CTCCAAGGCA ACGGGAGGAA CCATTCGGA GATCGAAGCA 180  
 70 AACTCCATCC TACATATANA CAATCTTCT TCCCTGAGA TCGTATCGGC CAATCCCTGG 240  
 AGCATGCTCA CAGGCAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCGA AGCCATCGGC 300  
 CAAGCCAAAA ATAATCCCAA CATAACCGGT ATCTTCCTCG ATCTGGACAA CCTTCCGTC 360  
 GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTCAGG ATTCAAGAT GTCGGGCAAG 420  
 TTCGTGAT CTATGCGGA CAGATACACC CAAAGGGTT ACTACCTCTC CAGTATTGCA 480  
 75 GACAAACTCT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA 540  
 ATGTTCTACA AAGATGCCCT CGACAAATTC GCGTGAAGA TGGAGATCTT CAAGGTAGGC 600

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5 ACCTACAAGG CAGCCGCTAGA GCCATTCATG CTCAACAGGA TGAGCGATGC CAATCGCGAA 660  
 CAAATCACCA CATACATAAA CGGGCTTTGG GACAAGATCA CATCCGATAT TGCAGAGTCG 720  
 CGCAAGACGG CAATGGATTG CGTGAAAATG TTTGCCGACA AAGGCGAAT GTTCGGTCTT 780  
 GCCGAGAAAG CGGTGGAGAT GAAGCTCGTG GATGAGCTGG CTTACCGTAC CGATGTGGAG 840  
 AAAGAACTCA AAAGATGTC CCAACGCGGA GAGAAAGATG AACTTCGGIT CGTATCGCTT 900  
 TCTCAGGTTC TGGCCAAATGG CCCGATGAAC AAAACGAAAAG GCAGTCGGAT CGCCGTTCTC 960  
 TTTGCCGAAG GTGAAATAAC GGAAGAAATA ATAAAGAAAG CGTTCGACAC TGACGGTAGC 1020  
 TCCATCACAC AAGAACTCGC CAAAGAAATC AAGGCAGCAG CCGATGACGA TGATATCAAA 1080  
 GCGGTAGTAC TTCGTGTCAA TTCTCCGGGA GGTAGTGCTT TCACTTCGGA ACAGATATGG 1140  
 10 AAGCAGGTAG CCGATCTCAA GGGCAAAAAG CCTATCGTGG TCTCCATGGG CGACGTAGCA 1200  
 GCCTCGGGCG GATACTACAT AGCCTGCGCA GCCAACAGTA TCGTGCGAGA GCATACGACT 1260  
 CTGACCGGCT CCATCGGCAT ATTCGGCATG TCCCCGAATC TCGCGGGCGT AGCCAAGAAG 1320  
 ATAGGAGTGA ATATGGACGT CGTACAGACA TCCAAATATG CAGACTTGGG CAACACCTTC 1380  
 GCTCCGATGA CGGTGGAAGA TCGTGCCCTC ATCCAACGCT ACATAGAGCA GGGCTACGAC 1440  
 15 CTCTTCCTCA CTCGCGTATC GGAAGGCGCG AACCGCACA AGGCACAGAT CGACAGCATC 1500  
 GCTCAAGGCC GTGTATGGCT CGGCGACAAA GCTCTTGAC TCGGTTTGGT GGATGAGCTT 1560  
 GGAGGTTTGG ACACAGCTAT CAAACGGGCC GCGAAGCTGG CTCAGCTCGG TGGCAACTAC 1620  
 AGCATAGAGT ATGGAAGAC CAAGCGCAAC TTCTTCGAAG AGTTGCTCTC CTCATCAGCA 1680  
 GCGGATATGA AGTCTGCCAT CCTGAGTACC ATTCTCTCCG ATCCGGAAT AGAAGTTCTG 1740  
 20 CGCGAACTCC GCTCCATGCC GCGCCGCTCT TCGGCGATAC AGGCACGTCT CCCCTATTAC 1800  
 TCTATGCCGT AC 1812

## (2) INFORMATION FOR SEQ ID NO:12

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 972 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...972  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

CTAACGTTGT TTTGTTGCAA CTATTTCAAA CAGATGAGAG CAAACATTG GCAGATACTT 66  
 TCCGTTTCGG TTCTCTTTT CTTCGGGACA GCGATCGGAC AGGCTCAGAG TCGAAACCGT 120  
 50 ACATACGAGG CITATGTGAA ACAGTACGCC GACGAAGCTA TCCGACAGAT GAGCCGCTAC 180  
 AATATACCGG CAAGCATCAC CATAGCACAG GCTTTGGTGG AGACAGGAGC CGGAGCCAGT 240  
 ACACTGGCCA GCGTACACAA CAATCACTTC GGGATCAAT GCCACAAATC GTGACGGGCG 300  
 AAGCGCACCT ATCGTACCGA CGATGCGCGG AACGAATGCT TCCGACAGTA TTCGGCCGCT 360  
 CGCGAATCGT ATGAAGATCA TTCCCGATTT CTGCTCCAAC CACGCTATCG TCCCTGTGTC 420  
 55 AAACCTGACA GAGAAGACTA TCGGGGCTGG GCTACGGGGT TGCAACGCTG TGGCTATGCC 480  
 ACCAATCGGG GCTATGCCAA TCTGCTGATC AAGATGGTGG AGCTGTATGA GCTATATGCT 540  
 TTGGATCGCG AGAAGTACCC CTCATGGTTC CACAAGTCTT ACCCGGGGTC CAACAAAAA 600  
 TCCCATCAA CGACCAAGCA GAAGCAGAGC GGAATCAAGC ACGAAGCTTA CTCAGCTAC 660  
 GGACTGCTCT ACATCATAGC CAAGCAAGGC GATACCTTCG ATTCTTTGGC CGAAGAGTTC 720  
 60 GACATGAGAG CCTCCAACT GGCCAAATAC AACGATGCTC CCGTGGATTT CCCGATCGAA 780  
 AAGGGCGATG TGATCTATCT GGAGAAAAAG CACGATGCTC CCATCTCAA ACACACACAG 840  
 CACGTAGTGC GTGTGGGCGA TTCATGTCAC AGTATCTCCC AACGCTATGG CATCCGGATG 900  
 AAGAACCTCT ACAAGCTCAA CGACAAGGAT GGCGAATATA TACCCAAGA GGGCGATATA 960  
 CTGCGCTTGC GC 972

## (2) INFORMATION FOR SEQ ID NO:13

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1599 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 75 (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

15	AGGATCCCCG	ACGAGCAGAC	CGGACGTATC	ATGGACGGAC	GTCGATATTC	GGATGGCCTC	60
	CATCAGGCTA	TGCAAGCCAA	AGAGCATGTG	AAAGTAGAGG	CTGCGACACA	GACATTGCA	120
	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	TATCATAAGC	TGGCAGGGAT	GACCGGTACT	180
	GCTGAACCTG	AAGCGGGAGA	GCTTTGGGAC	ATCTACAAAC	TGGACGTTGT	AGTTATTCCG	240
	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	AATGATCGTA	TCTATAAGAC	GGCAGGTGAA	300
	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	CGTCTGTGCG	AAGAGGGCAG	ACCTGTACTT	360
20	GTCCGCTACTA	CTTCGGTGGG	AAATATCCGA	TTGTTGAGCC	GTATGTTACG	CTTGCCTGGC	420
	ATCCCAACCA	ATGTACTCAA	TGCCAAATTG	CATCAGAAAGG	AGGCCGAGAT	TGTAGCTCAG	480
	GCCGCTCAGA	AAGGAACCTG	TACCATCGCA	ACGAACATGG	CCGTCGTGG	TACCGACATC	540
	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	600
	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	660
25	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	CATCTGATGC	GCCTCTTGGC	CACAGAAAG	720
	ATTGCTATCAT	TGATLGATCG	TTTAGGTTTC	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	780
	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	AAGGTGGAGG	AGAACAACCT	CGGTATCCGT	840
	AAACATCTGC	TTGAGTACGA	TGATGTAATG	AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	900
	CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	GGTATGGATG	TACTCAATAC	CATATACGAC	960
30	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	GAAGCCAATG	ATTTCGAAGG	CTTCAAGGAA	1020
	GATCTGATGC	GTGCACTCGC	GATAGAATCT	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	1080
	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	GATGAAGCTT	ACAAGTCTTT	CCAAGGTAAG	1140
	ATGGATCTGA	TGCGAGAAGT	GGCCACCCCT	GTGGTTCATC	AGGTATTCTGA	GACCCAAGCC	1200
	GCCGCTGACG	AGCGCATCTT	AAUCCCCATT	ACGGATGCTA	AACGTGTCTA	TAACATAGGA	1260
35	TGCAATTTCG	GTGAAGCGGA	TGAAACTCAA	GGGAAAAGCA	TCATCAAAGA	ATTTGAGAAA	1320
	GCTATCGTAC	TGCATCATAT	CGATGAGTCT	TGGAAAGAAC	ATCTGCGTGA	GATGGACGAG	1380
	CTTCGTAATT	CGGTTAGAAA	TGCCAGCTAC	GAAAACAAAG	ATCCACTACT	TATCTATAAA	1440
	CTCGAATCTT	ACGAACGTGT	CCGCAAGATG	GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	1500
	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	GAGGCTCCTT	CCCAAGAGA	GCTGGAACAC	1560
40	AGGCGGCCAA	TAGAAATCCG	ACATGCAACC	CAACAACGT			1599

(2) INFORMATION FOR SEQ ID NO:14

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
60 (B) LOCATION 1...2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

65	AAATCTTGCC	GTGTTATTGG	CCAGACGAGG	CGATACGGAT	GCTGCCCTGT	CGGACTACGA	60
	CCGTGCCATC	AAAGCCTATC	CGGAGTTTGC	CGATGCCTAT	TTCAATCGCG	GCCTGCTGTT	120
	GCTTTCCGCG	GGAAAGGCCA	AAGAAGGCAT	CGCCGATCTG	AGTCGGGCAG	GCGAATACGG	180
	GCTCTACAAG	GCGTACAACA	TCATCAAAAC	AATGAGCACG	AAGTCATGAT	CTCCGTCAT	240
70	AACTGACATG	TGATTTCCGG	CACCCGTLTG	CTCTTCGATC	AGGTATCATT	CGTCATCAAC	300
	AGGCGCGACC	GTATCGCTCT	TGTAGGGAAG	AACGGTCCCG	GCAAGAGTAC	GCTGCTCAAG	360
	CTGATTGCCG	GATGGAAGA	ACCGACATCC	GGACACATAG	CACGCCCAAA	GGGGATCCGC	420
	ATAGGCTATC	TGCCCGAGGT	GATGCGTTTG	CAGGACGGAC	ACACGGTTTA	CGAAGAGGTC	480
	GAGCAGGCTT	TCAACGATAT	TCGCCAAATA	GAGGAAGAGA	TACGGCCTCT	GTCCGATGAA	540
75	ATGGCCGGAC	GTACGGACTA	CGAATCGGAT	GACTATATCC	GACTGATAGA	GCATTATACG	600



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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1965 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ACAAACGAAAG	AAAACGAGAC	AACACAAAA	AACGAATAA	GAATTATGGG	AAAAATCATT	60
GGAAATTGACT	TAGGCACAAC	GAACCTCTGT	GTCTCTGTAT	TGGAAGGTAA	CGAACCTATC	120
GTTATTACAA	ACAGTGAGGG	CAAGCGCACA	ACGCCCTCGG	TAGTGGCTTT	TGTGGATGGT	180
GGCGAGCGTA	AGGTGGGCGA	TCCGGCCAA	CGTCAGGCCA	TCACCAATCC	GACCAAGACG	240
ATATACTCTA	TCAAACGCTT	CATGGGCGAA	ACTTACGATC	AGGTTTCCAG	AGAAGTGGAG	300
AGAGTGCCAT	TCAAGGTAGT	ACGTGGGGAC	AATAATACTC	CGCGCGTAGA	TATAGACGGT	360
CGTCTCTATA	CGCCGCAGGA	AATTTCCGCC	ATGATCCTTC	AGAAGATGAA	GAAGACGGCC	420
GAAGACTACC	TGGTCAGGA	AGTAACGGAG	GCCGTGATCA	CTGTGCCCCG	ATACTTCAAC	480
GACGCTCAAC	GTACGGCAAC	GAAAGAAGCA	GGAGAGATCG	CCGGCCGTAA	AGTTCGCCGT	540
ATTGTGAACG	AGCCTACGGC	AGCTTCTCTG	GCCTACGGTC	TGGACAAGTC	CAATAAGGAT	600
ATGAAGATCG	CTGTCTTCGA	CTTGGGTGGC	GGTACCTTCG	ATATCTCTAT	CTTGGAAATTG	660
GGCGACGGCG	TTTTCGAAGT	GAAATCGACC	AACGGTGATA	CGCACCTCGG	AGGAGACGAC	720
TTCCGACCACG	TGATCATTGA	CTGGCTGGCA	GAAGAGTTCA	AGTCTCAGGA	AGGTGTGGAT	780
CTTCGCCAGG	ATCCTATGGC	TATGCAGCGT	CTGAAAGAAG	CTGCCGAAAA	AGCCAAGATA	840
GAGCTCTCCA	GCACTTCATC	TACGGAGATC	AACCTCCCTT	ATATCATGCC	GGTGAACGGC	900
ATCCCCAAGC	ACTTGGTGAT	GACGCTTACA	AGGGCTAAGT	TCCAGCAGTT	GGCCGATCGT	960
CTGATTCAGG	CATGTGTGGC	ACCCTGCGAA	ACGGCCTTGA	AAGATGCCGG	TATGTCACGT	1020
GGCGATATCG	ATGAAGTGAT	TCTCGTAGGT	GGTCCACAC	GTATTCCTGC	TATTACAGGAG	1080
ATTGTGGAGA	AGATCTTCCG	TAAGGCTCCG	TCCAAAGGGT	TGAATCCCGA	CGAAGTGGTA	1140
GCTGTGGGTG	CGGCTATTCA	AGGCGGTGTT	CTGACCGGTG	AGGTAAGGGA	TGTCTTGCTG	1200
TTGGACGTTA	CCCCCTTGTC	GCTCGGTATC	GAGACTATGG	GAGGCGTGAT	GACTCGCTTG	1260
ATCGATGCCA	ATACCACTAT	CCCGACGAAG	AAGAGCGAAA	TCTTTACCA	AGCAGTGGAC	1320
AATCAACCTT	CGGTAGAGAT	TCATGTACTT	CAGGGTGAGC	GTTCTTTGGC	TAAGGACAAT	1380
AAGAGCATCG	GCCGTTTCAA	CTTGGACGGT	ATTGCTCCGG	CGCCCGTCA	GACACCGCAG	1440
ATCGAAGTAA	CGTTTGACAT	CGATGCCAAC	GGTATCCTGA	ATGTAACGGC	TCAATGACAAA	1500
GCTACCGGCA	AGAAGCAGAA	TATCCGCATC	GAAGCCTCCA	GCGGTTTGTC	CGATGATGAG	1560
ATCAAGCGCA	TGAAGGAAGA	GGCGCAGGCC	AATGCCGAAG	CAGATAAGAA	AGAGAAAGAA	1620
CGTATCGACA	AGATCAATCA	GGCCGACAGC	ATGATCTTCC	AGACGGAAAA	GCAGTTGAAG	1680
GAGTTGGGAG	ACAAATTCCC	GGCCGACAAG	AAGGCTCCGA	TCCGATACCG	TCTCGACAAA	1740
CTGAAAGAG	CACACAAAGC	ACAGGATGTA	GCTGCTATCG	ATACAGCCAT	GGCCGAAGCTG	1800
CAACCCGCTC	TTTCCGCGAG	GGGCGAAGAG	CTTTACAAGA	ATGCCGGAGC	AGCCCAAGGT	1860
GGCGCACAA	CCGGTCCGGA	CTTCGGCGGT	GCTCAAGGTC	CCTCTGCCGG	TGATCAGCCC	1920
TCTGACGACA	AGAACGTCAC	AGACGTAGAC	TTCGAGGAAG	TGAAG		1965

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1401

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:17

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5  AAGTGGGCAC GTACAACTAC TTTAAGGATA TCGAACGCAA CAATCTATAA AACTATGCGC 60
   TACGACTTAG CTATCATCGG TGGAGGGCCG GCCGGTTATA CGGCTGCCGA ACGTGCTGCC 120
   AAGGTGGGCC TGAACCCCT CCTAATTGAG AAGAATGCTC TCGGTGGTGT ATGCTCTAAC 180
   GAAGGATGTA TACCGACCAA GACGCTACTC TACTCGGCCA AAGTGCTACA TCAAAATTGCT 240
   ACGGCATCTA AATATGCAGT AAGTGGAACG GCGATGGAC TTGACCTCGG CAAGGTGATT 300
10  GCCAGAAAAG GTAAAATCAT TCGCAAGCTG ACTGCAGGCA TCCGTTTACG CCTGCACAGAG 360
   GCCGGAGTAG AGATGGTGAC GGCAGAAGCT ACCGTAACTG GATGCGATGC AGACGGCATC 420
   ATCGGCATTA CTGCGGGCGA AGCAGAGTAC AAAGCTGCGA ACCTGCTACT ATGTACCGGT 480
   TCGGAGACGT TTATTCCACC CATCCCCGGA GTGGAGCAGA CAGAGTATTG GACAAACCGT 540
   GAAGCTCTAC AGAACAAAGA GATTCCGACC TCTCTCGTCA TCATCGGTGG TGGAGTGATC 600
15  GGATGGAGT TCGCTTCTTT CTTCACCGGT ATCGGTACGC AAGTGACAGT GGTGGAGATG 660
   CTGCCGGAAA TACTCAACGG TATCGATCCC GAACATGCAG CTATGCTACG CGCTCACTAT 720
   GAAAAAGAAG GAATCAAATT CTACCTCGGG CACAAAGTAA CATCGGTTCC CAACGGAGCT 780
   GTTACGGTAG AATACGAAGG AGAAAGCAAA GAGATCGAAG GAGAACGTAT CCTGATGAGT 840
   GTGGGACGTC GCCCGGTGCT GCAAGGATTC GAGTCGCTCG GATTGGTGCT TGCCGSCAAA 900
20  GGTGTAAAGA CTAATGAGAG GATGCAAACT TCCCTGCCCA ATGTCATATG TGCAGTGAT 960
   ATTACAGGCT TCTCGCTTTT GGCACATACC GCTGTACGGG AAGCAGAGGT AGCAGTAGAT 1020
   CAGATTTTGG GCAAAACAGA CGAAACGATG AGCTACCGTG CCGTACCAGG TGTGGTGATC 1080
   ACCAATCCCG AGGTCCCGGG TGTGGGAGAG ACGGAAGAAT CGCTTCGCAA AGCAGGACGT 1140
   GCCTACACTG TTCGTGCGCT TCCTATGSGC TTCTCCGGTC GATTGTGAGC AGAAAAACGAA 1200
25  CAAAGCAATG GAGAGTGCAA ACTACTACTT GATGAAGAGA ACCGCTTGAT CGGAGCACAC 1260
   CTCATTGGCA ATCCGCGCGG CGAACTCATC GTAACCGCTG CCAATGGCCAT CGAGACCGGC 1320
   ATGACGGATC GACAAATCGA ACGAATCATA TTCCCTCATC CGACTGTAGG CGAAATCCTA 1380
   AAAGAAACTC TCGCCGGAGG T
   
```

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(2) INFORMATION FOR SEQ ID NO:18

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   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2835 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: circular

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
       (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

   (ix) FEATURE:
       (A) NAME/KEY: misc feature
       (B) LOCATION 1...2835
   
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:18

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55  CCTAAGATAC TTATGGAATT GAAAAGATTT TTATCACTTG GTCTTCTGCT TGTGGGATTC 60
   ATTCGGATGA AGCTTTCTGC CCACAGGCT CAGCCAATCC CTACAGATCC GGCTGTTCTG 120
   GTCGGTAACT TGGACAACGG ATTGACTTAT TTCATCGTTC ACAACGAGAA CCCGAAAGAT 180
   CGTGCAGATT TCTTTATCGC ACAAAGGTA GGTTCATTC TTGAAGAAGA TAGCCAGTCC 240
   GGTTCGGCTC ACTTCTTGA ACACATGGCT TTCAACGGTA CGAAGAAGTT CCCCAGTAAG 300
   AACTTGATCA ACTATCTCGA AACGATCGGT GTACGTTTCG GTCAGAACCT GAACGCTTCT 360
60  ACOGGATTTC ACAAGACGGA ATATACGATA ATGGATGTGC CGACTACACG TCAGGGAATC 420
   ATCGACTCCT GCTTGCTTAT CCTGCATGAT TGGAGTAACA ATATTACCTT CGACGGGCAT 480
   GAGATCGACG AGGAGCGCGG TGTGATCCAG GAAGAGTGGC GTGCTCGTCG CGATGCCAAC 540
   CTTGATATGT TCGAGGCTAT ACTTGCCAA GCTATGCCGG GTAATAAATA TGCAGAACGC 600
   ATGCCCATCG GTCTGATGGA CGTCGTGCTC AACTTCAAGC ATGATGAGCT GCGCAACTAT 660
65  TATAAGAAAT GGTATGCTCC CGACTGCAA GGTCTGGTGA TCGTGGGAGA TATCGATGTG 720
   GACTATGTGG AGAACAGAT CAAGAAGCTC TTCAAGGACG TTCCTGCTCC CGTGAATCCA 780
   GCAGAGCGTA TCTATACGCC GGTAGAGGAC AACGATGAGC CTATCGTAGC CATTGCTACU 840
   GATGCTGAGG CTACTACCA GCACTCTCC ATCAGCTTCA AGAGCGACCC CACTCCTCAA 900
   GAAGTGGGAG GATCGATATT CGGACTTGTG GAAGACTATA TGAACAGGT GATCACTACA 960
70  GCGGTGAATG AGCGTCTGTC CGAGATTACT CACAAGCCTA ACGTCTCTTT CCTCAGTSCA 1020
   GGAGCTTTCT TCTCTAACT CATGTACATC ACCCAGACTA AGGACGCATT CAATTTGTT 1080
   GCCACGGTTC GTGAGGGTGA AGCGGAGAAA GCGATGAACG CATTGGTGGC AGAGATAGAA 1140
   AGCCTCGGTC AGTTCCGGTAT CACCAAGGCG GAATACGATC GTGCACGCAC GAATGTGCTC 1200
   AAGCGATACG AGAATCAATA CAACGAAGA GACAAGCGTA AGAACAATGC TTATGCCAAT 1260
75  GAATACTCCA CTAATCTCAC CGATGGCGGC TATATCCCGG GTATTGAGGT GGAATATCAG 1320
   
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5 ACGGTGAATG CTTTGTGCTC TCAGGTTCTT CTGGAAGCAT TCAATCAGGC TATTGCCCAA 1380  
 ATGATCGATC CGGTGAAGAA TGCTGTGCTT ACCCTCACCG GTCCCTTCAA GGCTGAAGCC 1440  
 AAGATTCCGA GCGAAGCAGA CTTCCTCGCT GCTTTCAAAG CTGCTCGTCA GCAGAAAGTA 1500  
 10 GAAGCCAAAG AAGACGAAGT CTCCGACCAA AAATTGATGG AGAAAGCTCC TAAGGCCGGA 1560  
 AAGATCGTTT CCGAGAAGAA AGATCAGAAG TTCGGTACCA CGGAACCTAC CCTTAGCAAT 1620  
 GGCAATCAAAG TATACCTCAA GAAGACCGAT TTCAAATCAA ACGAAATCCT GATGAGTGCT 1680  
 CTCAGCCCGG GTGGTATCCT CTCCGGAAAG CATGCTCCCA ACCAATCTGT GATGAATTCT 1740  
 TTCATGAACG TGGGTGGCTT GGGCAACTTC GATGCTATCC ACCTGGATAA GGTGCTGACA 1800  
 15 GGTGCTGCTG CTTCCTATC TCCCTCTTTG TCTCTGCTCA GTGAAGGTCT TTCGGGCAAA 1860  
 ACUACTGTAG AAGATATGGA AACTTTCTTC CAGTTGATCT ATCTCCAAAT GACTGTAAAC 1920  
 CGCAAGGATC CCGAAGCGTT CAAGGCCACA CAGGAAAAGT TGTACAATAA CTTGAAAAAT 1980  
 CAGGAAGCCA ACCCGATGGC TGGCTTATG GACTCTATCC GTCATACCAT GTACGGCGAT 2040  
 AATCCGATGA TGAACCCAT GAAAGCTGCT GACGTGGAGA AAGTAAATTA CGATCAGGTA 2100  
 20 ATGGCTTTCT ACAATGAGCG ATTGCTGAT GCCGGCGACT TTATGTTCTT CTTTATCGGT 2160  
 AATCTGGATG AAGCCAAAGT GAAGCCATTG ATCGAAACTT ATCTGTCTTC ATTGCCCAAC 2220  
 CTCAGCGCTG GCGATAAGAT GAATAAGGCT CAGGTACCGG CTGCCCGTTC GGGAAAGATC 2280  
 GATTGCAAGT TCGAGAAGGA AATGGATACT CCTTCGACTA GTATATTCTG TGTGCTGTCC 2340  
 GGAAATGTGG AATATACGCT CAAGAACAGT CTCCTGCTGG AAGTCTTCTC AGCCGTAATG 2400  
 25 GATCAGGTGT ACACGGCTAC CGTTCGCGAG AAGGAAGGCG GTGCATACAG TGTGGCTGCA 2460  
 TTCCGCGGTC TCGAGCAATA TCCTCAGCCC AAGGCTCTGA TGCAGATCTA TTTCCCCACG 2520  
 GATCCTGCTC GTGCCGAGCA AATGAATGCT ATCGTTTTTG CTGAGTTGGA GAAGCTTGCC 2580  
 AAGGAGGGCC CCAATGTGGA ATACTTTAAG AAGACTATCG AAAACCTGAA TAAGCAGCAC 2640  
 AAAGAAAGTC TGGGTGAGAA TCGTTTCTGG CTCGAAGCCA TGAAGGCGTC TTTCTTCGAA 2700  
 30 GGAAATGACT TCATCACAGA CTACGAATCC GTACTGAACG GTCTTACTCC TGCTGAATTG 2760  
 CAAAAGTTTG CGGCAGACCT CTTGAAGCAG CAGAAATCGG TTGTTGTCAT GATGGCTCCT 2820  
 GTTGCAAAAG CTCAA 2835

## (2) INFORMATION FOR SEQ ID NO:19

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2058 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 40 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2058  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA GTAAGAAAGG AACAAATCGGG GTAACGAGCG ACAATATATT CCCCGTCATC 60  
 AAAAAAATCC TGTACAGCGA CCATGAGATA TTCTGCGGTG AGATCGTCTC CAATGCGGTG 120  
 GATGCTACCG AGAAGCTGAA AAGCCTTACA TCCGTGCGCG AATTCAAAGG CGAGACGGGT 180  
 55 GACCTCCGCG TAACGGTCAG CGTGGATGAA GTGGCAGCA CGATCAGGT CAGCGACCGC 240  
 GCGGTAGGGA TGACCGAAGA GGAGGTGGAG AAGTACATCA ATCAGATTGC TTTCTCCAGT 300  
 GCGGAAGAGT TTCTTGAAAA GTACAAAGAC GACAAGGCGG CCATTATCGG CCACTTCGGA 360  
 CTCGGATTTT ACTCGGCTTT CATGGTGTCC GAGCGAGTGG ACCTGATCAC GCGCTCTTTC 420  
 60 CGAGAAGATG CTACGGCGGT GAAATGGAGC TGCGACGGAT CGCCGAATA CACGCTCGAA 480  
 CCTGCGGACA AGGCTGACCG TGGCACCGAC ATCGTGATGC ACATCGATGA GGAGAATAGC 540  
 GAGTTCCTCA AAAAAAGAAA GATAGAGGGG CTCCTCGGCA AATACTGTAA GTTCTTACC 600  
 GTGCCGATCA TTTTCGGCAA GAAGCAGGAA TGGAAAGACG GCAAGATGCA AGATACGGAC 660  
 GAGGACATTC AGATCAACGA CACACATCCT GCTTGGACCA AAAAGCCTGC CGACCTCAAG 720  
 65 GACGAAGACT ATAAGGAATT TTACCGTTTC CTCTATCCCA TGTCCGAAGA GCCTCTCTTC 780  
 TGGATCCACC TCAATGTGGA CTATCCGTTT AATCTGACAG GTATCTCTA TTTCCCGAAG 840  
 ATCAAAAACA ACTTGGATCT GCAGCGCAAC AAGATTGAGC TCTACTGCAA TCAGGTTTAC 900  
 GTCACCGATG AAGTACAGGG TATCGTGCCG GACTTCTCA CCTCTGCA CGGGGTCATC 960  
 GATTGCGCGG ATATTCCCTT CAACGTATCG CGCTCTATC TGCAGAGCA TGCCAAATGTG 1020  
 70 AAGAAGATCT CGTCTCATAT CACCAAGAAG GTGGCAGACC GTCTGGAAGA AATTTTCAA 1080  
 AACGACCGCC CCACATTCTG GGAGAAATGG GATAGTCTGA AGCTCTTCTG CGAATACGGT 1140  
 ATGCTGACGG ATGAAGATT CTATGAGCGT GCAGCCAAAT TCTTCTTTT CACCGATATG 1200  
 GACGAGACCA AGTACAGGTT CGACGAATAC CGAAGCTCG TCGAAGGTGT ACAGACGGAT 1260  
 AAGGACGGAC AGGTAGTGTA TCTCTATGCT ACGGACAAGC ATGGACAGTA CAGCCACGTG 1320  
 75 AAACGTGCAT CCGCAAAAGG CTACAGCGTG ATGCTGTTGG ATGGTCAGTT GGATCCGCAT 1380  
 ATCGTGAGCC TGCTGGAGCA AAAGTTGGAG AAGACACACT TTGTCGCTG CGATAGCGAT 1440

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ACGATCAACA	ATCTGATCCG	CAAGGAGGAA	AGAGCCGAAG	TGAAACTGTC	CGATACGGAG	1500
CGCGCCACTC	TCGTGAAGCT	GTTTGAAGCA	CGCCTGCCAC	GGGACGAGAA	GAAGCACTTC	1560
AATGTAGCTT	TGGAATCGCT	CGGAGCCGAA	GGTGAAGCCA	TCCTTATCAC	ACAAGCCGAA	1620
TTTCATGCGCC	GTATGCGCGA	TATGGCACAG	CTGCAGCCGG	GAATGAGCTT	CTACGGCGAA	1680
CTCCCGGATT	CGTACAACTC	GGTACTTAAT	ACCGATCATC	CGCTCATCGA	CAGGGTACTC	1740
TCCGGTGAGA	AAGAATCGGT	AGAGCCTTCG	CTCACAGAGC	TTAGAGCGAA	AATCGCCGAG	1800
CTGAAAGCGG	AAGAGGCCAA	GCTGCTCGAT	GAGGAAAAAG	GGAAGAAACC	GGAGGAAATC	1860
CCTGTTGCCA	CGAAGGAAGC	CAAGGAGAAC	AACGCCGTCG	AACAGGCCAA	AACCGAAGGC	1920
AGTATCAACG	ATCAACTGAC	CAATATGCT	CAGGACAACG	AGCTGATAGG	TCAGCTCATC	1980
GACTTGGCTC	TGCTCGGAAG	CGGATTGCTG	ACGGGAGAGG	CTTTGGCCGA	ATTCATTCGT	2040
CGCAGCCAGC	GTCTTCTC					2058

## (2) INFORMATION FOR SEQ ID NO:20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

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GACAATCGAC	AGAAAAGACC	GTGCTTCAAC	GCCAAATTTGT	ACTTTTACCG	TGCAATGGAA	60
AAACTGATCG	ATATTTTGGT	CGTAGACGAT	GATGTGGCAG	TCTGTGCCGC	ACTGCGTCTG	120
GTGCTCAAGC	GAGCGGGCTA	TAATCCCGTT	ATAGCCAAACA	GTCCCGACGA	AGCTTTGTCC	180
ATAATGCGGA	ATCCTGATGG	CGGCTGTAA	CCGGCTGTGA	TTCTGATGGA	TATGAATTC	240
TCCCTTTTGA	CCTCCGGCAG	GGAAGGATTG	GAAGTACTGG	AGAAGATGCA	GATATTCACT	300
TCCTGCCCTG	TCATACTGAT	GACGGCTTGG	GCTTCGATTTC	CACCTGGCAST	GGAGGGAAATG	360
AGGCTTGGAG	CTTTGACTTT	CATAGGCCAAG	CCATGGGACA	ACGATCGGCT	CCTTCGTACC	420
ATAGATACGG	CCTTGCACTC	GGCTGCTCCC	TCAGCTGTGG	CGAATCCATC	GGAACAGTCT	480
GACAGAGATA	CAGCCCGTCA	GCCGAAAGCT	ACAGTCCAAG	AGAATGACCC	CTGTGCCCAT	540
ATCATAGGCC	GGAGCGATGC	CATCTGTAAG	ATCAAGGAAC	GGATACGCCG	CATAGCTCCC	600
ACCCATGCCT	CTGTGCTGAT	CACGGGCGAG	AGCGGTACGG	GCAAAGAGTT	GATAGCCGAA	660
GCTCTGCACC	GTGGGAGCAA	ACGAGCCTCA	GCCCATTCG	TCAAGGTCAA	TTTGGGTGGG	720
ATTCCCGAAA	GTTTGTTCGA	AAGTGAGCTG	TTGCGACATA	AGAAAGGAGC	TTTTACCAAT	780
GCTTTTTCGG	ACAGGAAAGG	ACGGTTCGAG	CTGGCTGATG	GCGGCACGAT	CTTTCTGGAC	840
GAAATAGGCG	AACTACCGGT	CGGCAACCAA	GTAAVACTGC	TGCGAGTGCT	ACAGGAACAG	900
ACATTCGAGC	CGTTGGGCGA	GAGCGTCTCC	CACCGATGGG	ACATCCGTGT	GGTATCGGCT	960
ACGAATGCTT	CCTTGGAGCG	AATGGTAGCC	GAAGGACGTT	TCAGAGAGGA	CCTCTACTAT	1020
CGAATCAACC	TGATACATCT	GCATCTGCCT	CCGCTGCGTG	AGCGTCAGGA	GGATATACAG	1080
CTGCTGGTGG	AAGCCTTCAG	TGAAGCCTTT	GCCCAATCGA	ACGGATTGCC	CCATGCCGTT	1140
TGGAGTGCGG	AAGCTATGCG	ACGTATCTGT	GCCATGCCCC	TACCGGGCAA	TGTACGCGAA	1200
CTGAAAAACG	TAGTGGAGCG	TACGCTATTG	CTCTCGGGAT	CGAGAGAAAT	CAGTGCCCGG	1260
GATGTGGCTG	ACTTCGGTTC	GCAGGTGACG	GCAGCAGACC	ACTCCGACGA	ACGGGCTTTG	1320
ACCGACATGG	AGGAAGCTGC	TATCCGAGAG	ACGCTGACTA	AATACAACGG	CAACGTTAGT	1380
CGTGTGACAC	GAGCCTTGGG	ATTGAGCCGG	GCAGCTCTTT	ACCGGCGAAT	GGAGAAATAC	1440
GACTG						1446

## (2) INFORMATION FOR SEQ ID NO:21

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

AGATCTCTGC	AATCATTTC	AAATAAAAA	CACTCAAGTA	TGCTTAAGAT	AAAGAACCCTC	60
CACGCCACAG	TACAGGGCAA	AGAGATATTG	AAAGGAATCA	ATCTGGAGAT	CAATGCCGGA	120
GAGATTTCATG	CTATCATGGG	GCCGAACGGA	TGGGGGAAA	GTACGCTCTC	TTCCGTTTGG	180
GTGGGACATC	CCTCCTTTGA	AGTCACGGAA	GGAGAGGTGA	CATTCAATGG	AATCGACCTG	240
CTCGAACTCG	AACCGGAAGA	ACGTGCACAC	CTCGGACTCT	TTCTCAGTTT	CCAATATCCG	300
GTCCGAGATCC	CGGGCGTCAG	CATGGTGAAT	TTCTATGAGG	CAGCTGTCAA	TGAACATAGG	360
AAAGCGATCG	GAGCAGAACC	CGTATCGGCA	AGCGACTTCC	TCAAGATGAT	GCGAGAGAAG	420
CGTGCCATTG	TGGAGCTGGA	CAACAAATTG	GCCAGCCGTT	CTGTGAACGA	AGGCTTCTCC	480
GGTGGAGAAA	AAAAGAGGAA	CGAAATCTTC	CAAATGGCTA	TGCTCGAACC	CAAGCTGGCT	540
ATTTTGGACG	AAACCGATAG	CGGGCTCGAT	ATCGACGCTC	TCCGCATCGT	AGCAGGCGGG	600
GTAACCGGAC	TCCGCTCTCC	GGAGAATGCT	GCTATTGTGA	TCACACACTA	TCAGCGTTTG	660
CTCGAGTACA	TCAAGCCGGA	CTTCGTACAC	GTCTTTACA	AGGGGCGCAT	CGTCAAGTCG	720
GGAGGAGCCG	AGCTGGCTCT	CACGCTCGAA	GAAAAAGGCT	ACGACTGGAT	CAAGGAAGAG	780
ATAGGAGAA						789

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AGCATGGCTA	AGGAGAAAAC	GATCTACGTC	TGCCGTTTCT	GCGGAACCAA	ATACGCCAAA	60
TGGCAAGGCA	ACTGCAATGC	CTGTGGAGAG	TGGAAGTSCA	TTGATGAGGA	GAAGGTGCCG	120
GCACCGGCAT	CGGGCAAGCA	TGCACCCAAG	AGTTTATATG	CTCGGGAGCA	GGACAACCGG	180
CCAAGACTCT	TACAGGATGT	GGAGTCCGGC	GATGAAGAGC	GTATTGCGCT	CGGCGATGAA	240
GAGTTCCGAC	CGGTACTGGG	TGGAGGAATT	GTCAAAGGAG	CATTTGTCTT	GCTTGGCGGC	300
GAGCCGGGAA	TCCGTAAGTC	CACGCTTATC	CTCCAGACGG	TGCTGCGTCT	GCCGCAGTTG	360
CGCACGCTCT	ATGTGTCCGG	CGAAGAAAGT	GCCCGACAAC	TGAAGATGCG	CGCCGAACGA	420
CTGGGGCAAG	CCATGAATGG	GTGCTACGTA	TACTGCGAAA	CGAATATAGA	GAGGATACTC	480
TCCCGTGCAG	AAGAACTCAC	ACCGATCTTC	CTCGTGATAG	ACTCTATACA	GACGCTCTAT	540
ACCGAGGAAA	TGGAAGCTC	GGCCGGCAGC	GTGGGGCAGA	TCCGCGAATG	TGCCCGCTTA	600
CTGCTCAAAT	ACTGCAAGAC	TACGGGTATC	CCCGTCATCG	TCATCGGACA	CATCACCAAA	660
GAAGGTAGCA	TAGCCGGACC	GAAGGTGCTG	GAGCATATAG	TGGATACGGT	GCTTCTCTTC	720
GACGGGGATA	AGCATCATCT	CTACCGGATA	CTCCGAGGAC	AGAAGAACCG	CTATGGCAGT	780
ACTTCCGAGC	TGGGGATATA	CGAGATGCGG	CAGGACGGTC	TGCGTGGCGT	GGAGAATCCG	840
AGCGAACATC	TCATCACACG	CAATAGGGAA	GACCTCAGTG	GCATAGCCAT	AGCCGTAGCG	900
ATGGAGGGCA	TTCCGCCGAT	ACTCATCGAA	GCGCAGGCTT	TGGTCAGCTC	GGCCATTAT	960
GCCAAATCCG	AGCGTTCGGC	CACGGGCTTC	GATATTCCGG	GGATGAACAT	GCTCTTAGCC	1020
GTACTGGAGA	AACGTGCLGG	CTTCAAGCTC	ATACAGAAGG	ATGTGTTTCT	GAACATTGCT	1080
GGAGGTATCA	AAATAGCCGA	TCCGGCTACG	GATCTGGCCG	TTATCTCGGC	AGTGTGGCGG	1140
TCCAGTCTGG	ACATCGTTAT	CCGCGCGGCC	GTATGCATGA	CGGGCGAGGT	CGGACTCTCC	1200
GGAGAGATAC	GTCCCGTGAG	CCGCATCGAG	CAGCGCATAA	CGGAAGCGCG	TCCGATAGGG	1260
TTCAVAGAGA	TATTGGTACC	GGCCGATAAT	TTCCGGCAGG	AGGATGCGCG	CCGCTTCGGT	1320
ATTCCGCTCG	TGCCGCTCAG	AAAGGTGGAG	GAAGCCTTCC	GCCATCTGTT	CTCGAAAGGA	1380
AGAGAA						1386

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## (2) INFORMATION FOR SEQ ID NO:23

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

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25  GGGTCTTGTG GAAGTAGCCC AGCAATTGGC CGATCAGGCT GTTCGCGTTG TGATCSCCGG      60
    ATTGACATG GACTTTCGAC GTCACCCCTT CGGACCTATG CCGGGCTTGT GTCCCATAGC      120
    CGACTCCGTG ACCAAAGTTC ATGCCGTGTG TGTGGAATGC GGCCGATTGG CCAGCTATTC      180
    TTCCCGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGCCG GAACTGAACG AATACAGTCC      240
    CCTCTGCAGA ACCTGCTACA GGAAATGCAG TTCTCCCCCA CAAACAGAAG AAATCCATTC      300
    GACAATATGA ATAGCAGACA TCTGACAATC ACAATCATTG CCGGCCTCTC CCTCTTTGTA      360
    CTGACATTGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAG      420
    CTCTTTACTT CCGCGTGGAT ACAACGTTTG GCCGAATATC AAGCGCTTTG CATTGAGGCA      480
    TACAACATCG CTACGGAAG AGTGGAGGCT CTACCGGCAG AACGTAAACA AGGAGATAGG      540
    CCTTATGCCA TGGTAACGGA CATAGACGAA ACCATTTTGG ACAATACGCC TAACTCCGTG      600
    TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG      660
    GCCGATGCCG ACACACTGGC AGGAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG      720
    ATCGAGGTCT TTTACGTCAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC      780
    CTTGAGGTTT ACGGATTCCT CTTGCGGAT GAAGAACATT TGCTTACGAC CCATGGGCCA      840
    TCCGACAAAG AACCCGTCG GCTCAAAATA CAAGAACAGT ATGAAATAGT ATTGCTCATA      900
40  GGAGACAACCT TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAAA      960
    CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGCCGGCACT TCATCATGCT GCCCAATCCC      1020
    AACTACGAT CTGGGAACC GGCATGGTAC GGCGGAAGT ATCCGCCACT GCCCGAAAGA      1080
    GACAAAGCAC TTAACAACCT GCACTCAGAG AACAGCAGA                               1119

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## (2) INFORMATION FOR SEQ ID NO:24

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

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70  CGTTGGGGTT TTTCTAATTT TGTGGCCATG AGCACCATA TAGATGTACA ACAGATCAAA      60
    CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA      120
    CAGGTGGCTC CTACCGACAT GTCGCTCCTC GTGACGGGCG AGAGCGGTTT GGGGAAAGAG      180
    TTCTTCCAC AGATAATCCA CTAATAACAG GCCCGGAAC ATCATAGCTA CATTGCAGTC      240
    AATTGCGGAG CCATCCCCGA AGGAACCATC GATTCCGAGC TGTTCCGACA CCGCAAAGGT      300
    TCCTTTACCG GAGCCGTATC GATCGCAG GGTACTTCC AAGAAGCATC CGGCGGCACG      360
75  ATCTTTCTGG ACGAAGTGGG CGAACTGCCT TTGCCACGCG AGGCGAGGCT GCTGAGGGTG      420

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CTGGAGACGG GCGAGTTCAT CCCCCTAGGA GCCAGCCAGT CGCAGAAGAC GGATGTCCGT 480  
 ATCGTAGCGG CGACGAATGT GAACCTCAAG GAGGCGGTAG CGAACGGGAA GTTCCGGGAA 540  
 GACCTCTTCT TCCGGCTCAA TACGGTACCG ATCGAGGTGC CTGCGCTGCG TATCGGACCG 600  
 GACGACGTGC CCTTGCTTTT TCGCCGATTC GCGCCGACA GCGCCGAGAA GTATCGGATG 660  
 5 CCTCGCTGC GCCTATCGGA CGAAGCCCGT ACCATATTAA TCGGTACCG CTGGCCCGGC 720  
 AATGTGCGAG AGCTGCGCAA TATAACCGAC AGGCTGAGCA TCCTGGAGGA GGAGCGGACG 780  
 GTATCGGCAG AGACCATCAC TCGCTACCTG GACGCTGAGG GGATGCAAGA CCTCCACCCC 840  
 GTCGTGATCC GACGGAACGA AACGACCGAA GCGGACAAAC AAATCCCCCA TTACGAGCGC 900  
 GAAATCATCT ACCAGGTGCT ATACGATATG AAGAAAGAGA TAGCCGATTT GAAGGGGATG 960  
 10 ATGAACCGCC TGGCGCACCA CGAACAGCCC TCATGGCCTG TAGGGTCGGA CGTCTGGGGC 1020  
 AACGACGACA AGCGACCCGC AGATCCGAAG TGGGGCGTCA GCACGCACAA GGCCCCCATC 1080  
 GCGAACGCGG CAGAAGCCGT GGAGCCGATA CAGGAAGCCA GCGAATACAC CGAGGATCCG 1140  
 GTTTCGCTGG AGGAGGTAGA GAGAAATG ATTTCCCTTG CATTGGAACG CCACCGCGGA 1200  
 AGGCGCAAGC AGACAGCCGA GGAAGTGAAG ATTTCCGAGC GGACACTATA CCGTAAATC 1260  
 15 AAGGAGTATG GACTGGAA 1278

## (2) INFORMATION FOR SEQ ID NO:25

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1959 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: FORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1959

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

AAAAATCTTC CGAGGTACGC TCCGGCATTT GGCAGAAATC GTAAAAGGGA ACAACCTGAC 60  
 CCTGACAACG ATGATAGTCG TGGGAGAAGC CATAGACAAT CGGGAAGGGC TGTCAACGTT 120  
 GTATGCCGAC GAATTCAAAC ACCTCTTCCG CACATGATCC TACTCTTCGG CGGTACTACG 180  
 GAAGGCCGTG CCGCAGCTCG CGTGCTGGAT GAAGCGGGAA GTCCGTTTTT CTACTCCACC 240  
 45 AAAGGCAATC TGCAAGAGAT CCAGAGTAGC CACGGCCATC GTCTGACAGG AGCCATGACG 300  
 GTTGCCGACA TGGTTTCGTT TTGTCCGAAA GAAGAGATCC GACTGATCGT GGACGCCGCT 360  
 CATCCCTTTG CCGAAGAATT GCACGCTTCA GTGGCAGAAG CCTCTGAACA AACAGGTATC 420  
 CCGTAGTAA GATACGAGAG ACAATACCTT CCACGCGAAG AAGGTATCGT CTGSGTGCA 480  
 AACTACGATA CGGCTGCCGA GCGGATGCTT GGCGATGGCG TGCAGCGTCT GCTGATGCTC 540  
 50 ACAGGAGTGA ATACGATCCC CAAGCTGGCT GCTTCTGGA AAGAGCGCAC CACCTTTTGC 600  
 CGCATATTGA AGCGAGACGA ATCGGTTGCT TTGGCAGAGA AGAACGGCTT TCCTGCGGAG 660  
 CGCATCGTTT TCTTCGAACC GCATGCGGAC GAGGAGCTGA TGCAAGCCGT TCGCCCGGAT 720  
 GCCATTATCA CAAAAGAAAG CGGAGAGAGC GGTACTTCC GAGAAAAGAT AGAAGCTGCC 780  
 CGACGGATGG GCATCCGTAT ATATGCCGTC GTACGTCCCC CTTTGCCTCC TTCAATTCATT 840  
 55 CCGSTAGGGG GCGCTGTGCG TTTGAGACGG GCGGTAGAAC GCCTCGTGCC GGGATTCCTT 900  
 TCACTCCGAA GCGGATTAC TACCGGCACC ACAGCTACCG CTGCAGTAGT AGCAGCCATG 960  
 TACCGATTGA TGGGGCTTGG CTCTCTCGCC GAAGCTCCCG TAGAATTGCC TTCGGGCGAA 1020  
 ATAGTCAGTC TGCCCATAGC GGAATTCGA GAGGAAGAAG ATGCTGTGCT ATCCGCGATC 1080  
 CTGAAGAGAT CAGGTGATGA TCCGGATGTG ACCAATGGCA TGGCGGTATG CGCTACGATC 1140  
 60 AGGCTCAATC CCGAACATGA GGAAGTCCCG TTCCTGCAGG GTGAAGGGGT GGGGGTATG 1200  
 ACGCTCCCGC GCCTCGGTCT GGAGGTCCGA GGTCCGGCTA TCAACCTCGT ACCTCGACGA 1260  
 ATGATGACAG CAGAGGTACG CCGACTCTAT GCGCAGGGAG GTGTGGATAT TACGATTAGC 1320  
 GTAACCGAAG GCGGAGAGGC TGCTACCCAG ACATTCAATC CCGGACTCGG CATACGGGAC 1380  
 GGCATCTCTA TTATCGGAAC ATCGGGAGTC GTGAACCTT TTTCGGCGGA AGCGTTCGTT 1440  
 65 GGTGCCATCC GTAAGCAAGT GGGTATTGCC ACCGCCCTGG GAGCCATCA TATCGTCTC 1500  
 AATTCCGGAG CCAAGAGTGA GCGTTATGTA AAAGGAGCCT ATCCGCGACT CATTCACAG 1560  
 GCCTTTCTGC AGTATGGCAA TTTCGTCCGC GAATCACTCA GTTGTGTAGC TTCTTCCCT 1620  
 TCTGTCCSTT CGGTAACGGT AGGAATCATG CTCGGCAAAG CAGTGAAACT CGCCGAAGGC 1680  
 70 TATCTGGATA CGCAGAGTAA AAAGGTAGTG ATGAATCGGG ATTTCTGCA CGAACTGGCT 1740  
 CGTCAGGCAG GTTCTTCGGA AGACATCCAT GCCAATATAG ACAGCTGAA TTTGGCTCGT 1800  
 GAGCTATGGA CTATGCCGAG TCGGAGGAGC AGCGATCGAC TGCTACGAAA GATTGCCGAA 1860  
 CGATCTTGGG AAATTCGCCG CCCATCGGTA CCATCGGCCG AATTAGAATC CCTGCTGATC 1920  
 GATGAGTCCG GAGCGATTCT TTTTCGTATC GGTGGAGAA 1959

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## (2) INFORMATION FOR SEQ ID NO:26

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1353
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

25 CAACAAAGAC CACATAGAAT TATTATGTTG AGGACTTTCC GAATCGGTGG TATTCACCCC 60  
 CCGGAAAACA AGTTGTGGGC AGGCAAGCCC GTAGAGGTGT TGCCTATCCC CTCACAGGTA 120  
 GTCAATCCCTC TTGGTCAGCA CATCGGTGCA CCGGCAACTG CCACGGTCAA GAAAGGGCAT 180  
 GAAGTTAAGG TCGGGACTAT CATTGCTCAG GCCGGAGGAT TCGTATCAGC TAATATCCAC 240  
 TCATCTGTGT CCGGTAAGGT GCTGAAGATC GATAACGTAT ACGACTCAAG CGGCTATCCC 300  
 AAGCCCGCAG TCCTCATTAG CGTAGAAGGT GACGAATGGG AAGAGGGCAT CGATCGCTCA 360  
 30 CCAGCCATCG TCAAGAATG CAATCTGATG GCAAAAGAAA TCGTAGCCAA AATTTCGTGA 420  
 CCGGTATTGG TGGGTCTTGG CGGTGCTACC TTCCCTACCC ATGTGAAGCT GTCCCTCCT 480  
 CCGGGCAACA AAGCTGAGAT CCTGATCATC AACCGGTAG AGTGCGAGCC TTATCTGACG 540  
 AGCGACCATG TCCTTATGCT GGAGCACGGC GAAGAGATCA TGATCGGCGT GAGTATCCTG 600  
 ATGAAAGCCA TTCAGGTAAA CAAGGCCGTC ATCGGAGTTG AGAATAATAA GAAAGATGCT 660  
 35 ATTGCTCACC TCACCAAACT GGCCACTGCA TATCCGGGCA TAGAGGTAAT GCCGTGAAG 720  
 GTGCAATATC CTCGAAGCGG TGAGAAGCAG CTGATCGATG CAGTGATCCG CAAGCAGGTA 780  
 AAAAGCGGTG CCTTGCTAT CAGCACAGGT GCCGTAGTAC AAAACGTGGG TACGGTATTC 840  
 GCCGTGTACG AAGCAGTACA GAAGAACAAG CCTCTGGTGG AGCGCATCGT GACGGTTACT 900  
 GGAAAAAACA TGCTCGTCC GTCTAACCTC CTCGTTCGTA TAGGTACTCC TATTGCGGCT 960  
 40 TTGATCGAAG CAGCAGGTGG CTTGCCGGAG AATACGGGCA AGATCATCGG CGGAGGTCCG 1020  
 ATGATGGGAC GCGCTCTGCT GTCAACGGAT GTGCCGTGTA CCAAGGCCAG CTCGGGAGTA 1080  
 TTGATTCTCG ATAGAGAAGA GGCAGTTCCG AAGCCTATGC GCGACTGTAT CCGATGCGCC 1140  
 AAGTGGCTCG GAGTGTGTCC GATGGGACTC AATCCGGCTT TCCTTATGCG CGACACCTTA 1200  
 TATAAGGCT GGGAAACAGC GGAATAAGGC AACGTGGTTG ACTGTATCGA ATGCGGTTCT 1260  
 45 TGCAGTTCA CTGTCCGGC CAACCGTCCT CTGCTGGATT ATATCGGCA AGCCAAGAAG 1320  
 ACTGTGTGAG GTATCCAAAG AGCACTAAG CAA 1353

## (2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1467 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

75 ATGAACTCTC AAAAGAAAGA GGCTTTTAAT ATGAAAAGAA TACAACCTAC TCTTATCGCT 60  
 CTCTTCGCCG CTGTTCGCCG TTGGTTCGCT CAAATGCTT ACGAGGGAGT AATTTCATAT 120  
 AAATTTGCT TGGACAAAAC CGGAAACAAG GTTGTACTGA ATGGTCCGGC AGATATGAGT 180  
 AATTTAAGC TCAAGAGCAC TCAGATGATC ATTGTTACGC CTATTCTTCG TTCAGAAGAT 240

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5 GGTACCAGCC GGGTGGAAIT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAACCT 300  
 CTCAGCGGTG AAATCGCATT TAGTTCGGCT TTGCCCAAG CAAAACATGC AGCTCAATAC 360  
 ATTCGCCGTC ATAATGGGAA GAGCGAGCAG TTTGCTTTTA CAGGAGAACA TGCTTATGCA 420  
 TCATGGATGA TGGATGCCAA GTTTGTGGTT CGTGAGGAGG TACGAGGTTG TGCTAAATGC 480  
 CCTGTAGGTC TCTCGAGTAA TATTGTCTCT TTTGATCCAC TCTTCAATCC GGCAGAGGCT 540  
 CCTTATTGT TGGCACACAT TACTCGGCA GAAGAAGTGG AAAACAGCG AGAGTCCAGC 600  
 TTCGATGCTT ATATCAACTT CAAAGTCAAT AAGGCAGATG TCCTTCCTGA GTATCGCAAC 660  
 AATAAGGCGG AGTTAGAGAA AATCAAAGAA TTTGTAAGCA CCGTTAAGGC TAATCCAAAC 720  
 10 TATTGGGTCA ATAAATGAT CATCGAAGGG TTTGCTTCTC CCGAGGCTTC AATAGCCAC 780  
 AATAAGGCTT TGTCGGAGCG CCGTGCTAAA AGACTCGCGG AAGATTGGT GCGTAAGTAT 840  
 GGCAAAACAT TGCCGAATAT AACCACTGAA TTCGSCGStu AAGATTGGAA GGGGCTGAAA 900  
 CTGGCTATCG AAAAGAGTGA TATAGCCGAT CGTGACCGCG TATTGGAGAT AATCAACTCC 960  
 GATAAATATG CCGATGATGA TGCACGTGAA CAGGCTCTGA AGCAACTTTC GTCTTATCGT 1020  
 15 TATATCTTGG ATCAGATCTA TCCGAATTG CGTGCAATA CGATAACCAT GGGGTATATC 1080  
 GTTCGTGATT ATACCCTCGA AGAAGCTCGT GAAATCATA AGACTGCTCC GAAAGAACTT 1140  
 AGTGAGGCGG AAATGTACCG TGTGGCAATG TCTTATCTG AGGGGCACCA AGAGCGTTTG 1200  
 TTTGCTCTGA ATACGACCCT TAAGTATTTT CCTGAAAGTG TAACGGGCGG AATCAATTTG 1260  
 GCTGTAGCCG CTTTAAATGG TGGAGAGGTT CAACAGGCAA TTGCTCTGTT GAGTCCGATT 1320  
 20 CAGACAGAAA AGGGGTGAAG CAATATCCTT GGAGCTGCTT ATGCTCGTAC GGGAGATTTT 1380  
 GCTCGTGCCG AACCTTCTT CCGTAAGGCC GTTGCAGAAG GAGATGCAAA TGCGCAGCGC 1440  
 AACCTCGATA TGCTGCTTGG CAAAAAG 1467

## (2) INFORMATION FOR SEQ ID NO:28

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

50 GACATGGCAG AAAAAAGAGA CTATTACGAA GTCCTCGGTG TATCGAAGAA TGCCACCGAC 60  
 GATGAAGCTA AAAAAGCATA TCGCAAGAAG GCTATCCAAT ACCATCCTGA TAAGAACCCC 120  
 GGTGACAAGG AGGCCGAAGA GCACTTCAAA GAGGTAGCTG AAGCTACGA CGTATTGAGC 180  
 GATCCGCAGA AGCGCAGTCA ATATGACCAG TTCGCCCATG CCGGATTGGG CCGAGCTGCC 240  
 GGTGAGGTTT TCAGCGGAGG CGGTATGTCC ATGGAGGATA TTTTCAGTCC CTTCGGTGAT 300  
 CTATTCCGTG GGTTCGGCGG TTTCCGCCGA TTCTCCGATA TGGGCGGTGG CAGTCCGAGA 360  
 CGTGTTCGCA GAGGCTCTGA CCTGCGAGTA CGAGTGAAGC TTTCTTTGGC CGATATAAGT 420  
 55 AAAGGTGTGG AGAAGAAAGT GAAGGTAAAA AAGCAGGTAG TGTGAGCAA ATGTCGTGGC 480  
 GATGGCACGG AAGAAGCCAA TGGCAAGACT ACCTGCCAGA CCTGCCATGG AACCGCGGTG 540  
 GTTACACGTG TGAGCAACAC TTTCTTGGG GCCATGCAGA CCGAGAGCAC TTGTCCCACT 600  
 TGCCACGGAG AGGGTGAGAT CATCACGAAG CCATGCTCCA AGTGTAAGGG CGAAGGTGTG 660  
 GAGATCGGCG AAGAGGTGAT CTCATTCCAC ATCCCTGCCG GTGTAGCCGA AGGAATGCRA 720  
 60 ATGTCCGTGA ACGGCAAGGG AAATGCCGCG CCCCAGGAGG GCGTGAATGG CGACTTGATA 780  
 GTCGTGATCG CCGAGGAACC GGATCCGAAT CTGATCCGCA ATGGCAACGA TCTGATATAC 840  
 AATCTGCTTA TATCCGTTCC GTTGGCTATA AAAGGAGSTA GTGTGGAAGT GCCGACGATA 900  
 GACGGACGAG CCAAGATCCG CATCGAGGCG GGGACACAAC CCGGCAAGAT GCTGCGTTTG 960  
 CGCAATAAGG GGTGCCCCAG CGTAAACGGC TATGCCATGG GAGACCAACT GGTGAATGTC 1020  
 65 AATGTCTATA TCCCCGAATC GATCGATGCC AAAGATGAGC AGGCTATCGC AGCGATGGAA 1080  
 AACTCGGACA GCTTCAAAAC TACCGATGCT GCTCGTAAGG ATATAGACAA GAAATACAGA 1140  
 GAGATGCTGG AT 1152

## (2) INFORMATION FOR SEQ ID NO:29

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 927 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

CGATTGCGATT	CAACAACATA	TGCTCACA	ATTAATTTAA	GAACAGAGAT	GAAAAAACTG	60
ATTTTAGCGA	CTTTGGGACT	TATGGCCATT	GCCATGCTCT	CATGTTCAAG	CAACAACAAG	120
GATTTGGAGA	ACAAAGGGGA	GGCTACTCTT	TTGGTAACGT	TTGGTAGCTC	CTATAAAGCT	180
CCACCGCGAA	CCTATGCGAA	GATTGAGAAG	ACTTTTGCCG	CAGCTTATCC	CGATCAAAGG	240
ATAAGCTGGA	CATACACGTC	TCTATTATC	OGAAAGAAAC	TGGCTCAGCA	GGGTATTTAT	300
ATCGATGCTC	CGGATGAGGC	TTGGAGAAA	TTGGCTCGTC	TGGGTATATA	GAAGATCAAT	360
GTACAGAGTC	TTTATGTGAT	TCCCGGCCGA	GAATATGATG	AGATGATCGA	CTTTGTCAAT	420
AAGTTTAAGG	CAGCACATAG	TGATATTACT	GTGAAGTAG	GGGCTCCGCT	TTTCGATACC	480
GATGAAGATA	TGGCGGAGGT	GGCAGAGATC	TTGCACAAGC	GTTTTCAGCA	AACGATAGAG	540
AAAGGTGAAG	CTATTGTATT	CATGGGACAC	GGCACCAGAG	ATGCTGCCAA	TGACAGGTAT	600
GCCCGTATCA	ATAAGATCAT	GAAGAACTAT	AGCAAGTTCA	TGATCGTCGG	AACCGTCGAG	660
TCCGATCCCT	CTATCAATGA	TGTTATTGCC	GAAGTGAAG	AAACCGGTGC	CACGGCCGTA	720
ACAATGATGC	CGCTGATGAG	TGTGGCAGGC	GACCATGCTA	CGAATGATAT	GGCCGGAGAT	780
GAGGACGATA	GCTGGAGAGC	TTTGTGACC	AATGCCGGCT	ACACAGTTTC	TATAGACAAG	840
CTGGACAATG	GCAATTTCTC	AGCTCTTGGG	GATATAGAAG	AGATCCGGAA	TATCTGGCTC	900
AAGCATATGA	AAGCCACCTC	TGCTCGC				927

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

CGGAGAGATG	CGCGGAGGCA	ACTGGTACGC	CGTAGGAGGA	AAGAGCTATC	TGGCACAGCA	60
AATACGCGAT	GCCGAGGAG	AGTATTTCTT	GAAAGACGAT	CAGCGATCCG	GTGGTGTTC	120
CCTCGACTTC	GAGACGGTCT	ACAGCCGATC	CGATTCCGGT	CGCTACTGGC	GAATCCTCAA	180
CAGCTATCCC	GGGAGTTCG	GTTACGAAGC	TTTGAAGGCC	GAAGACAGCC	GATATGCCGA	240
TTTCAGGGCA	TTCAAGGAAA	AAGGCGTGAT	ATACTGCAAC	CTGAGGGAAA	CAGCCTTCTA	300
CGAACTCATG	CCCATGCATC	CCGATTGGGT	GCTGGCCGAT	CTTATCGCTA	TCITGCACCC	360
CGGACTACTT	CCCGACCACC	AACCCGATTT	CTATTATTTC	CTCCAATGAC	ATCUGTCAGC	420
CACCTACGTA	CAATTTCTGT	CGCAGGTATC	CTGGCTGCGC	TGGGAGGGGC	TGTACTCATT	480
CTCTTCGGGG	TTAATCTCTT	CCTCGGCTCG	GTGGCTATTC	CGATGAGCGA	GATCTTCCGA	540
CATCTTTTTT	CAGATCGTCC	CGAAGGAGGA	GAAGCACTCG	TGCACTACAA	TATCCTATGG	600
AAATCCCGCC	TGCCCGAAGC	CCTCACGGCT	GCTTTTGCCG	GCGCAGGTTT	ATCCGTAGT	660
GGCTTGCAGA	TGCAGACCGT	CTTTGCGAAT	CCTTTGGCCG	GTCCGTCCGT	TCTCGGCATC	720
AGCTCCGGTG	CCAGTTTGGG	TGTTGCTTTG	GTCTGCTCTG	TGAGCGGCTC	GCTGGGAGGA	780
GTGGCATTGA	GTAGCCTGGG	TTATATGGGC	GAGGTGGCCA	TGAATATAGC	CGCTGCCGTA	840
GGCTCGCTGG	CAGTAATGGG	GCTGATCGTT	TTTGTACGCA	CCAAGGTGCG	CAGCCACGTT	900
ACGCTGCTCA	TTATCGGCGT	TATGATCGGA	TATGTAGCCA	CTGCCGTGAT	CGGGGTATTC	960
AAGTTTTTCA	GTATCGAAGA	AGATATTCGG	GCATACGTAA	TTTGGGGGTT	GGGCAGCTTT	1020
TCCCGTGCCA	CGGATTGCGA	ACTGAGTTTC	TTTGCCATTG	TGATGTTGAT	CTTTATTCGG	1080

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5 GCCGGTATGC TCCTTGTCAA GCAGTTG/AT CTCTTATTGC TGGGAGAAAG CTACGCACGT 1140  
 AATCTGGGAC TGAATACTCG TCGGGCACGG CTGCTCGTGA TCTCTTCCGC CGGTTTGCTC 1200  
 ATCGCTACCG TCACGGCCTA TTGCGGTCCC ATCGGCTTTT TGGGGATGGC TGTGCCACAC 1260  
 TTGGCACGSG TTATCTTTCA CACATCGGAT CATCGGATCC TGATGCCTGC TACCTGTTTG 1320  
 ATTGGAAGTG CTCTGGCTCT TTTCTGCAAT ATCATTGCTC GTATGCCGGG GTTTGAGGGG 1380  
 GCTTTGCCCG TCAATTCCGT AACGGCTTTG GTGGGAGCAC CTATTATCGT CACCGTTTTG 1440  
 TTCCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

## 10 (2) INFORMATION FOR SEQ ID NO:31

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2289

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

35 CATTTTTTAG TAACGATTAT GCGGACAAAA ACTATCTTTT TTGCGATTAT CTCTTTTATT 60  
 GCTCTATTGT CGTCTTCTCT GTCCGGCTCAG AGCAAAGCCG TTTTAACCGG TAGTGTGTCTG 120  
 GATGCCGAAA CCGGAGAGCC TCTTGCCGGT GCTCGAATCG AAGTCAAAAC CACCAACATA 180  
 GTAGCCGGTG CGATGCGCGG CGGACATTTC GAGATCAAGA ACCTGCCGGC AGGGCAGCAT 240  
 ACTATTATAT GTTCGTTGGG GGGGTATGGA CAGAAAGAGG AGGTGGTTGC CATCGAAGCC 300  
 GGACAGACCA AAACGATCTC TTTTGCAATT CGATGCGGAA CGAACAACTT GGAGGAAGTC 360  
 GTCGTTACCG GTACCGGTAC ACGTTACCGC TTGGTCCGAT CTCCTGTGGC AACGGAAGTC 420  
 40 CTTACCGCTA AGGACATAGC CTCCTTCTCG GCTCCTACTT CCGAGGCTTT ATTGCAGGGG 480  
 CTGAGTCGCT CTTTGTGACT CGGCCCAAT CTGATGGGCT CTTTCATGCA GCTGAACGGC 540  
 CTTAGCAGTA AGTATATCCT CATCCTTATC GATGGTAAGC GTGTGTACGG CGATGTAGGC 600  
 GGTGAGGCGG ATTTGAGTCG TATTTCTCCT GATCAGATCG AACGGATCGA ACTGGTGAAA 660  
 GGTGCTTCGA GTTCGCTCTA CGGATCCGAT GCCATCGCCG GGGTAATCAA TGTGATCACA 720  
 45 AAAAAGACCA CGAATCGACT GAGTGCATAT ACGTCACATC GCATATCGAA GTACAACGAT 780  
 CGGCAAAACCA ATACTTCGCT CGATATAAAC ATCGGTAAGT TCAGTAGCAA TACCACTAT 840  
 TTCTTCTACC ATACGGATGG CTGGCAGAA ATGCCGTTCC AATAAAAAA GAAAAAAGGA 900  
 TCCGGCGAAC CGGTCTTGGA GGAACGATAT AAGAAAACTT TTCGTGCACA GAAAAATCAG 960  
 GGTGTAAGCC AATCGCTTTC CTATTATGCA ACTAACCAATC TTAGCTTCAG CGGAAATGTG 1020  
 50 CAGTACAATA AACGTGAGT CTTCACTCCG ACTTTTTCCG AAAAAGAGGC CTATGACATG 1080  
 GATTATCGTG CTGTGACGSC TTCACTCGGT ACGAACTATC TTTTCCCAAA TGGTCTGCAT 1140  
 ACGCTTTCTT TCGATGCCGT CTACGATCGC TTCGTTTCG GATATTTGTA TCATGACAAG 1200  
 GACAGCAGTG AGAGCCTGAT CAACAACCAA GGTGAGACCG AGCAACCCAC ATTCTTTCCG 1260  
 GGTGAGCTAC GCAATAAAAA CGATCAGATC CGATACACCG CAGAGGCTCG CGGTGTATT 1320  
 55 AACTGCGCTT ATGCGCAGAA ACTGACCGGC GGTITGGAGT ATTCCGTTGA GGAATTGATC 1380  
 TCTCCCTATA ATTTGATTAC CGACAAGGCA GATGCTTCCA CGCTCTCTGC TTATGTACAA 1440  
 GATGAATGGA AACCGCTCGA TTGGTTCAAT ATGACAGCCG GTTTCGCTCT GGTACACCAT 1500  
 CAGGAGTTCT GTACACGAAT GACGCTAAG GTATCCATAC TCGCCAAATA TGGGCGCGTG 1560  
 AACTTCCGGC CTACGTATGC TAACGGCTAT AAGACTCCCA CGCTGAAAGA GCTTTTGTGA 1620  
 60 CGGAACGAAC TCACCACTAT GGGTTGCGAC AATCTCTATC TCGGCAATGC GGATCTTAAG 1680  
 CCACAGATGT CGGATTATTA TGCTTTGGGC TTGGAGTACA ATCAAGGCCC TATCTCGTTC 1740  
 AGTGCAACGG TTTATGACAA TGAACCTCGC AATCTGATCT CCTTTATGGA TATACCGACC 1800  
 TCACCGGAGC ACGAAGCTCA GGAATCAAG AAAACCAAGC AGTATGCCAA CATAGGAJVA 1860  
 GCTCGCAGCC GCGGCTTGA TGTCTTATGT GATGCTCTA TCGGTTGGGG TATCAAGTTA 1920  
 65 GGAGCCGGAT ACAGCCTCGT GGAAGCTAAG AATCTCCAGA CCGATGAGTG GCTGGAAGGA 1980  
 GCTCCACGTC ATCGTGCCAA TGTGACGCCC GATTGGGTTT ACTACTGGGG TCAGTATAGA 2040  
 CTTGGCGTGA GCCITTTCCG CCGTATTGAG AGCGAGCGTT ACTACAAAGA CGGCAATGCT 2100  
 CCGGACTATA CCTTGTGGCG ACTCGCCACA TCGCATCGTT TCGCTCATTT CCGCCACATC 2160  
 70 ATCCTGGATG GAACGCTCGG TATAGACAAC CTGTTTGACT ACGTGGATGA TCGTCTCATG 2220  
 GGTGTCAATT ATGCTACCGT AACGCCGGGA CGTACTTTCT TTGCTCAAAAT AGCGATTCTGA 2280  
 TTCAACAAC 2289

## 75 (2) INFORMATION FOR SEQ ID NO:32



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(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1095 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

1	TGCTGCGCAA	GGCTTCGGGA	CACCTCTCCC	CGGAAGAAGT	CGTTTCGGAA	TGATACCGTT	60
2	TTTCCTTATT	TCGTTATTCA	TCTGATCAAA	CATATTATCA	TTATGACGGA	CAACAAACAA	120
3	CGTAATATCG	TATTCOCGGC	GTTCCTCCTC	TTGCTGGGAG	TCATCGCAGT	GGTGACGATC	180
4	GTTCGGTTTT	TCATGCTCAG	ACCGGCCGAG	GAGATTATCC	AAGGACAGAT	AGAAGTGACC	240
5	GAATACCGAG	TGTCCAGCAA	AGTGCCCGGG	CGCATCAAGG	AACCTAGGGT	ATCCGAGGGA	300
6	CAGCAGGTGC	AGGCCGGCGA	TACCCTCGCT	GTCAATCAAG	CCCCCGACGT	AGCGGCTAAG	360
7	ATGGAGCAGG	CAAAGGCTGC	CGAAGCAGCT	GCACAGGCTC	AGAACGCCAA	GGCTCTCAAA	420
8	GGAGCAGCCA	GCGAACAGAT	ACAGGCAGCC	TATGAGATGT	GGCAGAAAGC	TCAGGCCGGC	480
9	GTAGCCATAG	CGACCAAGAC	ACACCAAGCC	GTGCAGAAC	TCTATGACCA	GGGAGTGGTA	540
10	CCGGCTCAGA	AGTTGGACGA	AGCCACTGCC	CAGCGCGATG	CGGCCATCGC	TACGCAAAAA	600
11	GCGGCCGAAG	CCCAAGTACAA	TATGGCTCGC	AACGGTCGCG	AACGCGAAGA	CAAGCTGGCA	660
12	GCTTCTGCCC	TCGTGATAG	AGCGAGAGGA	GCCGTCGCGC	AGGTGGAGTC	GTACATCAAC	720
13	GAAACCTACC	TCATCGCCCC	ACGGGCGAGC	GAAGTGTGCG	AGATATTCCC	CAAGCCGGGC	780
14	GAACTCGTAG	GTACCGGGCC	ACCTATCATG	AATATCGCCG	AGATGGGCGA	TATGTGGGCC	840
15	AGCTTTGCCG	TTCTGTAGGA	TTCTCTCAGC	AGCATGACCA	TGGGAGCCGT	TCTGGAGACT	900
16	GTGGTGCCCG	CTCTGAATGA	AGAAAAAGTA	CCCTTCAAGA	TCACATTTCAT	CAAGAACATG	960
17	GGTACCTATG	CTCCCTGGAA	AGCGACCAAG	ACAACAGGGC	AGTACGACCT	GAAGACCTTC	1020
18	GAGGTAAAGG	CCACCCCTTC	GGATAAAGAC	AAGGCACAAA	AGCTACGCCC	GGGTATGTCC	1080
19	GTGATCATAC	GCAAG					1095

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 960 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

1	CCGCAATCCT	CTCCTGATCG	AAGAAGCTTC	CAAAACGTCA	TGAATAAATA	TCATTCTCAA	60
2	AGCGTTTTAG	AGGTGCGCAA	AATTGGGATT	GTGATTATCT	TTGGGCCCAT	AGTACGGAAT	120
3	GTACATCAAC	AACCCCTTTT	TTTAAGCCAT	AAATCAATTA	TGCGTATTGT	CAGTAATTTT	180
4	TTGTTCTGCT	CTTTTTCGGT	TTTGCTTTTT	GCATCATGCC	GTTCACAGCG	AGAAAAAGTC	240
5	CTTTACCTGC	AAGATATCCA	AACCTTTTAT	CGGGAGATT	TCGCTAAACC	ATATGACGTA	300
6	AAATTTGAGA	AGGACGATGT	GCTGAACATC	CTTGTCAGCA	GTAGAGACCC	GGAGCTTTCA	360
7	ACGCCCTACA	ACCAAGTGTT	GACCACTCGT	GCACTGGCCC	GCAACGGCTA	TGGAACGAAC	420
8	TCGAACGAAG	GCTTCCTGGT	CGATTGCAAA	GGGTACATCA	ATTATCTTAT	TTTAGGCCAG	480
9	ATCTATGTAG	AGGGCCCTAC	TCGTACCGAA	CTGGAGAAGG	AGATACAGAA	GAGGATTATT	540
10	TCCAGTGGAT	TTATCAAGGA	TCCTACGGTA	ACGGTGACGC	TTCAAAATTT	CAAGGTGTCG	600

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5 GTTTTGGGAG AGGTGAATCA TCCGGGTTCC ATGTCGGTAA AAGGAGAGCG AATAACTCTT 660  
 TTGGAAGCGA TCGGAATGGC CGGAGACCTG ACAATCTATG CTCGCCCGCA TCGGGTTTTT 720  
 GTGATTAGAG AAACCGATGG GCATCGCGAG GTTTTCCAGA CGGATCTCAG AAAGGCCGAC 780  
 TTGCTCGCAA GCCCGGTGTA CTATCTGCAT CAGAACGACG TCATCTATGT GGAGCCGAAC 840  
 GACAAGAAAA CACAGATGAG CGAGATCAAC CAGAATAATA ACGTAAACGT ATGGCTGAGT 900  
 GTTACCTCCA CTTTGGTATC CATTTCACG CTGACGATTA CGATAATAGA TAAGACCAAA 960

## (2) INFORMATION FOR SEQ ID NO:34

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1746 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1746  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

TCAAAAATAG TACTACGAAA GTTTTGTACC TTAGCGCGCA TGAAAAAGAC CAATCTGTTT 60  
 TTATCTCTGC TGGTGATCTT TATCACCAGT AGTTTATAGA CTGCCTGTGC ACAGAAGTCC 120  
 35 AAGACGAACA AACTCACCAG AGAAGATCGG AGCCGCAATG AGTATGTACA GTCGATGGAT  
 GTGCTTAGCA ATATTATCGG TAACGTCAGG CTGTATTTCG TCGATACCAT AAGTATCAAA 180  
 CATATGACTC GGCCTGGTAT AGATGCGATG TTGGGCGGGC TTGACCCCTA TACCGAATAC 240  
 ATTCCTTAGC AGGAAATGGA TGAAGTAAA TTGATGACTA CGGAGAGATA TGCCGGAGTC 300  
 GGAGCTATCA TATCGCAGCG CCCGGATAGT GCTGTGATTA TCCAGAGACC TATGGAAGGT 360  
 40 ATGCCCCGAG ACGAAGCAGG ATTGATAGCA GGCGACCGCA TCCTGACTAT CGATGGGAAA  
 GACTTCCGCA AATCCACCAC ACCGAAAGTA AGCGAACGAC TGAAAGGGAT AGCCGGTACT 420  
 GTTGCAAAGG TGACAGTAAT GCGCTATGGC GAAACCAAAC CTCGTACTTT TTCCGTGAAA 480  
 CGTCAAAAAG TGATATGAA TTCCGTCACT TACAGCGGAA TGCTCGATGG CTCGATAGGA 540  
 TATATCCGCT TGAACAACTT TACGGACAAA AGTGCAAGAG AGGTGCGCAC GGCCTTGTG 600  
 45 GATCTCTGTC ACAAACNAGG AGCGAAAGGT CTCATTTTGG ATTTAAGAGG CAATGGTGGC  
 CGACTGATGC AGGCTGCTAT CGAGATAGTC AATCTGTTCG TCCTAAGGG CAAAGAGGTG 660  
 GTAACGACCA AAGGTGCGAT TGCAGAGTCG GCGTCCGTAT TTGCGACATT GACTGAACCG 720  
 ATCGACACGA AACTCCCGAT AGTAGTCCTG ATCGATGGAC AATCGGCATC TTCTCGGAG 780  
 ATTGTAGCCG GAGCACTGCA GGATATGGAC AGGGCTGTAC TGATGGGACA AAAGAGCTAT 840  
 50 GGCAAGGGTC TTGTACAAAC GACTCGTCAC CTACCATACA ACGGCGTGAT CAAATTGACT  
 ACGGCCAAGT ACTACATCCC AAGCGGACGT TGTATTACGC GTTTGGACTA CAGCCGCACC 900  
 AATCGGACAG GTATGGCAAC GGCCATTCCCT GACAGTCTGC ACAAAATCTT TTACTGTCT 960  
 GCCGGAAGAC GTGTAGAAGA TGCAGGAGGA ATCCTGCCTG ACATCGAGGT CAAACAAGAT 1020  
 ACAGCTGCGA CATTACTTTA TTATATGGCC ATCAATATG ACGTTTTCGA TTTCTGCACA 1080  
 55 GGTATGTGTC TCAAGCATAA AACGATTGCC AAGCCGGAGG ATTTTCCAT AACGAACGAG  
 GACTATGCAG CTTTCTGCAA GATGATGGAA GAAAAGAAAT TTGACTATGA TCGCCAGAGT 1140  
 GGCAAGATGC TTGACAACTT GGAGGAAGTG GCTAAGATAG AAGGCTACCT GCCGGAAGCC 1200  
 AACTCGGAGC TTAAGCACT ACAGCAAAAG CTAACACCCA ACCTGTCCGG TGATCTGCTA 1260  
 CGATTCAAAA AGGAGATAAC AACTATCTC AACAATGAGA TTGTCACTCG CTATTATTAT 1320  
 60 GAGCGAGGCA GTATCCGCCA GAGTTTGGCG GAAGATAAGG TAGTCAAGA AGCTATTAAG  
 CTGCTGAAGG ACCATCCGGA ACAAAATCGA CAGATCCTTG CAGCTCCGAA AGCAGAGAA 1380  
 AAAGGG 1440  
 1746

## (2) INFORMATION FOR SEQ ID NO:35

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2955 base pairs  
 (B) TYPE: nucleic acid  
 70 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 75

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

GTAACAGACA AAATGCCAAA CAAAGGATTT GTGATTGTTA TCACATCGGC TCTGGCCATC 60  
 ATCTGTGCGT TTTACCTGTC ATTCTCTTTC GTTACGAACC GTTACGAAAA GAAGGCTAAG 120  
 GCGATGGGCG ATGTTGCCGG AATGGCCTAT CTTGATTCCA TGTCGAATGA GAAGGTCTGG 180  
 TTCGGCTACA CGCTGAAAGA AGCTCAAGCC CAGCAAATTG GTCTTGGCCT TGACTTAAAG 240  
 GGGGGTATGA ACGTTATCTT GAAACTTAAC GCAAGCGATC TGCTTCGTAA CCTCTCTAAC 300  
 AAAAGTTTGG ATCCCAACTT CAACAAGCT CTGAGAATG CTGCCAAGAG CACGGAGCAA 360  
 TCCGACTTCA TCGATATTTT CGTGAAGGAA TATCGCAAGC TCGATCCCAA CGGTGCGTTG 420  
 GCGGTTATCT TCGGTTCCGG TGACCTTCGC GACCAGATTA CCGCAAAGTC TACGGATGCA 480  
 GACSTAGTGC GTCTGCTCAA AGAAAAATAT AATAGTGCTG TAGAAGCTTC GTTCAATGTG 540  
 CTCGGTGCTC GTATCGATGC TTTCCGTTGT GTTGACCTTA ATTTGCAGCG ATTGGAAGGG 600  
 CAAAGGCGTA TCCTTGTCGA ACTCCCGGA GTGAAAGACC CTGAGCGTGT TCGTACCTTT 660  
 TTGCAACGCA GTGCCAACCT ACAGTTCTGG CGTACATACA AATTGGAAGA GGTGAGCGGA 720  
 GACTTGATCG CTGCCAATGA TCGTCTGAGC GAATTGGCTA TGAACAACAC GGATGCTACC 780  
 CCGGAAACAG AGCCTGCAAC TACTGACTCT GTAGCTGCAA CAGCCGATTC TGCTGCTGTA 840  
 CAAGCTGTAG CTGATTCTGC TAC1GTAGCA CAAAAGAGAG CCAAGGATGC TACTCGTAAA 900  
 GACGCACTCT TCTCTCTGCT TACTCCCGTG AATCGTGGCG GTGCAGTAGT GGGTGTGGCT 960  
 CGTCTGTCTA ATATGGCTCA GATATCTGAA ATGCTCCAGC AAGCTCAGCA TCTGAAGGTT 1020  
 ACACGTGAAG ATGTGCTTTT CCTCTGGGCT GCTAAAGCAA TCGAAGACCC CGAAACCAAA 1080  
 AAGGAGACCG ACCTCTACGA ACTCTATGCT ATTCGTACCA ATCGTACGGG AGATCCTGAT 1140  
 TTGGGAGGTE ATGTAGTGAC TTCCGCCAAG AGTGATATCC AAAATGACTT CGGTGCTTCC 1200  
 GAACCGATCG TTTCGATGAC GATGAATGAA GAAGGTGCTC GTAAATGGGC GCGTATCACA 1260  
 AAGGATAACG TGGGACGGGC AATCGCTATC GTTTTGGATG GTGTGGTTTA TTCTGCTCCG 1320  
 AACGTGAATG ATGAGATCAC GGGCGGTGCG TCTCAGATCT CCGGGCACTT CACCGTGGAG 1380  
 GAGGCGGTTG ACCTTGCCAA CGTACTCAAC TCCGGTAAAA TGGATGCTAC GGTAAAGCATC 1440  
 GAACAGGAAA ACGTGATTGG TCCTACGCTG GGTGCCGAGT CCATTAAAGC CGGATTCCTG 1500  
 TCGTTCTCTG TCGCTTTGGT TATCCTGATG TGTACATGT GTCTGGCTTA CGGTTCTTGT 1560  
 CGGGGCTCTA TCGCAAAACG CGCATTGATT GTAAACAGCT TCTTCACATT GGGCGTATTG 1620  
 GCTTCTTTCC ATGCCGTGCT GACCTCTCG GGTATCGCAG GTTTGGTGTCT GACGCTGGGT 1680  
 ATGGCTGTGG ATGCCAAGCT ACTTATCTTC GAGCGTATCA AAGAAGAGCT TCGTGCCGGT 1740  
 AAGACTCCGA TTCGTGCCGT TACGGATGGT TATGGCAACG CTTTCTCTGC CATCTTCGAC 1800  
 TCGAACGTTA CCACTATTAT TACCGGTATC ATCCTATTCC TCTACGGGAC GGGGCCGATT 1860  
 CGCGGTTTTC CCACTACGTT GATTATCGGT CTTATCGCTT CTTTCATTAC GGC1GTCTTC 1920  
 TTGACTCGTA TCGTCTCGA GAAACTGGCG AAAAAAGGTC GTTTGGATTA GATTACATTC 1980  
 ACTACGAGCA TTACTCGCAA TCTCCTTGTC AATCCCTCAT ACAACATCTT GGGTAAGCGC 2040  
 AAGACCGGCT TTATCATTCC GGTGATTATC ATCGTTTGG CACTTATAGC TTCATTTACA 2100  
 ATCGGTCTCA ATAGGGGTAT TGAATTCTCC GGAGGACGTA ACTACGTAAT TAAATTCGAC 2160  
 CAGCTGTAT CTTCGAAGC CGTTCGTTCC GCCTTGCTTT CTCCCTGCA GGAAGAGGTA 2220  
 TTGTTTACCT CCATCGGTAC TGAAGGGACA GAGGTGCGTA TATCTACGAA CTATAAGATC 2280  
 CAGGAGGAAA GCGAAGAAAC TGAAGCAGAG ATTAAGTACA AATTGTATCA GAGCCTGAAA 2340  
 GGTTCCTACA CCCAGCAGCC TACTGCTGAT CAGTTCTTGG ACAATATCAT TAGCTCTCAG 2400  
 AAAGTAAATC CCAATATGTC GAGTGACATC ACGAGAGGTG CTATTTGGGC TGTGCTGTTA 2460  
 TCGATGATCT TCATGGCCAT TTATATTCTG ATTCGCTTCC GTGACATTTT TTTCTCTGCC 2520  
 TGGAAATTCG TATCTGTGGC CGCTACTACA TTCTGCATTA TTGCTCTGTA TGGCTTGGTG 2580  
 TGGAAATTCG TGGCCTTCAC CATGGAGATC GATCAGAACT TCATCGCTGC TATCTGGGCT 2640  
 ATCATCGGTT ACTCGCTCAA TGACACCGTG GTTGATTTTG ACCGTATCG AGAGACGATG 2700  
 AAATTTGATC CCAACAGAGA TCGCTATCAG GTGATCAACG ATGCCCTTAA TTCAACATTG 2760  
 GGTCCGAACAT TAAATACGTC TTGACTACG TTTATCGTTA TGTGGTAAAT CTTATCTTTT 2820  
 GGAGGTGCTA CGATGCGTAG TTTCAGTTTC TCGATCCTGC TCGGTATCGT TATCGGTACA 2880  
 TACTCTACGC TCTTTGTTGC TACACCCCTT GCCTACGAGA TCCAAAGCG CAAGCTCAAC 2940  
 AAAGCAGCTA AGAAA 2955

(2) INFORMATION FOR SEQ ID NO:36

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3138 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3138

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GACTTCCCTT	GGGTTAGGCT	AAAACCGGAG	AAGAAAGAA	AACAACATAA	CAGTAATAAT	60
TTTAAGTTTA	ACGCAAAAGA	AAAGTCTATG	AAAAGAATGA	CGCTATTCTT	CCTTTGCTTG	120
CTGACGAGCA	TTGGGTGGGC	TATGGCCAG	AATAGAACCG	TGAGGGGTAC	AGTTATCTCC	180
15 TCCGAGGATA	ATGAGCCCT	GATCGGCGCG	AATGTCGTGG	TTGTCGGAAA	CACCACTATC	240
GGTGCTGCAA	CGGACTTGGA	TGGCACTTC	ACGCTTAGCG	TGCCTGCCAA	TGCCAAAATG	300
TTGAGAGTGT	CCTATTCCGG	TATGACTACC	AAAGAGGTGG	CCATCGCTAA	TGTGATGAAG	360
ATCGTACTGG	ATCCGGACTC	TAAGGTTCTG	GAGCAGGTAG	TTGTATTGGG	TTACGGTACG	420
GGACAGAAAC	TCAGCACTGT	TTCCGGTTCT	GTGGCCAAAG	TGTCCAGCGA	AAAGCTCGCG	480
20 GAAAAGCCCG	TTGCCAATAT	CATGGATGCC	CTCCAAGGTC	AGGTAGCCGG	TATGCAGGTT	540
ATGACTACAT	CGGTTGACCC	TACTGCCGTC	GCTTCTGTGG	AGATCCATGG	TACAGGGTGG	600
TTGGGGGCAA	GCTCTGCACC	ATTGTATATC	GTGGATGGTA	TGCAAACTTC	TTTGGATGTT	660
GTGGCTACGA	TGAATCCGAA	TGATTTTGAA	TCTATGTCGG	TTTGTAAAGA	TGCTTCTGCA	720
ACATCTATTT	ATGGAGCTCG	TGCTGCAAAC	GGAGTCGTTT	TCATTCAAA	GAAGAAAGGT	780
25 AAAATGAGCG	AGAGAGGTGG	TATTACCTTT	AATGCCAGTT	ACGGGATTTC	TCAATCCTG	840
AATACTAAGC	CCCTTGATAA	TATGATGACT	GGAGATGAAT	TGCTGGATT	TCAGGTGAAG	900
GCAAGTTTTT	GGGGGAACAA	TCAAACCGTT	CAGAAGGTTA	AAGATATGAT	CCTTGCCGGA	960
GCTGAAGATT	TGATGGCAA	TTATGATTCT	TTGAAAGATG	AGTATGGTAA	GACATTGTTC	1020
CCAGTGGATT	TTAATCATGA	TGCAGACTGG	CTCAAGGCTT	TGTTTAAAC	AGCACCACC	1080
30 AGTCAAGGTC	ATATTCTTTT	CTCCGGAGGG	TCTCAGGGAA	CTTCATATTA	TGCTTCTATA	1140
GGGTACTTCG	ATCAGGAAGG	TATGGCTCGT	GAACCGGCAA	ATTTTAAAGC	GTATAGTGGC	1200
CGGCTCAACT	TGGAAGTCG	TATCAATGAA	TGGCTGAAAG	TTGGTGCAAA	TTTGTCTGGT	1260
TCCGATAGCGA	ATAGACGATC	TGCCGACTAT	TTTGAAAGT	ATTATATGGG	GTCAGGTACT	1320
35 GCGGTGTTT	TAAOGATGCC	TGTTTATTAT	AACCTTTTGG	ATGTGAATGG	GGATTAGCA	1380
ATGTGCTATT	ACATGTATGG	AGCTACCAAG	CCTTCTATGA	CAGAACCCTA	CTTCGCAAAA	1440
ATGAGACCGT	TCAGTTCGGA	ATCACATCAG	GCCAAATGTA	ATGGTTTCGC	CCAGATTACT	1500
CCGATCAAGG	GCCTTACTTT	AAAGGCACAG	GCTGGTGTTC	ATATTACTAA	TACTCGCACT	1560
160 TCTTCTAAGA	GAATGCCCAA	TAATCCGTAT	GATTCTACTC	CTCTGGGGA	AAGAAGAGAA	1620
AGAGCTTATC	GAGATGTTAG	CAAGTCTTTT	ACAAATACGG	CTGAATATAA	GTTTCTCAAT	1680
40 GATGAAAAAC	ATGATCTTAC	AGCATTGATG	GGGCATGAA	ATATTGAATA	TGAAGGGGAT	1740
GTTATTGGGG	CATCTTCTAA	AGGATTGAA	AGTGATAAGT	TGATGTTACT	GAGCCAGGGA	1800
AAAACCGGAA	ATAGTTTGTC	TTTGCCCTGAA	CACAGAGTCG	CTGAATATGC	CTATTGTCT	1860
TTCTTTAGTC	GTTTAAATTA	CGGTTTGGAC	AAATGGATGT	ATATAGATT	CTCTGTTCTG	1920
AATGACCAAT	CCTCTCGATT	CGGATCCAAT	AATAGAAAGC	CGTGGTTCTA	TTCTGTCGGT	1980
45 GGAATGTTTG	ACATATATAA	TAAATTCATT	CAAGAAAGTA	ATTGGCTCAG	TGATCTTCGA	2040
CTGAAAATGA	GTTATGGTAC	AACGGGTAA	TGGGAGATTG	GTAATTACAA	CCACCAAGCA	2100
CTCGTTACTG	TGAACAATTA	TACTGAAGAT	GCTATGGGGC	TTAGCATTTT	TACAGCAGGC	2160
AAACCGGACC	TCTCGTGGGA	AAAGCAGTCT	CAGTTCAACT	TGGGTTTGGC	TGCAGGGGCT	2220
TTCAATTAATC	GCTTATCTGC	AGAGGTAGAT	TTCTATGTCC	GCACTACGAA	TGATATGTTG	2280
50 ATTGATGTCC	CGATGCCTTA	TATCAGTGGT	TTCTTCTCAC	AGTATCAGAA	TGTAGGCTCT	2340
ATGAAAATAA	CGGGTGTAGA	CCTTCTCTTT	AAGGGGACGA	TCTACCAAAA	TAAGSACTGG	2400
AATGTATATG	CTTCTGCGAA	TTTCAACTAC	AATAGACAGG	AAATAACAAA	GCTTTTCTTC	2460
GGTCTCAATA	AGTACATGTT	GCCTAATACC	GGTACTATAT	GGGAAATTGG	GTACCCCAAT	2520
TCGTCTTATA	TGGCTGAATA	TGCTGGAAAT	GACAAAAAAA	CCGGTAAGCA	GTTGTGGTAT	2580
55 GTTCCTGGTC	AAGTCGATGC	GGATGCTAAT	AAAGTTACAA	CAAGCCAGTA	CTCAGCTGAC	2640
TTGGAGACAC	GAATGTATAA	GTCTGTACT	CCTCCTAATA	CAGGTGGTTT	CTCCTTAGGT	2700
GCTTCTTGGA	AAGGACTTTC	TTTAGATGCT	GATTTTGCCT	ACATCGTTGG	TAAATGGATG	2760
ATCAATAATG	ACGTTACTT	TACAGAGAAT	GCAGGTGGAT	TGATGCRAAT	AAATAAGAT	2820
60 AAAATGCTAT	TGAATGCCCTG	GACAGAGSAT	AATAAAGAAA	CAGATGTTCC	AAAATTGGGA	2880
CAGTCTCCTC	AGTTTGATAC	GCATTTGTTG	GAGAATGCTT	CTTTCCTGCG	TTTGAAGAAT	2940
CTCAAACTCA	CCTATGTACT	CCCCAATAGT	CTTTTGTCTG	GGCAGAAATG	GATTGGTGGA	3000
GCTCGTGTCT	ATTTGATGGC	GCGCAATCTG	TAACTGTTA	CSAAGTATAA	AGGCTTTGAC	3060
CU'GAAAGCAG	GGGGGAATGT	GGGAAAAAAT	CAATATCCTA	ATTCTAAGCA	GTACGTTGCG	3120
65 GGTATTCACT	TGCTTTTC					3138

(2) INFORMATION FOR SEQ ID NO:37

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2607 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (Rule 26) (RO/AU)

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTCATCGGCT	TTGAAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCUCCATTTT	CTTCTACAAG	CGGTTTATAT	CGCCGCTTAC	ACCGCTTCA	180
TGCGGGTTTA	CCCCCTCATG	TTCGTCTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTACCCCGTG	GGGTGGAAGT	300
GGCTATGACC	CCGTTCCG					318

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2583 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TTAGAGATGG	CATACGACTT	TACACAAACA	TTCCGCAACA	GCCTGGAGTA	CAGCTATCAG	60
GAAGCAACCC	GTCTCGGCGT	CGTAGCCGTG	ACGCAAGATA	TGCTCGTACT	CGGTATCATT	120
CGCGACGGAG	ACAATGGCGC	GATCGACATC	ATGCGGCACT	ATGGGATCAA	CTTGTACGAA	180
CTCAACCGGT	TGATCGAGTT	GGAAGCCATC	GCCGAGAGTT	TGCTGCTTTC	GCCTGAGGGA	240
TGCGCCATCT	TCACCCCTTC	GGCTCGGGAG	GCTATCGATG	ATGCCACAGA	CATCTGTGCC	300
GACATGGAGG	ACGAGGCCGT	CAGCCCGGTC	CATCTGTTGC	TGAGTATCCT	CAACTCGACA	360
CAGGAGAGCT	TAGTACAAAA	GATAITTTAT	AAACAAGGTA	TAAVATACGA	CACCATCCTG	420
TCGGATTACT	TCGGACAGCG	CAACCCCTCC	GAAGGGAAGT	CTCCCTCCGA	AATGGAGATC	480
CTCGACCGGT	ACCAAGACAA	CGACTTCGAC	GACGAAGAGG	ACGAATCCTC	TCCGCCTTCC	540
GGGAATAGCG	CGACAGGCGG	AGGCTCCGGC	GACGCCCCCG	AACAGAATAC	CGCGGAGGCG	600
GATACTACCA	CCACGACACG	GAGTGGAGGC	GACACGCCCTG	CACTGGACAC	CTTCGGCACC	660
GACATCACTG	CCATGGCGGC	AGCAGGCAAG	CTCGACCCCG	TAGTGGGTGG	GGAGCAGGAG	720
ATCGAAAGGG	TGATACAGAT	ACTCAGCCGG	CGCAAAAAGA	ACAATCCGGT	GCTCATCGGC	780
GAACCCGGTG	TAGGCAAGAG	TGCCATCGTG	GAAGGACTGG	CCGAACGCAT	CGTGAACAGG	840
AAGGTGAGCC	GTATTCTTTT	CGACAAGCGG	ATCATCAGCC	TCGATTGGCC	TCAGATGGTA	900
GCCGGCACCA	AATATCGCGG	ACAGTTGCGA	GAGCGGTTGA	AGCCCGTGCT	CGATGAGCTG	960
AAGAAGAATC	CGCAGATCAT	CCTCTTCATC	GACGAGATAC	ATACCATCGT	GGGAGCAGGC	1020
TCTGCAGCCG	GATCGATGGA	TACGGCCAAT	ATGCTCAAAC	CCGCTCTTGC	CCGTGGACAG	1080
GTACAGTGCA	TCGGAGCCAC	TACGCTGGAT	GAGTATCGTA	AGAACATAGA	AAAGGACGGA	1140
GCACTCGAAC	GCGGCTTCCA	GAAGGTGCCG	ATAGCCCCCT	CGACTGCAGA	AGAAACGCTG	1200
ACCATCCTCG	AAACATCAA	AGAGAAATAC	GAGGACTATC	ACGGTGACG	CTATACGGAC	1260
GAAGCGATCA	AAGCGGCAGT	GGAAGTGAAC	GATCGCTATG	TATCCGATCG	TTTCTTCCCA	1320
GATAAGGCGA	TAGATGCCAT	GGACGAGGCC	GGCGCGAGCG	TCCATATCAC	CAATGTGGTG	1380
GCTCGGAAG	AAATCGAGAT	ACTGGAGGCC	GAATTGGCAT	CGGTGCGAGA	GAACAAGCTC	1440
TGCGCCGTAA	AGGCTCAGAA	CTACGAACTG	GCTGCCTCCT	TCCGCGATCA	GGAGCGGCGC	1500
ACTCAGCAGC	AGATAGCGGA	AGAGAAGAAA	AAATGGGAAG	AGCAGATGTC	CAAGCACCGC	1560
GAGACGGTGG	ACGAGAATGT	AGTGGCGCAT	GTAGTGGCGT	TGATGACAGG	CGTTCGGGCT	1620
GAGCGGCTGA	GCACGGGCGA	AGCGCAACGT	CTGCGCACGA	TGGCAGATGA	TCTCAAGACC	1680
AAAGTAGTAG	GTCAAGGACAC	AGCCATCGAA	AAGATGGTGC	ATGCCATCCA	CGCAATCGT	1740
CTGGGACTTC	GCAATGAAAA	GAAACCGATC	GGTTCTTTCC	TTTTCTCTCG	CCCCACGGGG	1800
GTAGGCAAGA	CCTATTGSGC	CAAGAAGCTC	CGCGAATACC	TGTTGAGGGA	TGAGAATGCC	1860
ATGATCAGGG	TGGATATGAG	CGAGTATATG	GAGAAGTTCT	CGGTTTCCGG	TCTCGTGGGT	1920
GCCCCCTCGG	GATATGTGGG	CTATGAAGAA	GCGGCGCAAC	TGACGGAGCG	CGTAAGACGC	1980
AAACCTTATT	CGGTGGTTCT	CTTGGATGAG	ATCGAAAGGG	CGCATGCCGA	TGTCTTCAAT	2040
CTGCTCTTAC	AGGTGATGGA	CGAAGGTGAG	CTGACCGACA	GTCTGGGACG	GGCGGTGAAT	2100
TTCAAGAACA	CGGTGATCAT	CATCACCTCC	AACGTGGGTA	CACGCCAGCT	CAAAGACTTC	2160



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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...897

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

```

TTAAAAAAGG AGATAACTAT GAAACAGAAC TACTTCAAAA GAGTCTGCTC ACTGCTTTGG      60
CTGGTTTAC  CCATGCTTAT TATGCCATTG GAAGTAGCAG CTCAGAGAT  TATCCGAAC      120
GAAGAGCTGT TGAATCATT  GACTTTCGTT GCACCGGTTG AGGAGACAGA CGCAATAGAG      180
GCAGAGGTAG AAGCTCTGCA GGAGATAGTC GCTACTGAGG AGATTGCGGA GCAGGCTGTT      240
CGTTCTTTATA CTTACACGGT CTATCGTGAT GGCCTGAAGA TTGCTTCAGG ATTGACTGAG      300
CCCACTTTTC TCGATGAAGA TGTTCTGCTC GCGCAACATA CCTACTGCGT AGAAGTACAG      360
TATCAGGGAG GCGTATCCGA CAAAGTATGC GTGGACGTAG AGGTGAAGGA CTTCAAACCG      420
GTTACCAATC TCACCGGAAC TGCTTCCAAT GACGAAGTTT CTTTGGACTG GGACGGTGTG      480
15 GAAGAGAAAG CTGAAGAGCC GGCAAGTGAT AAAGCAGTCA GCTACAACGT CTACAAGAAAT      540
GGAACCTTGA TCGGTAATAC AGCTGAAACT CATATGTGG AGACCGGTGT AGCCAATGGT      600
ACATACATCT ACGAAGTGA AGTAAAGTAT CCTGACGGTG TATCTCCGAA GGTGGCTGTA      660
ACCGTGACCG TGACCAACAG CTCATTGAGC AATGTAGATG GACAGGCTCC TTACACATTG      720
20 CGAGTAGAAG GCAAGAAGAT TATTGCGGAA GCCCATGGTA TGATCACGCT CTACGACATC      780
AACGGACGTA CCGTGGCGGT AGCCCCGAAT CGATTGGAAT ACATGGCGCA AACCGGTTTC      840
TATGCAGTGC GCTTCGATGT GGGGAATAAA CACCATGTAT CGAAAATACA AGTAAGA      897

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## 25 (2) INFORMATION FOR SEQ ID NO:42

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## 30 (ii) MOLECULE TYPE: DNA (genomic)

## 35 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## 40 (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...1131

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```

TTGTTTAATC ATAAAAAATC ATGGTATGAA ACATTTCAT TTTATCTCGT TGTTTTCCGC      60
TCTGGCTTTA TTCTTTTGTG TGAATAATACC CTTGCACAAC AAAAAACAGA GGAGTTTGCA      120
CCTGTGTCGG ATTACGTGC  AGAAGCGTAC GGCTCTACCG TTTTCTCCA CTTGGACTCCG      180
CCGTATGACA ATCCGATGAT TCCTCTAAGC GAGAGTTTGG AATCAGGTAT TCCAGCTATA      240
TGGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTGAC CAATTCACG      300
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGGCGTCGG AGCTTTGACT      360
COGGACAATT ATCTGATAAC ACCCGAATTA AAACACCCA CAGACGCGTT GGTGGAAATA      420
ATCTAATGGG TATGTACTCA AGATCTCACT GCTCCATCGG AGCACTATGC CGTTTATTCC      480
TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT      540
GCCAAACGGA TACAATCCCC CGAGTTGATC CCGGGAATC GGACACAAGG TGTTTGGTAT      600
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTCC      660
ACGGATAAAT TCTGGCTCAA TTTGGATGAA GTATCTATCC TGTATACCCC TCTTCCCCGA      720
AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATCTG TATTCCGTGA TGGACAAAAG      780
ATAGCGAGTG GATTGTGGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA      840
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGTCTG CAAAAATATA      900
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTTCGCTT GACCGTGGTT      960
GGCAAGACCA TTGTAGCGAG TGCTTTCAA GGAGAGATCA CTCATTATGA CATTCGTGGC      1020
CGGCTGATAG CTTCCGGCTG CGATACGCTT AGGTACAAAG CGGAAAATGG TTTTACCTC      1080
65 ATTAAATAC AGGTAACCG AACTGTCTAT ACTGAGAAA TCCAAATCCA A      1131

```

## 70 (2) INFORMATION FOR SEQ ID NO:43

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2547 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75



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(ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 5 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 10 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2547  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43  
 15 TTCCGGAATAT CACCTTCAAT GAAAAAAGT TTTCTTTTAG CCATAGTAAT GCTCTTTGGC 60  
 ATTGCCATGC AGGGACATTC TGCTCCGGTT ACGAAAGAGC GAGCTTTGAG TCTGGCTCGG 120  
 CTGGCTTTGG GACAGGTATC CTTGCGAATG GGACAAACAG CAGTATCTGA CAAGATTTC 180  
 20 ATCGATTACG TTTATCGGCA AGGAGATGCT GAGAGGGGTA TCACATCACA AGAGGAAGGC 240  
 TCTCCTGCAT ATTTTATGT ACCTAATCGT GGAATAATG AGGGCTATGC TCTGTAGCA 300  
 GCAGATGACA GAATACCGAC AATTTTAGCC TATTCACCCA TTGCCGTTT CGACATGGAC 360  
 AGTATGCCGG ACAATCTTCG CATGTGGCTA CAAATTTACG ATCAGGAAAT AGGCCGTGATA 420  
 CTTTCCGGAA AAGCTCAGCT CAATGAAGAG ATATTACGTA CCGAGGGCGT ACCGGCTGAA 480  
 GTACATGCTC TGATGGATAA CGGTCAITTT GCCAACGATC CCATGCGATG GAATCAAGGT 540  
 25 TACCCATGSA ACAATAAGGA ACCACTGCTT CCTAATGGCA ATCATGCCTA TACCGGCTGT 600  
 GTTGCTACTG CTSCAGCACA AATCATGCGC TACCATAGCT GGCGGCTTCA AGGTGAAGGC 660  
 TCTTTGATTT ATCATGCAGG TTCAATAGTT GGCAACTGGT CCGGCACATT TGGTGAATG 720  
 TACGACTGSA TCAATATGCC CGGAATCCG GACCTTGATA ATCTGACTCA ATCTCAAGTG 780  
 GATGCCATCG CCACACTGAT GCGTGATGTG AGTGCACTCG TTTGATGAG TTTTATGAA 840  
 30 AATGGAAGTG GTACGTACAG CGTTTATGTA GTAGGAGCCT TGCGAAACAA CTTTGGCTAC 900  
 AAGGTTTCAC TGCAGCTACA TGTACGGGCC TTATATACCT CACAGGAGTG GCACGATATG 960  
 AATCCSGGGG AACTTGCTC CGGAAGGCGG GTCTATTATG CAGGGAATAA CCAGASCATA 1020  
 GGACATGCTT TCGTTTGGCA TGGTTATGCT TCGGATGGTA CTTTCCATTT CACTGGGGT 1080  
 TGGGAGGGTG TTTCCAACGG CTCTACAAA CTAACACTCC TCTCGCGAC TCTGTGGGT 1140  
 35 ATCGGAGGTG AGGGAATAGG TTTTACCATT TATCAAGAGA TCATCACCGG TATCGAACCG 1200  
 GCTAAGACTC CCGCTGAAGC CGGTACAGAT GCCTTGCCGA TCTTGCACT GAAAGACATA 1260  
 GAAGCCGAGT ATAAAGTGA ATCCGGATTG AACGTAGGGT ATTCGATATA TAATACAGGT 1320  
 GAAGAGCAAT CAAATCTTGA CCTCGGATAC AGATTGAACA AGGCTGACGG AGAAGTCATA 1380  
 GAGGTGAAAA CTTCTCTAT CAATATCTCT TGGTACGGAT ACGGAGAGCA TCCGAGAGT 1440  
 40 TTCTCATTTG CACCTAATCA GTTGTCACAA GGAATCAACA CCATCACCT ACTTTATCGT 1500  
 CGCACAGGCA CGAACAGTG GGAGCCGTA CGGCATGCAC AGGGAGGATA TGTCAATAGC 1560  
 ATTAAGTAA ATACGACAGA CCGGAACAAT GTCGTAGTCA CGGTAGATAA TAACGAAGGC 1620  
 AAGCTCAGTA TGCTCCCAA CAGCTTTGTC GCAGATCTGA ATTCTTATGA ACATAGTACG 1680  
 ATTACAGTAC AGTTCAATAG CGACAGCCCT GATGAGATCC GTACACCCGT AGCCTTTGCT 1740  
 45 CTATCTACAG GAGCTACTGC GGACGATGTA ATATCTTTGG GCTGGGTAAT GGCCTGAAGT 1800  
 CCGGGCGGTA GCAGCAACTA TCCGGTGGTT TGGTCTAAAG ACGTTCTCAC TCTCTCGGAA 1860  
 GSCGACTATA CATTGTGGTA TAGATTTTCC ATCAACAACC AAAAGGATGA ATGGAAGGAG 1920  
 ATCGGAAGCG TGTCAGTAAA AACACCGACA GAGTATACGC ACCCTTATT CGAAGTGGGC 1980  
 CATAATGACA CTTCTACCTA TACGCTGGAT ATGGACACA ACAGAGTATT GCCCGACTTT 2040  
 50 AACTCAAAA ATCTCGGATT GCCTTTCAAT GGTGAGTTGG TTGTTGTTT CCGCCAAACA 2100  
 CAATCCTCAT CGGGGTCTTT ATGGGAGCT CAAGAAACAG TACATATCAA GCAAGGAGAA 2160  
 ACTTTCGTAT ATAAACCTGT TGTCGAAGGC CCTATACCTG ATGGATCCTA TCGTGGACCC 2220  
 CTCCATGCAT TCGTAAACGG ACAACAACAG TTGTACCTCA AGGGGAAAAG GAACCTACAG 2280  
 GTGAAGATCG TCAATGGTAC AGCCGTAGAA GCAATAGAA CGTCAGAAGA GATCAGAGTA 2340  
 55 TTCCCTAATC CGGCACGCGA TTATGTGGAA ATATCGGCAC CTTGCATTCC CCAAGAAACA 2400  
 TCTATCATTC TTTTCGATCT GTCAGGCAAG ATTGTATGA AGAATAGTTT ATCAGCGGGG 2460  
 CATGGCAGAA TGGATGTAG CCGACTTCCT AATGGGGCCT ACATCCTTAA GGTGGATGGA 2520  
 TATACGACGA AAATAATAT AGTGCAC 2547

(2) INFORMATION FOR SEQ ID NO:44

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 885 base pairs  
 65 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 70 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...885

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

10	ACGAAGAAAA	CACTGATGAA	AAAGCTATTT	CTCTCGCTCA	CGAGTCTTGT	AATGGTCTTC	60
	GCTGTTGCAA	GTTGCGATAT	AATCGACAAG	GATCAAACCC	TCTTGCCGGC	TCCGACCAAT	120
	GTGACACCCG	ATAATCCGGA	TGACAATCCT	TGGGAGATCG	ACATTACGCA	GACGCACACA	180
	GAAAAATATG	TTTTGGCTGA	AGAATTTACC	GGCCAAAAAT	GTCTCAACIG	TCCGAAAGGT	240
	CATCGCAAAC	TGGCGGCTCT	CAAGGAGCAA	TACGGTAAGA	GATTGACTGT	TGTCGGTATA	300
	CATGCCGGCC	CTGGATCTCT	CGTGCCACCT	CTTTCCGTA	CAGAAAGCCG	AGACGCATAT	360
15	TATAGCAAGT	TGCCCAATAA	TACCCCTCTC	CCTGCGCTGA	TGGTTTCGCG	CAAAAAGTTC	420
	GGCTCTTUCT	ACGTTTATGA	TAAGAGCTAC	AAAACGTGGG	ACGTGCCTAT	TGCCGAGCAG	480
	ATGGAGCAAA	AGGCGAAGAT	CAATATCTTT	GCCGTGGCCG	AATACACCGA	TACCCAAAAG	540
	ATCAAGGTGA	CTGTAAAGGG	TAAATACTG	GAGGGGAATA	CACTCCCGAA	GTCCATGGTT	600
	CAGSTGTATC	TGTTGAGGA	TAAGCTGATC	GCTCCGCAGG	TGGATGGCAA	TACGACAGTC	660
20	GAGAAATTACG	AGCACAAATCA	CGTGTTCGGT	GGAGCCGTTA	ATGGTATTTG	GGGCGAAGAA	720
	TTTGTGAATC	TCAAAGATTA	TTTGATATACT	TACGCCGTTG	AACCGCTCTC	GGGTATGTCC	780
	TTCGTAGCCG	AGAATTATTC	GATTGTGGCT	TTTGATATAG	ATGTGCAGAC	GTTCGAAAGTG	840
	TATGACGTTG	TGCATGTAAA	GATCAATCCG	CAATCCGATG	GCAAAA		885

25

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...690

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

50	ACGAATAAAA	AAGAAGAGAC	ANTGAAGAAA	TCAAGTGTAG	TAGCCTCAGT	TTTGGCCGTG	60
	GCTCTCGTGT	TCGCCGGTTG	CGGACTGAAC	AATATGGCAA	AAGGCGGCCT	TATCGGCGCC	120
	GGAGTAGGAG	GTGCCATTGG	TGCCGGAGTA	GGTAACGTAG	CCGGAATAC	GGCTGTCGGT	180
	GCCATCGTCG	GTACTGCAGT	CGGTGGAGCA	GCCGGTGCTC	TCATCGGAAA	GAAGATGGAC	240
	AAGCAGAAAA	AAGAACTGGA	GGCCGCAGTA	CCGATGCTA	CGATTACAGC	AGTAAATGAC	300
	GGAGAGGCTA	TTCTGGTTAC	TTTCGATAGC	GGTATCCTCT	TTGCGACGAA	CTCCAGCACT	360
55	CTGAGTCCCA	ACTCACGCAC	TGCGCTGACG	AAGTTTGCTG	CAAACATGAA	CAAAAACCCG	420
	GACACGGATA	TTCTGTATCGT	AGGCCATACG	GACAATACCG	GCTCCGACAA	GATCAACGAT	480
	CCTCTGTCTG	AGAGACGTGC	AGCCAGCGTA	TATTCTTTCC	TGAATTTCTCA	GGGTGTGAGT	540
	ATGTCCGGCA	TGGCAGCCGA	AGGGCGTGGG	AGCCATGAAC	CGGTTGCAGA	CAATAGCACA	600
	GTTGCCGGAC	GTTCCGGCAA	CCGCCGTGTG	GAGGTTTATA	TCTTGCCGAA	TGCCAAGATG	660
60	ATCGAACAAG	CACAGCAAGG	TACGCTGAAG				690

65

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1026

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

MCAGGAACA	GAAATATGTC	GAAAAAATCG	ATCCTTCTGC	TTTGCTGTTT	GCTGTGCTTC	60
ATTTCTGCTA	CGAAGGCTGT	GACCCCGCTC	AGAAATGTGC	GCAATAGCCA	AGTGAACAGC	120
AAAGCAAAGA	CCGAACGTAC	AAAGOCCTCG	GACTCTGTAC	GGTACATTAG	CAACATGATT	180
GCAGATCGGC	TGGAGTTCCG	CAACAGATT	TCTTCCGAAA	AAGAGGTAAG	AAAAGCCGAA	240
15 TATGAAAATC	GGCTGGCGAT	GGAAGCACTC	AATTACCCTG	CCATAGATT	ATATGGTGAA	300
GATTCCTTGA	GCGAGTATGT	AAACCCCTTC	GTGGGTGCAG	GAACCGATGT	CGAAATTCCG	360
AACTCCTATG	ACATTGATTG	CTCTTCGTTT	GTGATGCCCG	TGGAAGATAA	GCAGGTCACC	420
TCTCAATTTG	GCTACCGTCG	GCGTTTCGGA	CGGATGCACT	ATGGTATTGA	TCTTTCAGTG	480
20 AATCGTGGCG	ATACGATACG	AGCAGCCTTT	GACGGGAAAG	TTCGTGTACG	CAGCTATGAA	540
GCGCGTGGCT	ATGGCTACTA	CATAGTCTTG	CGCCATCCGA	ACGGACTGGA	GACTGTGTAC	600
GGACACATGA	GTGACCAATT	GGTAGACGAG	AATCAGATCG	TTCGAGCAGG	ACAACCGATC	660
GGATTAGGAG	GCAGCACGGG	TGGAAGCACU	GGTCCTCATC	TTCACCTCGA	GACCCGCTTC	720
ATGGGTATTG	CCATCAATCC	GAGTAGCATT	ATAGACTTCG	ATAACGGAGT	GCCGCTCCGA	780
GACATTACA	CATTCAAACG	AGGGAGCAAT	TCTCGCTATG	CAAAAGCCCTC	TAAGACTTCT	840
25 TCTCGCTATG	CAAAAAAAGG	GAAGAAAGGC	AGACAAGCTT	CTTCTCCTAT	GACCTATAGA	900
ATCAAAAAG	GCGATACTTT	GGAAACAATA	GCCAAAAGGC	ACGGCACTTC	TGTTCAGAAA	960
CTCTGTGCTA	CCATGGGCAT	TGGCAAGAGT	AAAAATTTGA	CTCGGGGCAA	AGCCTTGAGG	1020
ATCAAA						1026

30 (2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...477

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

CCGAGCAAAA	CGATAATTAA	GACAATGGCA	AAAATCAATT	TCTATGCTGA	AGGCGTCAGC	60
CTTCCTCGGA	TCAGAAGACG	GATCGTCGGT	AAGTGGATAG	CCGAAGTATG	CAGCCGATAT	120
GGGAAAGCGG	TGGGAGAAAT	CTCCTATCTT	TTCTGTGATG	ACGAATATAT	CCTGAAAGCC	180
AATCAGGAAT	TTCTCGATCA	TGACTACTAC	ACCGACATCA	TCACCTTCGA	TTCTGCGGAA	240
GCGGATACGG	TGAATGGCGA	CCTGCTTATC	AGTCTCGATA	CCGTACGCTC	GAATGCCCGT	300
60 GCTCTTGATC	TTGATACGGA	AGACGAACTG	CATCGTGTCA	TTATCCACGG	CATACTGCAT	360
CTTTCGGGAT	TGAAAGACAA	GAGCAAAAAG	GATGAAGCCC	AAATGCGTGC	AGCCGAAGAG	420
AAAGCCCTTG	TCATGCTGCG	AGAAACCATC	GGATCGGAGC	TTTCCCTATT	GCATACA	477

65 (2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

AAAAATAAAA	CTATGAAGGT	AAAGTACTTA	ATGCTCACAT	TGGTTGGAGC	AATTGCACTG	60
AACGCAAGTG	CACAGGAGAA	TACTGTACCG	GCAACGGGGT	AGTTACCCGC	TAAGAATGTT	120
GCTTTTGCTC	GCAATAAAGC	AGGCAGCAAT	TGGTTTGTA	CACTGCAAGG	CGGTGTTGCA	180
GCGCAGTTCC	TCAATGACAA	CAACAACAAA	GACCTCATGG	ACCGCTTAGG	AGCCATAGGT	240
TCTCTTTCTG	TCGGAAAGTA	TCACAGCCCT	TTCTTTGCAA	CTCGTTTGCA	AAITTAACGGA	300
GGTCAAGCCC	ACACTTTTCT	CGGAAAAAAT	GGCGAACCAAG	AAATCAACAC	CAATTTTGGT	360
GCAGCTCACT	TCGACTTTAT	GTTTGATGTG	GTTAACTACT	TTGCACCATA	TCGCGAAAAAT	420
CGTTTCTTCC	ATTTAATTCC	ATGGGTAGGT	GTTGGCTACC	AACACAAATT	CATCGGTAGC	480
GAATGGAGCA	AAGACAATGT	GGAATCACTG	ACGGCGAATG	TAGGAGTTAT	GATGGGTTTC	540
AGATTAGGAA	AGCGAGTAGA	CTTTGTGATC	GAAGCACAAG	CAGCTCACTC	CAATCTCAAT	600
CTAAGTCGGG	CATACAATGC	CAAGAAAACT	CCCGTATTGG	AAGATCCCGC	AGGACGTTAT	660
TACAATGGAT	TCCAGGGGAT	GGCTACAGCA	GGTCTTAATT	TCGCGCTGGG	AGCCGTAGGC	720
TTCAATGCCA	TTGAHCCCAT	GGACTACGCA	CTTATCAATG	ATCTGAATGG	TCAGATTAACT	780
CGTTTGCGCA	GCGAGGTCGA	AGAACTCTCA	AAACGTCCTG	TATCATGCCC	CGAATGTCCCT	840
GAAGTAATCT	CTGTTACTAA	GACAGAAAAAT	ATACTGACGG	AAAAAGCTGT	ACTGTTCCGT	900
TTGACAGGCC	ACGTTGTGGA	CAAAGATCAA	TTGATCAACC	TGTATGACGT	AGCTCAGTTT	960
GTAAAAGAAA	CTAACGAGCC	GATTACCGTT	GTGGTTATG	CTGATCCTAC	GGGTAACTACT	1020
CAATACACG	AGAAAATGTC	TGAGCGTCGG	GCTAAAGCCG	TTGTTGATGT	TCGACAGGT	1080
AAATATGGTG	TGCCTTCCGA	ATTAACTCT	GTAGAATGGA	AGGGCGACTC	TACGCAACCG	1140
TTACGCAAGA	AAGCTTGGAA	TCGTGTTGTA	ATCGTTGCGT	CCAAG		1185

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

TATAAAATGA	CATACAGAA	TATGAAAGCT	AAATCTTTAT	TATTAGCACT	TGCGGGTCTC	60
GCATSCACAT	TCAGTGCAAC	AGCCCAAGAA	GCTACTACAC	AGAACAAGC	AGGGATGCAC	120
ACCGCATTC	AACGTGATA	GGCCTCCGAT	CATTGGTTCA	TTGACATTGC	AGGTGGAGCA	180
GGTATGGCTC	TCTCGGATG	GAATAATGAT	GTAGACTTTG	TAGATCGTCT	AAGTATCGTT	240
CCTACTTTCC	GTATCGGTAA	ATGGCATGAG	CCTTATTTCC	GTACTCGTCT	CCAATTCACA	300
GGATTGACAA	TCTATGGATT	CCCGCAAGGG	AGCAAGGAGC	GTAAACCACAA	TTACTTTGGA	360
AACGCCACCC	TTGACTTCAT	GTTCGATCTG	ACGAACTATT	TCGGTGTATA	CGTCCCAAT	420
CGTGTCTTCC	ATATCATCCC	ATGGGCAGGT	ATAGGATTGG	GTTATAAATT	CCATAGCGAA	480
AACGCCAATG	GTGAAAAAGT	AGGAAGTAAA	GATGATATGA	CCGGAACAGT	TAATGTCGGT	540
TTGATGCTGA	AAATCCGCGT	ATCAAGACTC	GTAGACTTCA	ATATTGAAGG	ACAAGCTTTT	600
CGCGGAAAGA	TGAATTTAT	CGGGACAAAG	AGAGGAAAAG	CAGACTTCCC	TGTAATGGCT	660
ACAGCAGGTC	TAACTTCAA	CCTTGGCAAG	ACAGAGTGGA	CAGAAATTGT	TCCTATGGAC	720
TATGCTTTGG	TCAATGACCT	GAACAACCAA	ATCAACTCAC	TTGCGGCTCA	AGTGGGAAGAG	780
TTGAGCGGTC	GTCTGTTTC	ATGCCCTGAA	TGCCCTGAGC	CTACACAGCC	TACAGTTACT	840
CGTGTAGTCG	TTGACAAATG	GGTTTACTTC	CGTATCAATA	GTGCAAGAT	TGATCGTAAT	900
CAAGAAATCA	ATGTTTACAA	TACAGCTGAA	TATGCGAAGA	CCAAACAACG	ACCGATCAAG	960
GTAGTAGGTT	ACGCTGACGA	AAAAACCGGT	ACTGCGGCTT	ATAACATGAA	GCTTTCAGAG	1020
CGTGTGCAAA	AAGCGGTAGC	CAAGATGCTT	GAAAGATATG	GTGTTTCTGC	GGATCGCATT	1080
ACAATTGAAT	GGAAGGGGTC	ATCAGAGCAA	ATCTATGAAG	AGAAGCCTTG	GAATCGTATT	1140

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GTAGTAATGA CTGCAGCGGA A

1161

5 (2) INFORMATION FOR SEQ ID NO:50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 585 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...585

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

GTAATTGGCA	TCATTATGGA	ATTTTTCATG	TTATTCATAG	CGGCGGTTT	CGTTAATAAC	60
GTCTGTCTGT	CGCAGTTCCT	CGGTATATGC	CCATTCTTAG	GCGTATCGAA	GAAGGTAGAC	120
ACCTCAATCG	STATGGGTGC	AGCCGTGACA	TTCTGATTGG	CACTGGCTAC	CTTGGTTACC	180
TTCTGATTTC	AGAAGTTCGT	TTGGATCGT	TTGGGATTGG	GCITTATGCA	GACCATTTGCA	240
TTTATTTTGG	TCATTGCCGC	CTTGGTGCG	ATGGTGGAGA	TCATACTCAA	GAAAGTATCT	300
CCTCCCCCT	ATCAGGCACT	GGGTGTATTC	TTGCCCTTGA	TTACGACGAA	CTGCTGTGTG	360
CTCGGTGTGG	CTATTTTGGT	TATCCAGAAG	GATTATACCC	TGCTCCAGAG	CTTCGTCTAT	420
GCAATATCCA	CGGCTATCGG	TTTCACTTGG	GCAATGGTTA	CTTTCGAGG	TATTCGAGAG	480
CAACTCGATA	TGACCAATCT	CCCCAAGCT	ATGAAGGGAA	TACCTTCGGC	ACTCTTGGCT	540
GCCGGTATAT	TGGCTATGGC	TTTCATGGGC	TTTCAGCGGA	TCGCC		585

40 (2) INFORMATION FOR SEQ ID NO:51

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2628

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

TACCGATCTT	ATCGTGGGAT	AGGGAGTGGG	ACACACTCTC	CTAACCTCAA	AAACCGACTA	60
AAAAGGATCG	GAATAAGGAT	ACCGAACAGA	CACTATATCC	ATATCAAGCC	AATCAAACCA	120
AAAAATAAAA	TGAACAACCT	AAACATTATC	AGCTTCATCA	TTGCTTTCCT	ATTCTTAGGA	180
ACGAGCGCAT	CGGCTCAGCA	ATCGGGCGGA	TCCGTTACAG	GTACCGTAGT	GGACAAVAGC	240
TCAAAAGAAC	CTATCGCATA	CGTACAAGTA	TTGTCAAAG	GAACCACTCT	CGGAACCTCC	300
ACGGATGCAA	ACGGAACCTA	CTCGATCAAG	GGAATCCCTT	CGGGTAATCA	AACTATCGTA	360
GCCCGACTCA	TGGGTTACTC	CACCTTGCAG	GAAAAAGTAC	ATATAGAAAA	GGGTGTTTCC	420
CGCCAGTAG	ACCTCTATCT	GACCGAAGAG	ATTCTCTCTC	TCGATGGGGT	AGTGGTATCT	480
GCCAATAGAA	ACGAGACTTT	CGCGCTCAA	GCACCTCTGT	TGGTAACGGT	ACTGTCGCGG	540
GAACTTTTCC	TCAAAACCAA	CTCTACCAAC	CTGAGTCAGG	GACTTAAGTT	CCAGCCCGGT	600
CTGCGCGTGG	AGGACAACTG	TCGAACTGCG	GGTTTCAACC	AAGTTCGTAT	CAATGGACTC	660
GAAGGAGCCT	ATTGCAAAAT	TCTTATCGAC	AGCCATCCCA	TCTTCAGTTC	GCTTGCCGGT	720
GTCTATGGCT	TGGAGCAGAT	GCCTGCCAAT	ATGATCGAAC	GTGTAGAAGT	AATTGCGGGT	780
GGAGGTTCCG	CTCTGTTCCG	CTCTAATGCT	GTGGGAGGCG	TTATCAACGT	AATTACGAAA	840

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5 GAACCGCTTC GCAATTCCGGC CGAGATCAGC CATTCTACGA TGACCTTCGA CCACGCGAAA 900  
 GGGTGGGGGA GCTTCCAAAA TACGACCCAG TTCAACGGTT CTATGCTGAC GGAAGACCGC 960  
 AAAGCCGGTG TCATGGTATT CGGCCAACAC AACTACCGTC CCGGACAGGA TATAGACGGC 1020  
 GACAACTTTA CCGAACTACC CAATCTGCGC AACCGCTCGC TCGGTTTCGG CTCATACTAT 1080  
 AAGACCGGTC TCTACAGCAA AGCAACCGTC GAATATCACA GCATGCAGGA GTACCGTCGT 1140  
 GGTGGCGACA GACTGGACAA TCCTCCTTTC GAAGCCGAGA TAGCGGAATA TCTCCAGCAC 1200  
 TATATCAATG GCGGAAGTTT CAAATTCGAT CAGGGCTTCA GCGGTGGCAA GGATTTCTTC 1260  
 AGTCTGTATG CTTACGACACA AGACGTTTCA CGTCGTAGCT ACTACGGGGG TGGCGACTAT 1320  
 ACCGAAAAATC TGTGTAACGG AGCAGTTTCA AGTGGGAAGCA CCGAATCGGA CGAATACAAC 1380  
 10 GATGCTTTCA CGGCTCTTAC TTCTACGGG ACTACCAAGG GATTCGATTT GCAAGGAGGA 1440  
 GGTATGTACC GTCATACCTT CGGAGAAAAC TGGGACTTTA CCGGCGGACT CGAATATATC 1500  
 TACCGCCAAC TCGATGACAG AAGCGGCTAC AGACCGAGCA AAATAGATCA GAATACCTCT 1560  
 ACTTTTATGC AGTACGACCA GCTCGAATAT AAGACGGAGA AGTTAAGTGC CCTTATCGGA 1620  
 GCACGTATCG ACTATGTTCT CCTCAATCAG GATGGCAAAC GCTATATCGA TCCGCTCTTC 1680  
 15 ATTTTCAGTC CTAGAGCCAA CGTACGATAC AATCCCAATA AGAATCTCAG CTTCCGACTC 1740  
 TCATACAGCG AAGGATTCCG CGCTCCTCAG TATTTGATG AAGATCTGCA CGTAGAGTTG 1800  
 GCAGGTGGTA CTCCTATCAG CCGTGTCTTT TCCCCCAATC TGAAAGAAGA ACGTTACGGA 1860  
 AGCATCAGTG CTCTTTTCGA TATATACCA AGAGCCGACG AATGGCAATT CAATATCATG 1920  
 GGAGAAGCCT TCTCCACCTT TATCAGCAAT CAGTTCAAAC CATOCGATAA GGTGGAACC 1980  
 20 ACGAGCGATG GCAAGAATG GATCATTCTG ACCATCTACA ACGACAAGGA TGGAGTATCG 2040  
 AAGGTATATG GTGTGAATCT GGAGGGAGA ATGCGCTACA ACAATCTGTT CGACCTCCAG 2100  
 CTGCGCGGTA CATGGCAGAG AAGCGGCTAC GGAAGCATCT ATACCGCTGT GGAAGCGGAC 2160  
 AAAACAACGG GACAAGCCGA GATCTCTGTG AAGAGCTATG TACGCACTCC GAATCTGTAC 2220  
 GGCTATTTCG TTGCTACGGT ACCTCTTACC GAGCACTTCG CCATCAATCT CTCGGTACA 2280  
 25 TTCACGGGCA AATGGATGT AGTACACGAA GCCTATGAAG GCGATATTCC CGCAGAACAC 2340  
 ATAGCTCCGG ACGGATCGTT CGACTTTGAA ATGAATGGTC AGCAATTCAG AGGTTTGGCC 2400  
 GAAGGTCATG CCAAGCTCGT CAAGACTCCG GCCTTCGCGG ATATAGACCT CAAGCTGAGC 2460  
 CACGACTTCC ACCTTGCTTC CACTATGACC TTGGAATTGA ATGCGGGAAT ACAGAACATA 2520  
 30 TTCAACAGCT ATCAGAAAAG CACGGACAAG GGACCGGGA GAGCTTCTAC TTACGTATAC 2580  
 GGTCTATGCG AGCCAGAAAG GATTTTCTG GGTACAAAGA TCAATTC 2628

## (2) INFORMATION FOR SEQ ID NO:52

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2697 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 40 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 45 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2697  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

55 ATATTGAATC ATTTGAGAAA GACTATGTAC AAAAAGATTA TTGCCGTAGC AGCTCTCTTC 60  
 TCGCGCCAGCA TAGGGATCCT GAAAGGACAG TCCTCGGATC TGACCCCTCA GGATACTATA 120  
 TATAGCCCTG AAATATCCTA TGCCAAGCCT ATTCATAAGA CCATAGCATC TATTGAGATC 180  
 GAGGGAATGA CGTCTTTCGA TGACTTTGTC TTGCGCAATC TTTGAGGCTT GGTGTAGGT 240  
 60 GATGAAGTCC TGATTCTCTG AGATGCCATG TCTGCTGCCG TGAATAGAAT TATGCGTCAG 300  
 GGCTACTTCT CAAATGTGCG AATCATCGCG GATAAATATG TCGGCAATAA AGTCTATCTG 360  
 AAAATCATTG TCACTGAACG TCCTCGCATC AGTAAGGTTA CTTTACGCG GGTAAAGAAG 420  
 TCTGAGAGAG AAGATCTTGA AATGAAAATC GGTCTTCGCG AGGGGATTCA GATGACCGA 480  
 AATATGTAAG ACAAGGTCAG GCAAATCGTA CAGAAGTATT TTAGTGAGAA AGGTTATCGC 540  
 65 GATGCCAGCA TACGGATAAC GCAGGAACCG GATCTTTCCA AAGATGGCTT TGTCAATGTG 600  
 CTTATCTCGA TTGAGAAGAA AAGCAAAACC AAGGTGAATG AATTTTATTT TTCGGGCAAC 660  
 AAGGCGCCTTA GCAATCATAA GCTAAGAATG GCGATGAAGA ACACCAATGC CAAATTCAGT 720  
 CTTAGAAACG ATATTGCTC ATCTTTCTTG AAATTTTITA GTACTCATAA GTTTGTGGAA 780  
 GAGAGCTACC GTGAAGATTT GGTCCGATTG ATAGAGAAGT ATCAGGAATA TGGATATCGT 840  
 70 GATGCTGAAA TACTGACCGA CAGTGTCGTG AAGGCTCCTG ACGGCAAAAG AGTGGATATT 900  
 TATCTCAACA TCGAAGAGGG GCAGAAGTAT TATATTAAAG ATGTCAACTT TGTGGGCAAT 960  
 TCACATATC CATCGGAGTA TTTGGAACGA GTGCTCGGAA TAAATCCGG AGATGTGTAC 1020  
 AATCAGAGAC GATTGGCTAA CGGTCTCAAT GAAGATGAAG ATGCTGTGGG GAACCTGTAC 1080  
 75 TATAACATG GCTATATTTT TGCTGGGTG GATCCCGTGG AAACAATGT AGTGGGGAT 1140  
 TCTGTTTCGC TTGATATTCG TATAGCGGAG GGAAGGACGG CCAATATCAA TAAGGTGATC 1200

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	ATCAAAGGAA	ATACTGTCGT	GTACGAAGAC	GTAGTACGCC	GAGAGCTTTA	CACAAAGCCC	1260
	GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AACTCTATT	GTCTCATCAA	TCAGCTTGGG	1320
	CATTTTCGATG	CCGAAAATC	TATTCCTCGT	CCGATTCCCA	ATCCCGAAAC	AGGAACAGTG	1380
	GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTTC	TGTCGGTTGG	1440
5	AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAACTTCTC	TGTCGGCAAC	1500
	TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GCAAACACTA	1560
	TCACTGAGTG	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTAC	ATTTATGGAT	1620
	CCATGGTTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTTCA	GTGCATTCTA	TTCCAAGACT	1680
	ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCTACTAT	1740
10	AATAGTACT	ACAACAATA	TAATAGTTAT	TACAACGGTA	TGTCGAATA	TACCGGCGAC	1800
	CTCTATACTC	AGGCCAGCGA	TCCGATCGT	TCCCTTCAGA	TGTTAGGTAC	TTCGATCGGT	1860
	TACGGTAAGC	GTITGACTTG	GCCGGACAAT	TGGTTCAGA	TITTACTTTC	TCTGAACACT	1920
	ACCTAGTATA	GACTGCGAAA	TTGGAGCTAC	AATACCTTCC	AAAAATTTCCA	TCATGGCTCG	1980
	GCTAATGATC	TCAACTTGGG	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTTAT	2040
15	ACCAGAAGCG	GATCGGATTT	CATGGTTTCT	GTGCTGCTA	CTCTTCCTTA	TTCTTTGTGG	2100
	GACAATCATG	ACTATGCCAG	CCAGAACCTC	AGCGTAAGCG	ATCGTTACAG	ATTTATCGAG	2160
	TATCACAAGT	GGAAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTAGGCAT	2220
	AAATATACAC	CGGTGCTCAT	GAGTCGAGTG	GAAGGAGCAG	TTCTTGTTTC	GTATTAATCC	2280
	AAATAAGAAAT	CTCCTTTTCG	TACTTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
20	GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CCTGGTTATA	AGAACGGATC	TATTGCCGCT	2400
	AATAACTACG	ACTATGCATA	TGCTTATATG	CGGCTTACGA	TGGAACTACG	TTTCCCGATT	2460
	CTGTTTGAAG	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTTG	CCGAAGCAGG	CAATGCGTGG	2520
	CGCAGTATCG	ACAATTATAA	TCCCTTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
	GTACCGTTAC	CGATGGTCCG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
25	GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTTC	2697

## (2) INFORMATION FOR SEQ ID NO:53

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 531 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...531

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

50	CAAATAAACA	TGAATGGCGA	TATGAAACGG	TTTTGATT	TGATCGGCTT	TGCACTGGCG	60
	GTAGCTTTCT	COGGTTTTTC	CCAAAAGTTC	GCTTTGGTAG	ATATGGAATA	TATCCTCAGG	120
	AATATTCCTG	ACTATGAGAT	GATGAACGAA	CAGCTGGAAC	AGGTGTCCAA	GAAATGGCAA	180
	AATGAAATCG	AAGCTCTCGA	AAATGAAGCC	CAATCTATGT	ATAAGAAGTA	TCAGAGCGAT	240
55	CTCGTATTCT	TGTCTGCTGC	ACAGAAGAAA	ACCCAAGAAG	AGGGTATCGT	AAAGAAGAG	300
	CAGCAAGCAT	CCGAGCTCAA	GCGGAAGTAT	TTCGGCCCGG	AGGGGGAGCT	GTATAAGAAA	360
	CGTCCGATC	TGATGAAGCC	TATTCAGGAT	GAGATTGGGA	ATGCTATCAA	AGAGATTGCC	420
	AAGCGTAACA	ACTATCAGAT	GGTGCTTGAT	AGAGGTACGT	CCGGAATTAT	CTTGCCAGT	480
60	CCGTCTATTG	ACATTAGCGA	CCTTGTAATG	AGCAAGATGG	GCTTTAGCAA	G	531

## (2) INFORMATION FOR SEQ ID NO:54

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 510 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

10	CGAATAAATA AACAAACACGA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT	60
	TTGAGCCTCT TGGCACAAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG	120
	CCGGAACAAAG TAGCTGCTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT	180
	CTCAAGAGTA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTTGTAAA GGAAGAAAGAC	240
15	TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACTCGT	300
	TATCAGCAGT CATACCAAAC GATGCAGGAG GATTTGCAA AGCGCCAACA ACAGCTTTT	360
	GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAACGTG	420
	GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGCTAT TGACTTGACC	480
	GCAAAGGTAA AAGCGAAACT CGGAATCAAG	510

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2484 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

45	ATCATGAAGG AAGCTATTCC CCGAAGAAGC AAGTATATAA AGCTCAACGG TATATACAGA	60
	TTGTGATTCA TTCTGCTATG CTGCCCTGCTA TGCTCTCAGG CAGCTATGGC ACAAGGCGTC	120
	AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAGAGCCGA TCCCGTTCCG CCGAGTCAAA	180
	GTGCGTGGTA CGGGGACAGG CGCAACGACG AATCTGAAAG GATACTACGA GTTTCGGATG	240
	AAGGCCACGA CCGGACAGCAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAGT	300
50	CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCGGAG	360
	ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAACGCA GACTCAACAC GATGGAGCCG	420
	GTCAATACCC GAGACCTTCG TGTCAATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC	480
	GGAAGCTACG CAGGAGTAAC GCAGAACAAT GAACCTAAGCT CGCAATACTC GGTTCGCGGA	540
	AGTACCTACG ATGAGAATAT GGTCTATGTA AACGAGTGG AGGTTTATCG CCGCTGCTG	600
55	GTTGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA	660
	CAGTTCTCCG CCGGAGGGTT CACGGCCGAC TATGGCGACA AGATGTCCTC CGTACTGGAT	720
	ATTGCTACA AGCAACCGCA GGAGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACATCG	780
	AGTGCCAAAT CGCTCTTGGG CACTACGGAC ACGAAAGCCG AATACGATCC GATCTATGCG	840
60	GACGGACAGA CATTCATGAC GTACCGTTTC AGCCCCAAGC TGTGCGTTAG TTTCTCGGC	900
	AATATTTGCG AATCTCGCTA CAAGTTTGTC CCTCAGACCC GTGAGACGAG CTTCGGTACA	960
	CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAAGA TCGTTTCCTG	1020
	ACCTACTTCG GTGCTTCAG CATGAATTC GTGCCGACG ACAAACAGCG GCATACGGTT	1080
	ACGCTTTCCG CCTTCAACAG TAACGAACCG GAGACCTACG ATATTGAGG AGAATACTTT	1140
65	CTGAACGATG TGCAGCTGGG GCGGACGGA ACTGCTTCCA TGGCTTCGGG CTCAGAGAAC	1200
	TCCAACGGCT TGGGCATCGG GCGCAATCAC GAGCATGCCG GCAACAGGCT GAGCTACCGC	1260
	GTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CCTGCAAGCC	1320
	GGCGTATCGG CACAGATGGA GAAATAGCC GACCATATCA CGGAATGGGA ACGGAGGGAT	1380
	TCGGTAGCAT ACAACCTACC TCACTCGGAG ACCGTATTGC TGATGTACAA TAACCTATAT	1440
70	CGCGATACCG AGATGAGGGG AACCGCGCTG TCGGCATTTC TACAGGATCG ATTCAACTTC	1500
	AGCATGGGAG GAGGTACATT TTCTCTCAT CCGGGTATCA GAGCTTCGTG GTGGAGCTTC	1560
	AACNAGGAGT TGCTCGTCAG CCCACGATC AGCGTGGGTT ATTCTCCGGA AAGCAACCCG	1620
	GCTTTGGTAC TGCGTGACGC CGCCGGAATT TATTATCAGG CACCGTTTTC CAAAGAGCTA	1680
	AGGCAGACGC ATAAGGATGC CGAAGGCAAT AACGTGGTTG TCCTCAACGA GATAGTCCGC	1740
75	TCTCAGGAG CTTTTACAT TCTCGCAGGA GCAGACTATA CCTTCGAAAT GGGGGGCGA	1800
	AAATACAAGT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCCGTATATA	1860
		1920

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5 ATAGAGAACG TGAAGATCCG CTATCTGGGC GAAACATCG GTTCGGGTTA TGCTGCGGGT 1980  
 ATCGATCTCA AGCTCTTCGG CGAACTGGTA CCCGGAGTGG ATTCGTGGCT GACGGGCTTCC 2040  
 ATTATAAAG CCCGTCAGAA ACTGGATGGC TACGGTTCTT TACCACTGAT GAACGCACCC 2100  
 ACTTACAATT TCTCCTTCTT CCTTCAGGAG TACGTGCCGG GCAATAAACG CATCACAGCC 2160  
 ACCCTGCGGG CTGCACTAAG CGGAGGATTG CCCAGCTCA ATCCGAGCAA AGGGCTTAGC 2220  
 TCGCCGGCCT TTACCGCACC GGCCTATAAG CGTGTGATC TGGGGGTAAT GTACAAATGG 2280  
 CTGACCCGG ATGACTCCTT TGCCGGCCGA AGCAAATGGC TAATGGGAGT AAAAGGGGCC 2340  
 TACATAGGG CTGACCTCTT CAATCTGTTC GACATGACCA ACSTCAATTC TTACTACTGG 2400  
 10 GTGTCGGATG CCTACCAACA GCAATACGCC GTACCGAACT ACCTGACACG CCGCCAATTC 2460  
 AACCTGCGTC TCCTCGTCGA ATTC 2484

## (2) INFORMATION FOR SEQ ID NO:56

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2037

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

35 CCTATCCCTT TTCTTCTTAA TATGTACAGC GGACATCATA AAATCCATTA TCCTTTTCTT 60  
 ATCCTGTTGG TATGCCTTGC TTTTGCTGCC TGCAAGAGCG TGAAGTTGAA AGATGCGGAG 120  
 AAGGCACATG ATCGCCAAGA GTATACCAAG GCTGCCGATA TGTACAATAC ATTATACAGG 180  
 CGTACCCGAC GAAAGCAGGT GGAGATGAAA GCTTATACGG CTTCGGATC CGGTGAAAAC 240  
 40 TATCGTGCAG CCGGCAGACA AGCCAAAGCT TTGCGTGGCT ATCTGAATGC CAGACGCTAC 300  
 GGGTATCCGG ATTCTGTGGT ACTGCTCCGT TTGGCACAGA CTTATCAGCA AGGAGGTAAC 360  
 TATAAGGAAG CCGAGGTACT CTTCCGTGGA TATCTGGAAG CTTATCCGAA AAGTTATTTT 420  
 GCAGCTATCG GTTTGGAGGG GTGTCTCTTT GCCCGCCAGC AAAAGGAATA TCCTACACGT 480  
 TACCGGATAC GCGAGCTGCG CGAGTGGAA TCGGCACGGG GCGACTTCGG CCCGCCCTAT 540  
 45 GCACCCGATG CTTCCGCTCT CTATTTCACA TCGAGCAGAA GCAAAGACGA CGGTTTGGAT 600  
 AATAGCAGCA TAACGGGACT GAAACCCAAC GACATTATA TCATCAACG AGATGCACAA 660  
 GGACGATGGG GACGTCCCGA TAGCGTGTCC GGAGGAATCA ACACCTCATG GGATGAAGGC 720  
 GTGCCAACGA TCACGCCCGA TGGTAGTACC ATATATTATA CGTTGGCGCA GCAAGGAGCC 780  
 GATTACGACC GTACGGTACA GATCTATTCC GCGCTCGGA GCGGAGAAGG CGGTTGGAGC 840  
 50 AACGGTTCG TCGTGGACAT TATGCGGAT TCGCTCCGTA TGGCTGCTCA TCCCTCTATG 900  
 TCGGCATCCG GCGATTACCT GTATTTCGTC AGCAATATAG GCGGTAGCTA TGGCGGCAAG 960  
 GATATTTATC GTGTCAAGGT GTCGGATCGT TCTTATGGTT CACCGGAGAA TTTGGGGCCT 1020  
 GATATCAATA CCGCGGGGGA CGAAATGTTT CCCTTCATAG ATGGGGATAG TACCCTTTTC 1080  
 TTGCGTTCGG ACGGACACGC CGGTCTGGGA GGACTGGATA TTTTCAAAGC CACGCTGGAC 1140  
 55 TCTACCGGCC AATGGCATGT AGTCAATATG GGACAACCGG TCAATTCCTC TGCCGATGAT 1200  
 TTCGGCTTGG CTGTGGAGCC TAAAGGCAAA AACAAAGAAG AAGCTTTGCC GGACAACGGA 1260  
 GTCAAAGGTG TATTTTGTTC CAACCGAGGC GATGCACGCG GATGGCCGCA CCTCTCCAT 1320  
 TTCGAACTGC CCGCTATCTA CACCGAGATT CAAGGTTATG TGATGGACAG AGAAGAAAAT 1380  
 CCCATAGCCG GAGCCACTGT CAGGATCGTA GCGGAACGCG GCCCGTAGG ACAGGGATTG 1440  
 60 GTGACTACTC GTGACGATGG CTCCTATAAG ATGAGCGTGC AGGGCGATAC TCGCTATGTA 1500  
 ATGCTTGCCG GAGCATCGGG TTATTGTAAT CAGTACGTAG AACTCAAGAC CGATACCGCC 1560  
 AAGCAGAGTG AGACCTACTA TGTGGACTTT TTCTTGCAT CGCGTGAGAA AGCCGAGGGC 1620  
 TTGCAAAATA TTTTCTATGA TTTCGATAAA GCTACTCTTC GCCCGGAAAG CATGAAGAGC 1680  
 TTGGACGAAC TGATTCTGAT CCTCACGGAC AATCCGATA TFCGATCGA ATTGGGTTG 1740  
 65 CATGCGGACA GGAAAGGCCG CGATGCTTAC AACCTCGGAC TATCTGACCG CAGAGCCAAA 1800  
 TCCGTGGTGG ATTACCTCAC GAGTCGTGGC ATAGCGSCCG ACAGGCTTAC GTGGAAAGGC 1860  
 TACGGTAAAT CTGTCCCCAA GACGGTGACA GCCAAAATTG CCGAACGGCA CGATTTCCTG 1920  
 AAGGAAGGCG ATGTGCTCAC CGAGGAATTC GTAGCACCTT TGACCGAGGA GCAGCAGTCA 1980  
 70 GTCTGCGACC AACTGAACCG TCGTACCGAG TTCCGTGTGA TCGAAGAAGA GTTGCCT 2037

## (2) INFORMATION FOR SEQ ID NO:57

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2316 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2316  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57  
20 CCTGCACAGC CGAAAACATA TTGCATACGA TACTTTCGGA GAGAGGTATC TCCGAGGAGG 60  
CAAAACAGAAA GGACATTGTA TCGCGACAAG ATGCGCCGGC ATATCGTCAA GTGCTGTCCC 120  
TCTGCTCCCA TACTCTTGCA AGAATACTCC ACAACAGAAT TATTCATTCA TCACTTTAAC 180  
ATATCAATTA TTATGAAAAA GTTTTCTTC GCGCTACTAT CGATTGGTAT TTCAGCGCAG 240  
GCTTTTGCCA AGACGGACAA CGTCCCGACA GATTGCTAC GAGTACACAA TCTTCAGACC 300  
25 GTCACGGTCT ATTCTACAGC CACGGCCGTA CTTCTGAAA AGATACGGC CAAGATGGAA 360  
CTCATCTCAT CGCGCAACAT CAAGCACTCC GCGTTTAA CAATGACCGA CATCCTCAAG 420  
ACGCAAAATT CGCTCGATGT CATACAATAC CCGGGCTTTA GTTCGAACAT CGGTATCCGC 480  
GGTTTCAAGC COTCCGGCAA GTATGTAACC GTATTGGTAA ACGGCATCCC TCGGGGAACG 540  
GACAAATCTT CTACGCTCAA CACGAGCAAC ATCGAACAAA TCGAGATCCT CAAGGGCCCG 600  
30 TTCTCTTCCA TCTACGGCAC CAATGCCATG GCGGTGTGG TGAACATCAT CACCCACAAA 660  
TCCAAGGACA AGATCCATGG CAACGTTTCT CTCTTCGGCG GTAGCTACCA GACCATGGCC 720  
GGATCATTCA ACTTGGGTGG CCGCTTCGAG GATATTTCT CATTCGATCT TAGTCTGGGC 780  
TTGGACAAGC AGAACAAAGG ATATAAGACC GGATCAAA CAATTCTATC CTTGAGCAAA 840  
CTGAAGAAG CTATAGTAGA TGTAAATGCT ACCAAAAACA AGAAATGAA GGGGAGCGAC 900  
35 TATACTGTAG CAACGGGACG TCTGCGTTTC GGTATCGACT TCACGCCCGA ATGGTCGCTG 960  
AATCTGTATC AAAACGTAAT CCTCGGAGAT GCGATCCCG TAGGAGGATC TATATGGGGC 1020  
GTTTACGGAG AATCCAAAAA AATCTGAAT CGTTCTTCA CCTCTTCA GCTGCTCGGC 1080  
AAACATGGCT GCCACACGCT TCATTTCTCC CCTACTTCA ACATAGAGAA ATCGGAGAAC 1140  
TATAACAATG CCGATCCAC CCGTTTCACT AACTACAAAA GCGACTACTA CACCTATGGT 1200  
40 GCGCTACTCC AGGACAAGAT TTCTTTGGA GGACAAAAA TCGTACTCGG TGTCGACAGC 1260  
CGAAACATGA CGATGGAGTC AGAAAGATTC GAGCAGGCAG GAGTGAATAC AAAGCCATAC 1320  
AACCCCGGAT ATGCCACGAA CAATATCGGT TTGTTGGGAC AGGCCAATTT CTACCTGCTG 1380  
AACGATGCTC TATCGATATC TGCCGGTGCA CGTGCCGACT TCATGTTCTT TGACCTGAAA 1440  
45 GCGAAGAGT ATCTCAACAA TGAAGCCAAA CAGGAAACTC ATAACGTAAT CAATCCGAAT 1500  
GTGGGAATCA AATATGAGTT TGTGAAAGGC CTTACAGCTC ATGGTACATT CGGTAGTGCA 1560  
TTCAATGCTC CCGATGCTTT CCAAAVAGCA GGCCAATACG TAGGCCCGTT CGGCACGACC 1620  
TATAGGAATC CTGACCTGAA ACCCGAAAAG TCCATGACCT GGGACTTCGG TATCGGATAC 1680  
AGCAATGCAC GCTGCGGGAT CCAAGCCGAC GTAACTTAA CCTATTTC CAACGACCAC 1740  
AAGATCTGA TCTGTCCAG CCTGACTAT GCTAATAATA TCACCACATA CATCAATGCC 1800  
50 GACAAGGCTC GTATGAGCGG TATCGAGGCC CTTTGTCTT ATGACTTCGG CAGCCTCTTT 1860  
GCCAACAAAT TCTCTCTCCG CGCATTTCGG AATGCCACGA TCATGCTCAA TTCGGAGATG 1920  
AAGAAAAGCC AGACCGATGC CCTTGGAGC GAAATGACT ACGTTCGCAA GCAGAACATC 1980  
ACCTTCGGTA TCGAATATCG TGGCAAAGAA GGACTTGAA TGATGCTCAA CCGTCGCTTC 2040  
ATGGGACGCA GGATCGAGCA AAAGTGGTAT GCTTACTACC CCGAAGTTCG CCGCGAACTC 2100  
55 CAGCAACTGC TTGCAGCAGA AGAGCCTGAA TTGGCTGCTC AGGGACTGCT CCGTCATCCG 2160  
CAGCAATGG TGTCAATGC CTCTGCTTAC TACCACATGA ACAAGTATCT CACCTTCGGT 2220  
GTGAACCTGA ACAACATCTT GGATGAGCTT TATACGGAGA AAGACGGCTA CCACATGCCG 2280  
GGACGTAA CAATGGGTAA GGTATGGTC AACTTC 2316

60 (2) INFORMATION FOR SEQ ID NO:58  
(i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 1452 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
70 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
75 (vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

39 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

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10  GGGCGGGCCT CTTCCCTTA CAGGCAAATG GATGGCATAC TAAACGATGA ATATAGACAA      60
    GCATCTATGA ACAGGTTTTC AAATCATTGG CCTGCATCC TCGTGGGGTT TGTACTCTGG      120
    TTTGTATCGG CGAGTCGGAC TGTGGCACAA AACGCCTCCG AAACGACGGT ATCGTACGAT      180
    ACGGATACCG CCGTACTCTC CGAAGCGGAT GTGCTTCGSA TCGCTCTTAG TGAGAATGCC      240
    ACAGTGAAAG TGGCCGATAI GGATGTGCGC AATACAGGAAT ATGCACGTAG GGCAGCACGT      300
    GCGGATCTCT TCCCGAAAGT AGACCTCAAT GGCCTTTACA GCCATACGCT AAAGAAGCAG      360
15  GTCTTATATA TAGATATGCC CGGTTTCAGC AGTAGCGAAG GTATCGAAAT GGGGCGGTACA      420
    CACAATACGC AAGGAGGGGT GAACGTCTCC ATGCCATTGG TGTCGGCACA GCTTTGGAAA      480
    AGCATTGCCA TGACUGGAGA ACAGCTCGAT CTGGCTCTGG AGAAAGCTCG CAGTCCCGA      540
    ATCGATTGGG TGGCAGAGGT GAAGAAGGCT TACCTCAGTG TATTGTTGGC CGAGGACTCT      600
    TATGGCGTAT TCAAGCGCAG CTATGACAAT GCTCTGGCCA ATTATAAGAA CATATCCGAC      660
20  AAGTTTCGATC GTGGACTTGT GGCCGAGTAT GATAAGATTC GAGCCAATGT ACAGGTACGC      720
    AACATCGAGC CTAACCTCTT GCAAGCGCAG AACTCCGTAG CCCTTGCTCT CTGGCAGCTC      780
    AAGGTCCTGA TGAGCATGGA AGTGGAAACT CCGATCAGAC TCTCCGGTTC ATTGTCCGAC      840
    TATAAAGAAC AAGTCTATAC CGGCTATTTT GCGGCCGATA CGCTTATTTC CAACAACCTCC      900
    TCCCTGCGTC AGCTCGATAT ACAGCGTCGT CTGGCTGTCA GTGCAGACAA GCTGAACAAG      960
25  TACAGCTTCC TGCCCTACACT CAATCTGGGA GGGCAGTACA CCTATTGCT CAACAGCAAC      1020
    GACATCAVAT TCTGGGGCGA GGGACAACGC TGGAGCCCTT TCTCCACCAT ATCGCTCAGC      1080
    CTGTACATTC CTATATTCAA TGGAGGCAAA CGTCTGTACA ACGTGAAGCA AAGTGCTTTA      1140
    TCGATCCGTC AGATCGATCT GCAACGACGC CACATAGAGC AATCCATCCG AATGGGAATC      1200
30  AAGAACCAAA ATGACCGTCT GCGTACCTGT ATGCAGAGAT TTGTGGCCTC GGAAGAGGCT      1260
    GTCCGAAGTG CAGAAAAGGG CTATCAGATA GCAGAGAAAC GCTATCAGAC AGGCGAAGGC      1320
    ACTCTCGTCG ACCTCAACGA TGCCGATGTG GCTCTTTTGC AGGCTCGACT CAATTATAAT      1380
    CAGGCCATAT TCGACTTTAT GACCGCAAGG GCCGAATTGG ACAAGATGAA CGGCATGGGG      1440
    ATTCGCGAAC AA
1452

```

(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

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60  TTTCATAACT TTGACTTCCT AAACGCTATA AAATTGTTT CGATGGCAAA TAATACTCTT      60
    TTGGCGAAGA CTGACGTTA TGTCTGCCTT GTCGGTTTCT GTTGGCTCAT GGCATGATG      120
    CACCTCTCTG GGCAGGAAGT CACTATGTGG GGGGACAGCC ATGGAGTGGC GCCGAACCAA      180
    GTGCGCGGAA CGCTGGTGAA GGTAGCCTTA AGTGAATCCC TTCTCCGGG TGCAAAACAG      240
    ATTCTGATCG GATTCTCTCT TCCGAAAGAA ACGSAGGAAA AAGTCACCGC CCTATATCTC      300
    CTGTGTAGTG ATTCTTTAGC GGTGCGCGAC TTGCCGGACT ACAAGGGCG AGTCTCTTAC      360
65  GATAGCTTCC CGATCTCAA GGAAGATCGT ACCACAGCCC TTTCTGCGGA TTCGGTAGCC      420
    CGACGCGCGT TCTTTTATT GGCTGCGGAT ATAGGGCCTG TTGCTTCTTT TTCCCGATCC      480
    GATACGCTGA CTGCCCGTGT GGAAGAGGTG GCTGTGATG GCGGCCCTTT GCGTTGAAA      540
    GAGCTGTGCG CTGCCCTCCG TCGTCTGTAT AGGGGGTATG AGGCCCTCTT TGTACCCGGT      600
    ATAGCGATGG CCGGGAACCTA TCGTATCCCG GCCATTTTGA AAACGGCTAA TGGAACTAC      660
70  GTCATGCGGC GCAGTACGGA CGGAGGGAAA TCGTGGAGCG ATCCCAGGAT TATCGTACAG      720
    GGAGAGGGGC GCAATCATGG CTTTGGCGAT GTAGCCCTGG TGCAAAACCA AGCAGGAAG      840
    CTCCTGATGA TCTTTGTGCG TGGAGTAGGC CTGTGGCAGT CTACCCCGA TCGTCTCAG      900
    CGCACTTATA TATCGGAAAG TCGGGACGAA GGAAGTACTT GGTGCGCTCC TCGGGATATA      960
75  ACCCATTTCA TCTTCGGCAA GGATTGTGCC GATCGGGGAC GCACTGCTG GTTGGCTCTC      1020

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SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

40 / 490

TTTTGTGCTT CGGGACAAGG GCTTGTGCTG CCATCCGGTC GTATCACGTT TGTGGCTGCC 1080  
 ATCCGCGAAT CAGGGCAGGA GTACGTCCTG AACAACTATG TCCTCTATAG CGACGATGAG 1140  
 GGCGATACAT GGCAGCTTTC CGACTGTGCA TACCGCCGTG GCGATGAGGC AAAGCTTTC 1200  
 TTGATGCCCG ATGCCAGGGT ACTGATGAGC ATACGCAATC AGGAGCGGCA GGAGAGCCGA 1260  
 5 CAGCGTTTCT TCGCTCTCTC CTCGACGAT GGCCTTACTT GGGAGAGAGC CAAGCAGTTC 1320  
 GAGGCGATCC ATGACCCCGG CTGTAATGGA GCTATGCTTC AAGTGAAAAG GAACGGAAGG 1380  
 GATCAAGTGC TGCACCTCCCT GCCTCTCGGC CCGGATGGGC GTCCGATGG AGCTGTCTAT 1440  
 CTCTTCGATC ATGTCTCCGG CCGCTGGTCC GCTCCCGTTG TTGTCAATTC AGGATCGAGT 1500  
 GCCTACTCGG ATATGACTCT GCTGGCGGAT GGAACGATCG GTTATTTTGT CGAAGAGGGC 1560  
 10 GATGAGATCT CATTGGTTTT CATTCCGGTC GTCCTTGAGC ATCTCTTCCA TGTCCGGCAA 1620

## (2) INFORMATION FOR SEQ ID NO:60

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...879

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

35 AAGTCTCGGA GCGATTCCGGC TTGCGGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC 60  
 GTCGGTGGGA AACGCATTAC TTGCTTATC CTGTATTCTA TGGCGATAAG AAGTAGTAAT 120  
 ATAGAATCAA TACAGTGCTT TGTGATGAAA AAAGAAAAAC TTGGATTGCG GATCGTCGCC 180  
 GGTTTGGCTT TCGTATTGGG CCTTTATGCT CTGCGCCGCA GTGTGCTCA GCTACGCCGC 240  
 40 TCTCAGCTT CGGTGACTGT GACCGGTATG GCGAGCGSTA ATTTCAAATC CGATCTGATC 300  
 GTTTGGACTG CTTCGTACCA GCTCCAGATG ATGGATCTCG AATCGGCCTA CAAGGCTTTG 360  
 AAGGAAAAAC AGATATTGGT AGCAGACTAT TTGAAAAACA AGCAGCTGCC CGATTGCTCT 420  
 TATATCTTCT CAAGCGTAGC CATCTCTAAA GAATACAACT ACTATTACGA TCCTCGGCAG 480  
 GAACAAAACG TCAGGACCTT TGCCGGGTAT CTGCTCAGCC AGACAGTTAC GGTGACCTCA 540  
 45 CAGGACATCG AACATGTGGA GAAATATCT CGCGATATAA CGGAGCTGAT CAATCAGGGG 600  
 GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTC 660  
 GAGATGCTGC GCAATGCCTC CGAAGACGCT TTCAATCGTG CTTCGGTCAT TCGGAGGGGG 720  
 AGCGGTTCTT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTCCA GATAGTGGGG 780  
 CTCAACTCGA ACGAAGATTA TAGCTGGGGA GCTTCGTICA ATACGTCTTC CAGATGAAG 840  
 50 ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG 879

## (2) INFORMATION FOR SEQ ID NO:61

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...840
- 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

WO 99/29870

PCT/AU98/01023

41 / 490

5	GGGAAACTCC	AAATGAAAAA	AAGAATTGCA	ATTATCGCCT	CAGCCCTCTT	GGCTTTAGGA	60
	GCCGTCGGCT	GTAAGAAAAA	TGCTGACACT	ACCGCTGTCA	GTGAAAAGGA	TAGCATAGCC	120
	TTGTCCATGG	GTATTTTGTG	CGGACAGGAT	TTTGCCATATC	AGTTCGAAAT	GTCCCGCTTG	180
	CAAGGCCAGC	CGATTGATTC	GGTAGCTTTC	TTGGACGGTT	TCAAAATATGG	TATCGATACG	240
	ACGCGCTTCT	CGTACAATCT	GGGAGCCATC	TATGCTTCCA	ATATAGCTCG	TCAGCTGGCT	300
	CATGATTCCA	TCGATATCGA	CAAGTTCTAT	GCAGCCATGC	GTGCGGCTCT	TCTTAAAGAC	360
	ACCGTATCTA	TCGCCATGAA	GCCTGCAGAT	GCACAGGCTT	TCATGCAACG	AATCCAAGCC	420
	AAAAAGCAGC	GAGAAAAACA	TATGAAGCAG	TTTGCCAGAG	ACATCGAAVA	GGGTAATGAA	480
	TACATCGATA	CCTTTAAAAA	AGAAGATGGT	GTAAGTGTTA	CGACAACTGG	TCTGGCATAC	540
10	AAGACTCTTC	AGGAAGGTAC	GGGAGCTACT	CCCTCTTTGG	CCGATACTGT	ACGTGTCAAG	600
	TATGTGGGTA	CTCTGGTCTG	TGGTAAAGAG	TTCGACAAVA	ACGAAGAAGG	AATCGAATTT	660
	GCCGTTACCG	GTGTGATTAA	AGGCTGGACG	GAGATGCTCC	AACTCATCAA	GGTCGGTCAG	720
	AAAGTTCGCG	TGGTAATCCC	ACAGGAGCTG	GCTTATGGGG	AGACCGGCAA	CTATACCATC	780
15	GAACCGTTCT	CTACCCTGAC	GTTTCGAGATG	GAACCTATCG	GGATCAAGCC	CGGAAAAAAG	840

## (2) INFORMATION FOR SEQ ID NO:62

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2409

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

40	TGTCGAAAGC	AGAAGCTCTC	AAACCCGAAG	AGGAGCCGGT	ATCCGTGCAG	ACGGATATCA	60
	TTCCGACAAA	CGGATAAGAA	TCCGATGAAA	GTATTACGGC	AAGTATTCCT	CCCCATCCTT	120
	TTTGTCCCTAC	TGACAGGTGC	CTGCTCCACC	ACAAAGAAATC	TGCGGGAAGG	CGAACAGCTG	180
	TATATCGGAA	TGGGCAAGAC	ACAGATACTC	CGGCAGGACA	AGAGCCACGC	CGGCCAACAG	240
	GCTCTGACCG	AAGTGGAGAG	TACACTGAAA	GTTACACCCA	ATGGAGCTAT	TTTCGGCAGT	300
45	GCAAGTGCCT	CCTTACCCAA	GATACCATTC	GGGCTATGGC	TATACACAGC	CTTCGTGGGG	360
	GATTCACACTG	TCATTTCGAA	ATGGATATTC	GACAAGTTTG	CAGCCAAGCC	GGTTTTCAATC	420
	AGTCAGGTCA	AATCCGATAG	CCGGGCTAAG	GTGGCGACGA	ACATCCTCCG	CGAACACGGG	480
	TACTTCGATG	CTAAAGTAAA	AAGCAGTGTG	ACCACTCTGA	AAAAGGACTC	GCTCAAAGCC	540
	AAATCTCCT	ATACGGTGGG	TATGGCCTCT	CCTTATCAAT	ACGACAGCAT	CATTCCCTTA	600
50	CCGATCAGCA	CTTCCCCGA	CAGCATTCTG	GCTTACAGGC	AGACTCCGTC	TTTGATCAGG	660
	AAAGGAGACC	AGTTCATATT	GGCAAGCTG	CACGAAGAGC	GTCCAGACCT	CAGTGCCTTG	720
	CTGAGAGACA	ATGGTTACTA	CTACTTCGGC	CCACAGGATA	TTATCTACGA	AGCCGATACC	780
	CTCCTCGTAA	GAGGTGCCGT	ATGCCGTGGA	GCCAAGCTCT	CGGAAGATAC	TCCACCCCAA	840
	GCCATGCGCC	CGTGGAGGAT	AGGGAAACGG	ACAGCAGTCC	TGCTCGGAAT	GAACGGAGAA	900
55	AGCCCGACAG	ACTCGCTCGA	AGTGGAGGAT	ATGAAAGTCC	TTTACTATCG	TAAAAATGCCG	960
	GTTCGCCCCA	AGATTTTGGC	CAAAACGCTT	CGTTCTTCT	CCGGCAATCT	GTATCGGCAG	1020
	AAAGACGATG	AGACGACACG	CAAAATCCTTG	GCTCGTTTGG	GAGCCTTCTC	CGTTATCGAT	1080
	CTCAATTTTT	TGCAACGCGA	TTCCATTTCC	GGCCTTTTGG	ATGTGCGACT	GCTAACCCACC	1140
	CTCGACAAAC	CTTGGGATGC	ATCATTAGAG	ACCTTGTTCA	CGAGCAAAAG	CAATGACTTC	1200
60	ATCGGTCCCG	GACTGAATTT	TGCTCTTGCT	CGGCGCAATG	TATTGGGGGG	AGGAGAAAAAT	1260
	CTTCTTGGA	ATATCGGTGG	ATCGTATGAG	TGGGAGACCG	GCAATCGTCC	CGAAAAATAGC	1320
	AGCAATCGGC	TGATCGATAT	AAATTGCTAC	AACATGAATA	CGGCCGTGAA	CCTCTCGTTT	1380
	CCCTCGATTG	TATTTCCCGG	TCTGCTGGAT	AAATACTATT	ACTACCCACG	GACTACGACT	1440
	TTTCAGGCTT	CTGCCACCGC	GCTGAACAGG	GCACACTACT	TTAGCATGTA	CTCTTTCGGC	1500
65	TTTTCGACCA	CCTACGAATT	TCAGCCCTCC	AAGGAACACG	GGCATGCTAT	TTTCCCGCTC	1560
	AAGCTCAACT	ACAACCTCCT	GGGGCATCAG	ACAGAACTT	TCCAGGCCAT	TACGGGGAAC	1620
	AATCGGCCCC	TGCTGCTCAG	CCTTCAGAGT	CAGTTCCTTG	CTCAAAATGGG	GTATATCTAT	1680
	ACGTTCAACA	AATCCGTTTC	AGAGAAAAGT	CCTCATCATC	TTTGGATGCA	ATTCCGACTA	1740
	TCCGAGCGAG	GCAATCTCCT	GAATCTGATC	TATCTGGCAG	CCGGCAAGAA	GTACAGCGAC	1800
70	ACCAAGATTT	TGCTCGGCGT	CCCTTCTCT	CAGTTCATCA	AAGCCACGGG	AGAACTGCGC	1860
	TATCTCTATA	CCATAGACCG	CAATCAGTCA	CTGGCAACCC	GTTTCGGGAG	AGGCGTGATA	1920
	TATAGCTATG	GCAATATGCG	AGTGGCACCC	TATAGCGAGC	AGTTCTATGT	AGCGGTGACC	1980
	AATAGTATCA	GAGCTTTCAC	CGTCCGTAGC	ATCGGCCCGG	GACGGTTCAA	TCCGATTCC	2040
	GACAATCAST	ATTCCTATTT	GGATCAGGTG	GGCGAATTC	AACTCGAAGC	CAACGTGGAA	2100
75	TATAGAGGCA	AGCTTTTCGG	GGATCTCCAC	GCAGCCGTTT	TCTCGATGTC	GGCAACGTT	2160

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

42 / 490

TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GCCGGTGCTC TGTCCGAAGT GGGATCGGTG 2220  
 AGCAATTTCC TGAATAGCAT CGCTCTCGGC ACCGGTGTGCG GCCTTCGCTA CGATCTGGCA 2280  
 TTTCTCGTGG TTCGTGTGGA TGTGGGCTTC GGTCTCCACC TTCCTTACAA TACGGGTAAG 2340  
 AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTCCCATTT GGCTGTCCGG 2400  
 5 TATCCCTTC 2409

## (2) INFORMATION FOR SEQ ID NO:63

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 15 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2349

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

TCTCTCTCCG CGTATATCCG TTTTCTATG TCCTCGCATT CCGTTCGSTA TCTAATCGGC 60  
 ATTGCCGGCT GCTTGCTCCT CATGCTTGCT TCCTCCTGCT CGGTCAACCG TTATGTGCCG 120  
 GACGGTAGCA GACTATTAGA CAGGGTAACG ATCGCAAGCG AAACGGGCAG TATCGCTCTG 180  
 35 CCGGAAGATA TTCGGGACTA TACCCTCCAG CAACCCCAATT ACAGACTGTT CGGGATGACT 240  
 CGCTGGCTAC TGGCGCTCTA TAGCAGCTCG AATCCGAACA GCACAGCTG GTGGAACCGT 300  
 TCGCTCCGGA AATGGGCGA ACCGCTGTG CTCATCGATT CTGTCTCAC CGATCGTACT 360  
 GCCAACCGTC TGGCAAAGGC GATGGCCGGC GATGGCTTTC TCGATGCTAC TGCTCGTGCC 420  
 GTGGTAGACA CCGGCTTGTA CAAGAAAGCT CGCATTAATT ATCTGATTCA GCCCGGAAGC 480  
 40 CGTTATTATA TACCAATAT GGCCTTGGAT GTGAAGAATC CACTCCTTCC TCCCGTTGCG 540  
 CTTGGCAATT CGCTTCCTTC GGCATACAAG GTCGGGATCA GCGAGGGTTC TCCTTGCTCG 600  
 CCCATCGTAC TCGATGAAGA GAGAAAGGCG ATAGCTCGTC ATATGCGCAA CAACGGCTTC 660  
 TGGAAATTC CCGCCGAGGA TGTTTATTAT GAAGCAGATA CTACCGTTTC AGGAGGATCG 720  
 GGTACGAAAT CTGCGGATCT GAAATTAGTG GTCAATGGCA TCGGGCGTTA TCCATATCGG 780  
 45 ATCGGCAGGG TATTCTTTCA TGCCGATTAT GATCCTCTCG AATCGGACTT CAGAGTTTCA 840  
 GAGCTGCCAC GTATCGATT GATTCGCGT GCGGATTACA CTGTTTACTA TGGGAGTAGG 900  
 GAGCTTTATA TCCGGGCATC GGCTCTCACG CGGTCCGTGT CCGTTACACC GGGAGCTTTT 960  
 TTCTSCGAGG ATGATGTGGA ACGCTCTTAT ATCAAGCTGA ATGCGCTCCC TATCGTTCCG 1020  
 AACGTGAATA TCCGATTGTG GGAGCACAAT GGTAAGGATG AGATTGCTCT GCGGATAGC 1080  
 50 TCTCGCCTTG TGGACTGCTA TATTCTTACC GTTCCGGCCA AGAGCAAATC GTTCGAAGCC 1140  
 GAAGTCCCTG GCACCAATTC CGCTGGAGAC TTCGGGGCGG CTTTGTCTCT CGGTTTCACC 1200  
 GATCGCAATT TGTTTCGTGG GCGCGAGATG TTCAATATCA AACTCAAGGG TGCTTACGAA 1260  
 GCCATTCCGA AGGGTTCGCA CAGCTTCTAT GAATATGGGG TGGAAAGCTC GCTCCGTTTC 1320  
 CCTCGTCTCC TCTTCCATT CATTTCTGAC GAAACGCGCC GCGGGCTACG CCCATCCACG 1380  
 55 GAATGGAAGA TCGGGTATAA TTACAGACA CGTCCGGAGT TTGATCGGGT GATTCTCTCC 1440  
 GCTCAACTCA ATTATTATG GCAGACCTAC CTGCACAATC GTCTGCGTCA TACGATCCGC 1500  
 CTGCTGGATG TCGATTATCT CCATCTCCCG TACATCGATC CCGACTTCGC CCAATCCCTT 1560  
 CCGCTACGA CTGCACTGTA TAACTACAG GAGCAGTTTA TCCTCGGCTC GGCATATATA 1620  
 CTGAATATA CCACGGCTTC GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1680  
 60 TTCAGTATCC AGACAGCCGG CAACCTGTG CAAGCCATTT CTTATCTGAC CGATTCTCCG 1740  
 AAGACGAAC ACGGGTTGTA TAAATGTTC GGTCTGCACT ATGCTCAGTT CGTCAAGCTC 1800  
 GATCTCGATC TGGCTAAAC CGTCTTCTC GAAAAGGACA ATACTTTGGC ACTGCATCTG 1860  
 GGTTCGGGAC TGGCTTTCCC TTATGGCAAT GCTCGCCATA TACCTTTGA GTTACGTTAC 1920  
 TTGCGCGAG GATCGAACAG CGTTCGGGCT TGGAGTGTCC GTACCTCGG CCCGGGAGT 1980  
 65 ATGAAGATGA CTCGGGACAA GACCTTCTTC GATCAGATGG GTGATATTCG TCTGGATCTG 2040  
 AATGTCGAAT ACAGGACAAA GCTGTTCTGG AAGTTTCGCG CAGCAGCTTT TGTGATGCC 2100  
 GGCAATGTCT GGACGATAAA GGAGTATGAG AATCAGGAGG ACGGTCTCTT TCGTTTCGAT 2160  
 CGCTTCTACA AGGAAATAGC TTTGGCTTAC GGTCTGGGSC TTCGTCTCGA CTTCGATTAT 2220  
 TTCTTGTGTC GGCTGGATGC CGGACTGAAA GCCTACGATC CTCAGCAGAC AGGGCGTTAC 2280  
 70 AAATGGGCTA TCACACGCC AAACCTTTCT TCCAATTTG CTTGGACAT TGCAGTAGGC 2340  
 TATCCGTTT 2349

## (2) INFORMATION FOR SEQ ID NO:64

- 75 (i) SEQUENCE CHARACTERISTICS:

WO 99/29870

PCT/AU98/01023

43 / 490

(A) LENGTH: 2625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

20	GTGGAATCTA	AATTGTTATG	TCTTATGAGA	AAAAGAATTC	TACAACTTTT	CCTGACCGCA	60
	TTGCTGCTGG	CATTAGGCTC	CTCTCTCGCC	ATAGCGCAAA	CAGTGGTGAC	CGGTAAGGTG	120
	ATCGATTACG	AAACGTCCGA	ACCGCTCATC	GGTGATCCG	TAAGCACCGG	TCAGGAGGCA	180
	TCCCTCGCGG	GTGTAACCAC	CGATATGGAT	GGTGGCTTCC	GATTTCGAAGT	ACCGGCCAAA	240
25	TCTGTCTTGA	CTTTCGGTTC	CGTAGGTTAT	GCTACCGTAA	CTCGCTCTAT	AGGCAGAGGT	300
	TCTCAAGAAG	ACCTCGGTAC	GATTCTCTCT	GATCCCCAGG	CCATCGGCTT	GGATGAGATT	360
	CAGGTAATAG	CCTCTGTGCT	GCCCAAAGAC	CGTATGACGC	CGGTACCGGT	TTCCAATATC	420
	CGTGTGGCTG	ATATTCAAGC	AGCATCGTTG	AATGTCGAAT	TTCCCGAACI	GGTTAAATCC	480
	ACTCCCTCTA	CGTATACGAC	AAAAGGAAGC	GGAGGTTTCG	GTGATGGTCG	TACCAATGTG	540
30	CGTGGATTGG	ACACTTACAA	CTTCGGTGTA	CTCATCAACG	GAGTTCCTGT	CAATGGTATG	600
	GAAGACGGGA	AAGTATATTG	GAGCAATTGG	AGTGGTCTGA	TGAATCAAGC	CAGTACCATT	660
	CAGATTACGC	GCGGACTCGG	AGCCTCCAAG	CTCGGTATCA	GCTCGGTAGG	TGGTACGATG	720
	AACATTATCA	CGAAGACTAC	GGACGCCAAC	ACCGGAGGTT	CGGCTTATGT	CGGTATGGGT	780
	AATGATGGAT	TGCACAAAGA	ATCGTTCTCC	ATTCTACGCG	GTATGACGGA	CGGTTGGGCT	840
35	ATCACCATTG	CAGGCTCCCA	TATGACGGGT	CTGGGTTATG	TGAAGGGGCT	GAAGGGACGT	900
	GCATTCTCTT	ACTTCTTCAA	CGTTTCGAAG	AAGTTCAATG	AACGTCATAC	CCTCTCTCTT	960
	ACCGGATTGG	GTGCACCAAC	ATGGCACAAC	CAACGTTCTT	CCAAATATTC	TGTAGCCGAC	1020
	TATGACAAAT	ACGGCATCCG	TCACAATCAA	TCCTTCGGCT	ATCTGCGAGG	CGAAGTGAAT	1080
	CCTACGGCTT	ATGCTTACAA	TACGTACCAC	AAGCCCCAGT	TCTGGCTGAA	CCACTTCTGG	1140
40	AAGATGGATG	AAAATACCTC	TCTTTATACC	gCANCTACG	CATCTTTGGC	TACCGGTGGA	1200
	GGTCTCGCGG	CTTATGGAAA	GAACAGTAAG	TGGGTATTGA	TCAACTACAA	CACCGGACAA	1260
	CCCTATGAAC	AAACAAGAGT	GACTCCCGAT	GGACTTATCG	ACTACGATGC	CGTACTGGCT	1320
	GCCCAATGCT	CGGCGAGCAA	TGGCTCGGAA	GCAATTTTTC	CCCTTGGGTC	CAACTCTCAC	1380
	AAGTGGTTCG	GTCTACTCTC	TTCAATCAAG	AAGAAACTTA	ATAGTTCGCT	GACTTTGACA	1440
45	CCCGGATACG	ATGGGCGTTA	CTACCGTGGC	GACCACTATG	ACAAGATCAC	CGATCTGCTC	1500
	GGCGGTAGCT	ACTACATAGA	GGATCCCAAG	ACAAAGCTCG	CATACCATGC	GGAAAGGTGAG	1560
	CAAGTGAAAG	TGGGTGACAT	TGTAAATCGG	GACTACACAG	GCGAAATCAT	GTGGCACGGC	1620
	CTCTTCGCAC	AGATGGAGCA	TTGTCGCGAA	TGGATCGATG	CATTCTGATC	AGGATCTATC	1680
	AACATACGAAC	TATACCGCAA	TCACAACTAT	GGCGGTAGCA	AGTCCACCGG	CTACCTGCCC	1740
50	GGCGTATCGC	CGTGGAAAAG	CTTCCTTCGG	TGGAGTGGCA	AGGCAGGTCT	GAGCTACAAG	1800
	TTGCGACAGG	GACACAATGT	ATTGCGCAAT	GGCGGTTTCT	TCACACGTGC	ACCACTCTTT	1860
	GGCAATATCT	ATGCTGCGGG	GGCTATCATT	CCCAATGACA	AAGCCAATAT	GGAAAAGGTG	1920
	CTTACAGGAG	AGGTGCGCTA	TGGATTACCG	AATCACAAA	ACTTCGAGTT	CAATATCAAC	1980
	GGATACATATA	CGAAGTGGAT	GGATCGCGTG	ACCTCGAAGA	GAATCGSAAA	CGAGTATGTT	2040
55	TATCTCAATG	GCGTTGATGC	TGTTCACTGT	GGGGTAGAGG	CTGAGGTGAG	CTATCGTCTT	2100
	ATTCTGTCAG	TGCACTTCG	CGGTATGTTT	TCTCTCGGTG	ACTGGACTTG	GCAAAACAAT	2160
	TTAAGTTACA	CTTCTTACGA	CGAAGCGGGC	AATGAGACAG	GGCAGGATAT	AACCTATATC	2220
	AAGGTCCTTC	ACGTGCGAGA	TGCAGCACAG	ATGACGGCTG	CTGTATCGGC	AGACATAGAG	2280
	CTGTTCAAGG	GTTTCCATGT	CATAGGTAAG	TACAACTTCC	TTGGCAAGAA	CTATGCAAGG	2340
60	TTCAACCCCG	CAACGCGTAA	TGCACAGCAG	TACGAAGCAG	ATGGCAAGAA	AATCGTGGAA	2400
	TCATGGAAGT	TGCCCCGATG	AGGTCTGTTT	GATCTGTCTG	CATCCTACAA	TTCGAAGCTT	2460
	GGTTCACCTA	GCACCACATT	CTATTTCAAC	ATGGACAACG	TAGCCGACAA	GCGATATGTG	2520
	AGCGATCCCG	ACGACAATAT	CATCGGTAAG	AAACACGATG	AGGCTTCGGC	TCTCGTATGG	2580
65	TACGGTTTCG	GCCGCACTTG	GTCTACCGGT	ATTCGTGTAA	ACTTC		2625

(2) INFORMATION FOR SEQ ID NO:65

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

15	AACAGATGTA ATCCCTCGCG TCAATACTTC CACCTATCGC AGAATGACGT TGGAAAGATCT	60
	CTCCGAGCTT TTCTAATCCA TCTATCTATG AAGTTTTCAG TCCGCTTTT CCTCTGCATC	120
	ATCTTTTCTCC TCTCTGCATT TATCTGCTT GCTCTCGGAC AAAATTCAG GCAGGTACAG	180
	CGACTTGAGA ASCAACCTAA GGAGGCCCTC AAAGCCATCG AAAAAACGA TCGCGAACTA	240
20	CGAAATACCA AGAAAGACAA GCAAGACAAA CAAAAGCATC TCAACCTCCT GAACAAGCAG	300
	GTGCTCAAC GCAAGCAGAT GGTACAATC TTGGACAATG AGGTCAAAGA GTTGCAATCC	360
	GACATTGATT CCATGACGGG TGTATGTCAT CAGCTCTCTG TAGAAGAGAA AGCCCGATCC	420
	GAAGAATATG CCCAAGCTCT ACAGTCTATG CAAAAGCGGA AACGCTCGTT GCATCGCATC	480
	CTTTTCATTT CATCGGCCAA GAGCTTTGAC GAAGGCATGC GACGATCGG TTTCTTGGAA	540
	CAATACGCTT CTGCATACAA GCTGGCATCT GTCCGGCTGC GCGATACAG TAGCAAGTTG	600
25	GAGACTGAAC GTGCGACTCT AGAAGACGCC AAAAGSAGA AAGGACATCT CTTAGTCATC	660
	AGAGAAGAGG AAAAAAGAA ACTCGAAGGA CAGLAAGCGG AGCAAGTGC GCAGGTGCAG	720
	GCTTTGGGAG CCAACAAAA AGACTTGGAA GCGCAGCTGC GAAAGCAGAA AAGCAAGCC	780
	GAAGCTCTGA ACAGAAAGAT CGAGAAACAG ATTGCCAAGG AATAGAGAG TCGCGAACGT	840
	CGTGCTCGAG AAGAACGTGA ACGGTGGCA CGCGAAGCCA AAGCCAAGGG TAAGCCGGTT	900
30	CGTGCGAAG CGGAACGGA GCGGAGAGCC AAAGCGGCT ATGCTATGGA TGCCTCTGAG	960
	CGTGCTCTCT CGGCGAGCTT TGCACAGAAC AAAGGTGCGC TGCCCGGCC CGTTCGCGGC	1020
	AGATACCGAA TCGTAAGCGA CTTTGGCGTG CATCAGCACA GTGAGCTGAA AAAAGTACAA	1080
	GTTAATAATG GAGGTATCGA CATCGCTGTA GCAACAGGAT CCGATGCTAC CAGCGTATTC	1140
	GATGGTGTAG TGTCCAGTGT ATTGCTGATA CCCGGTTATA ATTCCGCCGT AATGTTTCGT	1200
35	CACGCTAACT ATATCAGGTT TATGCGAAT CTGAGCAAGG TGTATGTAAA TTCGGGCATC	1260
	CGTGTTAAAA CGGGTCAGGC TCTTGGTCGT GCCTATACGG ATCCTTCCAA CAACAGACCC	1320
	ATTATTCATC TCGAAATCTG GAAAGAACGC AGCAACAAA ACCCAAGACT ATGTTTACGA	1380

40 (2) INFORMATION FOR SEQ ID NO:66

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
60 (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

	AGTTTTTATC AAGAAATAGA CAGACTTATG AAAAAGTATT TGTATATGC CTCGTTGCTA	60
	ACGAGTGTTT TGCTCTTTTC CTGTTCAAAG AACAATCCTA ACGAGCCGGT GGAAGACAGA	120
65	TCCATCGAAA TTTCTATAAG GGTAGATGAT TTCACCAAAA CGGGTGAGGC AGTACGCTAT	180
	GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCT CTTGTTGTTT	240
	GATCAGTCAG GGGCGAATCC GGCAGAAATC TATATTACCG GTAACACTTT CACCGGAGGG	300
	AGCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GGCAGGAGAG	360
	CGCAAGATAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGTGCTGTC	420
70	GCTAACGAAA GCGATTGCA GACTGTAAAG AGGACGACTG CAATGCCGTG GTCGACCGAT	480
	ATAGCCTCTC CTTTCTGAT GTCCGGAAGC AAGACACAGC ACTTCTTGGC CAATCGTCTT	540
	TTGGACAATG TGCCCTTGT GCGTGCCATT GCCAAGGTGG AGCTGAATAT CTCGCTGAGT	600
	GAGAAATTTT AGATTGTGCC GATAATTGTC AATGTTAGTT TGAAGTGAAT CAAGTTTACA	660
	TACGTAAACT TCGACAAGGA GACCTAGTA GTGAAGCCAA CGACCAAGCC GGACCAATCTC	720
75	ATTAGTTCTG CTAATGGTGT TTGGCTTCAG ATTACAGATT GGACTGTATG GGGTGCTTCC	780

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5 TTAATACTT CTCCTGCTCC GGATGCGGGC ACAGGTTATA CATTGGATGC AAATGGCAAG 840  
 GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA 900  
 GAGGTCGCAT TGCCTCGTGT GGATGATGGC ACCCTTCCTC CTCGGAATT CGGTCCGGAG 960  
 CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATCAAGTC 1020  
 GAGATT 1026

## (2) INFORMATION FOR SEQ ID NO:67

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- 20 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

30 AACCTTAGGA CACAGCCTTT CTTTTGGTA GATTTCGAAT CTATGATCAG AACGATACTT 60  
 TCACGATATG TATCCTCGAA CTTTGGGAGT CCGGGAGCTA CCTTTTTTTT CACGATTTTC 120  
 CCGGCCTTCA TCCTCGCCGC TACTGCTTTG CCGGCTTGTG GAGGGGGTAC TGCTTCAGGC 180  
 TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGGC 240  
 35 GATAAGTCGG TGCAGGTGGT GGCATTGGTA CCGGCCGACA GCAATCCGGA GGAATACGAC 300  
 CCTTCGCCCTA CCGTGATGAA GCGTTTGTCC GAAGCAGATG CCTACTTCTA TATAGGAGGA 360  
 CTGGGGTTTC AGCAAAGAAA TCTCGCTGCC ATTCCGGACA ATAACCCCTAA GCTCCCTCTT 420  
 TTCGAAATGG GCAAAGCCTT GGCGGATGCC GGAAGTGAG ATCTCCACGG CTCCTGCACA 480  
 40 GATCATTCTC ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG 540  
 GCAAAGGCAC ACMAAGGGCA CGACCGTCTC AACGGAGCTA TCGACAGCGT GAAGAGACTC 600  
 GTCGATACCA TGTITGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG 660  
 CTCAGCTTTT TCGCCCAAGA GTTCGGCTG CCGCAGATCG TCATAGAGGA AGATGGGAAA 720  
 45 GAGGCTACGG CTGCCCCAAT TCGTCGTGTG ATCGATCAGG CACGTGCCGA TGGTGTGAGA 780  
 ATCGTATTTA TCCAACCGA ATTTGAAACG CGTCAGGCGG AGGACATCGC ACGCGAGATC 840  
 GGTGCTCGTC CGGTAAGCAT CAATCCTCTG CGCAGCTCGT GGGACGAGGA AATTTTACAT 900  
 ATTGCTCGCG CTTTGGCTCA TGAACGG 960  
 987

## (2) INFORMATION FOR SEQ ID NO:68

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2634 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2634
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

75 GCAGATTCTA TTCGATATCC TCTTTACTTT TTTGGGCGGA ATCGGAAGAA ATGCTTTAGG 60  
 GAACCTATTG CCACCTTATA CAATAAAVAC ATGATCGGAA AAAAAATCTT TTTTATCCTG 120  
 CTGGCGCTCA TTGCGTTTCAG TGGGCTGAAC GCAGCGACAG AACTGAGTT CAAGTACCCG 180

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ACCGATGCCA ATATCATCGG TCACGTCAAA GACAGCAAGA CGGGTGAACA CCTTGTCCGT 240  
 ATCACTATTG CTATCAAAGG CACTACCTTT GGTACATCTA CAGATGCAAC CGGGCACTAC 300  
 TATCTTCGTA ACTTGCCTCC GGGTGAGATC ACTTTGATTA TGGGTGGCAT GGGCTATAAG 360  
 AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG GACAAGACTA TCGAGGTGAA TTTGCAAGCA 420  
 GAAGAGGATG CCATCAATCT GGACGAAATC GTGATTTCCG CCAACCCGGA ACTGACGCTT 480  
 CGCCGCTCTG CTCCCTACTCT GGTAAATGTA TTGAACGAAA AAGTCTTCTC GCAAGTCAAT 540  
 GCTTCTAACC TGGCTCAAGG CTGTGTCATT CAGCCGGGAG TTGCTGTAGA GAACAACCTGT 600  
 CAGAAGCTGT GTTTCATCA AGTTCGTATC AATGGACTGG ATGGTCGTTA TGCACAGATC 660  
 CTATCGACA GCGTCCCAT CATGAGTGCC CTTCGCCGTG TTTACGGTCT GGAGCAGATC 720  
 CCTGCCAATA TGATCGAAGC TGTGGAGGTA GTACGTGGTG GAGGATCGGC CTGTACGGT 780  
 TCTTCTGCTA TTGCCGGAGT GGTGAATATC ATCACCAGG AACCTTCTCA CAATTCTTTC 840  
 ACATTCATG AATCTCTGAG CTTTACCGGT TTCAGCAAGC TGGATAACAA CACGAACTTC 900  
 AATGCCFCCA TCGTCAGCGA TGACAACCGT GCCGGTGCCA TGGTATTCCG GCAGGCTCGT 960  
 TACCGCAACU ATGGGATGC TAACAATGAC GGTATTCCG AATTGGGTAA AATAGATGCC 1020  
 CGCTCGCTGG GAGCGCATTC TTATTTCGCG TTGAGCGACT ACAGCAAAAT GACGGGAGAG 1080  
 TTTCAACGTA TCAGTGAATT CCGCGGTGGT GGCATCGTA TCGATTTGCC TCCTCACGTA 1140  
 GTGGGTGTAG CTGAACAAAC TGACCATAGC GTATTTAGCG GAAACTTGAA ATACGATCTC 1200  
 TTCTCTTCCA ACTATAAACA CCACCTCCAG GCTTATACTT CCGGACAGAT CGTAAATCGC 1260  
 AAGAGCTATT ACGGAGGTAT CCGAGAGATT GACGTCAATG GCCACCCCGG TGGTACGGAA 1320  
 GGCTACCTCA TCCTCAAGA TCAATACGGC AATAATTATG GCGTGACCAA AGGCAAGACA 1380  
 TATATGGGCG GTATCCAGTA CAGCTACGAC TTGGACAAAT TCCTCTCAT GCCTTCGCAA 1440  
 CTTTTGTTCC GAGCCGAATA TACGCGTGAT GAACTCAATG AAGTGATGCC CATCCTTTCA 1500  
 TGGCAGACCG GCGAGGATGC CAATGGGAAT ACCATTCCCC TCTATCCCGA ATTGGATCAG 1560  
 AATATCAACA ACTACAGCCT ATTCGGTCAG AACGAATGGA AAAATGACAG ATGGAGCATC 1620  
 CTGTGTTGGG CTCGCTTGGG CAAGCATAGC GAAGTCAAGG ATATGATTCT GAGTCTCTGT 1680  
 ACCACACTGC GTTTCACAGT GAATCCGGAC ATCAACCTGC GCGCTACATA TGCAAAAGGG 1740  
 TTCCGCGCAC CCGAGGTATT CGATGAGAGC TTGCACGTAG GGGTTGTAGG CGGTGAGGCA 1800  
 CAGAAATAT TCACGATCC GAACCTCAAG CCTGAAATTT CTATGCATT CAGTTTGAGT 1860  
 GCCGATATGT ATCATCGTT CGGTAACGTC CAGACCAACT TCCTTGTGGA AGGCTTCTAT 1920  
 ACTCGTTTGC TGGATGTATT CACCAACGAG GAGCAGCGTG ATCAGCAAGA TGGCATCAAA 1980  
 CGCTACACCG CTATCAACGG TAGCGGAGCC AAAGTATTCG GTCTCAATCT GGAAGGTAAG 2040  
 GTGCGATACA AGTCTTCCA GCTCCAAGCC GGTCTTACCC TGGCCAGCAA CAATACGAC 2100  
 GAAGCAGAGG AGTGGGTCT GAATACGGTG AAAGACACCA ACGGAGCTTT TGTACCGAG 2160  
 GCCAATGCAA ATGGACAACA GGAATACAAG AACGAATCCA TGACGGATAC GCAGATCACC 2220  
 CGTACCCCCA GCGTATACGG TTATTTTACT TTGGCTTACA ATCTGTCTCA CTCATGGAAC 2280  
 ATAGCCCTTA CGGAGACATA TACCGGTGAG ATGTATGTAC CCAACGCTAT CGAATATGGT 2340  
 GTGAAGTCTG CCGAAGTGA TATTATGACG AACCAATCTG AGATTACCGA CGAAACCGGA 2400  
 AAGGCTCCCC GTATTGATGA GCTGAAGAAG ACACCTGCAT TCTTCGATT GGGCTTGAAA 2460  
 GTGGGTTATG ACTTCCAGCT ATTCCAGGCT ACTGAGGTTT AACTCTATGT AGGTATGAAC 2520  
 AATATCTTCA ACTCTTCCA GAAGGACTTC GATCGTGGAG CTGCACGTGA CAGCGGATAT 2580  
 ATCTATGGTC CTACGCAGCC GCGTACAGGC TACATGGGCT TGGTAGTGAA GTTC 2634

## (2) INFORMATION FOR SEQ ID NO:69

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...618

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC 60  
 ATTCTTTTTT CCTCACCTTC TCTTGTTCGG GCGCAAAATC TTTTCAGCAC CGAATATGTC 120  
 TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA 180  
 ACGGCAGGTG AGTCGGCATT TCCTTTTATA GACAAATCA TCAATCTCGG CCGCACTTTC 240  
 CTCGGCAAAAC CATATCGCTA TCGCGGTCCCT TCCCCATGGC CGATGGAGTG CTCGGGCTAT 300  
 GTGTCTTACC TCTACTCCAA ATTCCGACATC AAATCCACAC GTGGTGGCGG AGCAGAGAGC 360  
 CAATATACGA ATCCTATCGA GCGGAGGAT GTTCGTCCGG GCGACTCTCT TTTTTCAAA 420  
 GCGCGCAATG CACGAGCAAA CCGTATCGGG CATGTAGCTT TGGTCGTATC TGTCGATGAA 480  
 GATGATATTA CCATGATGCA CAGCGGCAAT TCGCGAGGGA TCGTATCGA AAAACTCAAT 540

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CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA 600  
GTGATCCAC GAAAAAGT 618

## 5 (2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1401

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

AAAGGTACGT GGATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAA CTCTCTGACG 60  
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTCTGTGCAC AAAATGAATC CGAAGCATCA 120  
30 ACCAATCCGA TGTCAGGCCT CTCCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC 180  
CTGAATCTCG GCAGACAGGA GATCGAACAA GAAACCGAA TCATTAGTCT CGATGCAGCA 240  
CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCCGACGT 300  
TCGAAAGACA AAACGGGAGT AACCGTAGAT CGCTCCTCGA TGAATACCAA TCTCAGCATC 360  
GGAGCTTCGG TGGAAATATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG 420  
35 TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAGCGCG GTGAAGACCT CAGCCTGCAA 480  
ATCGCGGCTC TCTATATCAA TTGTCTCTTC CGTCAGGAAA TGACTCGTAC GGCAGAAACA 540  
CAGTTGGCAC TGATTCGCGA GCAACGCAAT CGCACGGCCG AATGGTTCG CGTAGGTAAA 600  
TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC 660  
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAGC CCTCGAACTG 720  
40 GAGCAGCCCG AAAGCATTGC AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG 780  
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA 840  
CTCATTCGA GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG 900  
GCATACITCC CGAGCTCAG CCTCTCTGCC GGATACAGCA AUGGTTACTT CCGCGACCTC 960  
GGCAAGGAGT ATGCCGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAGAA CACGGCCAGC 1020  
45 TACAGTATCG GACTCTCTT GAATATCCCC ATCTTCTCTG CCATGCAAC GCATGATCGC 1080  
GTTCGGAGCA GTCCGCTGCA AATAGCTCA AGCGAGCTTC GACTCGTCGA AGAGAAAAAA 1140  
GCCCTGTATA AAGAGATCAG GCAAGCATA AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200  
GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAGGCAT ACGAATACCG TCCGACAGC 1260  
TTGAGGCGAG GCGGCTTGTC TGCTACGAA TATGCCGAGG CAAAACAAA ATAGCCCTC 1320  
50 AGCCAAGTGG AAGAACTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT 1380  
TTCTATCAGG GCAAAGACTT C 1401

## 55 (2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1353 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1353

75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

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5 AAAACATCAT ATCGGAATAA TATGCGTTTC CAACATTATC TCATCTGTAC GGCTGCCGTA 60  
 GCGGCTTTGG CTGCGAATCC CCTTACGGGC CAATCGAATA TGACCTCGA AGAGTGCATA 120  
 GACTATGCAC GCCGGCACAG TTCGGCCGTG GCGCTGTCCG CTGCGGAAC TGGAGCAGTCC 180  
 AAGGCCGATT ACCTTCAGGC CGTCCGCAAT TTTCTGCCCT GTGTATCGGC CGGAACCGGT 240  
 GCTTCGTGGA ATTTCCGACG CGGATTGGAT GCCGAGACGA ATACCTACAC CGACATCAAC 300  
 AGCTTCAACA ATTCGTACAG CATACATGCC ACGATGACCC TTTTCGACGG TTTGCAGAGT 360  
 GTCTATCGAC TGGCGATGGC GCATGCACGC CGGGAGGCTT CGCGCCTCTC CGTTCGCGAG 420  
 CAGCAGGAGC TGGCAGCTCT CGGCACCACG GAGGCCCTACT ACGACCTCGT CTATGCGCGC 480  
 10 CAAATGCAAG AGCTGGCCAAT GCAGAAGTAC GAGGAGAGCA GCCGCTCCA CGGCAGACG 540  
 GCTCGAATGG AAGAGCTGGG GATGAAGAGT CGTCCCGATG TCCTCGAGAT GCAGTCCGGA 600  
 ATGGCCCGTG ACCGTTTGGC CCTGACTCAA GCGGACAATC AGTGCATCAT CGCTCTGATC 660  
 CGGCTCAAG AAAAATGAA CTTCGCCATC GATGACGAAC TCCTCGTAGA CGATATGCGG 720  
 GCTGACAGTC TCTCCGCCGA CATGGCCGAA TCGGACAGCT CGGCCGGCGT CTTCGCCCGT 780  
 15 GCTGCCCATC ATCATCCCGT CCTCCTCCGT GCCAAACTCG ACGAGCAGGC TGCCACCCGAC 840  
 CGTTTCCGAG CGCGCGGAGG TGCAATTCCT CCGAGTGTGT CGGTATCCGG AGGATGGAAC 900  
 ACGGATTCTT CACGCTTTT GAATGGATCG GACTATACGC CCTTCAGCGA GCGATTTCGG 960  
 AACGTCGGG GGGAAATCGT CAGTCTGAAT CTGAGTATCC CCATCTTTTC GGGATTCAAC 1020  
 20 CTGTGTAGCC ATCTCGCTCA GCGCGGTGCC GAACGCAAGG CGGCAATCGT CCGACGGGCG 1080  
 GAAGCGGAGC GCAGGCTCTA CAGCGAGATC GCCCAAGCCA TGGCCGACCG GATGCCGCT 1140  
 CTGGCTTCTT ACCGCCAGGC GAAGGAGCAT ACCGACGCCA TGCAAAACCG TTACGAAGCC 1200  
 GTCTTGACGC GTTATGAGCA GGGGCTGAAT ACGGCCATCG ACCTGACCC TCAGGCCAAT 1260  
 CGGCTCCTGG ATGCCCGGT GCAGCGACTG AGAGCGGCCA TGACCTACCG GCTCAATATG 1320  
 25 AACTCATAG CCTATTACGG CTGCCTTTCG GAC 1353

## (2) INFORMATION FOR SEQ ID NO:72

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2886 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2886  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

50 GCCATTTTGT TCGTATCATT GCAAAATTGA AAAATAACAG AGAATAAGTA TAATTCAGAC 60  
 AAGAGCATGA ACAAAATTTA CAAATCACTT TTGCACTCAG GACTGGCTGC CTTCGTGTTC 120  
 ATGGCAACTG CACTGACCGC TTCTGCACAG ATTTCTGTTC GAGGGGAACC CTGAGTTTC 180  
 TCTTCAAGAT CCGCCGGAAC GCATTCAATC GACGATGCAA TGACTATCCG CCTTACTCCG 240  
 GATTTCAATC CGGAAGACCT GATCGCACAG AGCCGTGTGC AATCGCAAG AGATGGCCGG 300  
 55 CCGCTCCGGA TAGGACAAGT AATACCGGTG GATGTGGACT TTGCATCAA GGCTTCGCAC 360  
 ATCTCTTCCA TCGGAGACGT AGATGTATAT CGCCTGCAAT TCAAGTTGGA AGGAGCCAAA 420  
 GCCATTAGCG TTTATTACGA TGCAATCAAT ATTCCGGAGG GCGAGCGCT CTATATCTAT 480  
 ACCCCGAGCC ATGAAATTGT GTTGGGAGCA TATACGAACG CCACTCATCG CCGCAAGGGA 540  
 GCTTTTGCCA CAGAGCCGCT ACCGGGGAGT GAGCTTATTA TGGATTATGA AGTGTCTGCG 600  
 60 GGAGGGACTT TGCTGACAT CAAGATCTCC GGTGCGGGT ATATATTGCA CAAAGTCGGC 660  
 GGAGCGCCCG TAACGGATAA CCATTACGGG ATCGGTGAGG ACGATTCCGA TTCGATTGCG 720  
 GAGATCAACA TCAATTGTCC TGAAGGTGCA GACTGGCAGG CAGAGAAGAA CGGTGTGGTG 780  
 CAAATGATCA TGGTAAAAGG ACAGTATATC TCAATGTGCT CAGGCAACCT GCTCAATAAT 840  
 ACGTAAGGAG ACTTTACTCC GCTGATCATT TCTGCCGAC ACTGTGCTTC CATAACAACC 900  
 65 AATTTCCGTT TAACGCAATC CGAGTTGGAT AAGTGGATCT TCACTTTCCA CTATGAAAAA 960  
 AGAGGATGCA CCAATGTATC ATTGGCCATC TTCCGTGGCA ACGATATCAT CGGAGCTTCC 1020  
 ATGAAGGCTT TCCTCCCGAT CAAAGGTAAA TCCGATGGTC TCTGTCTGCA ACTCAACGAT 1080  
 GAGTCCCTC TGCGCTATCG TGTCTATTAC AATGGATGGG ACGTACGCC CGATATTCCC 1140  
 TCGAGCGGTG CCGGTATTCA TCATCCGGCC GGAGATGCCA TGAAGATTTC CATCTAAAG 1200  
 70 AAGACTCCGG CTCTGAATAC ATGGATCTCC TCCAGTGGTT CCGGAGGAGC TGACGATCAC 1260  
 TTCTATTCTA AATACGATCA AGGTGGTACG GAAGGAGGAT CGTCCGGTTC TTCTCTCTTC 1320  
 AATCAGAATA AGCAGTGGT CGGCACACTG ACCGAGGGTG CCGGCAATTG TGGCGGACG 1380  
 GAGTTCTACG GCAGACTGAA CAGTCATTGG AACGAGTATG CATCCGATGG CAATACGAGC 1440  
 75 CGCATGGACA TCTATCTGGA TCCCAAAAC AATGGCCAGA CGACCATCCT CAACGGAACG 1500  
 TATCGTGACG GTTATAAGCC TTGCCCCCTT GTGCCCCGGC TATTGTTGCA GTCTACAGGC 1560

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	GATCAGGTCG	AATTGAATTG	GACGGCTGTT	CCTGCCGATC	AATATCCATC	ATCTTATCAG	1620
	GTGGAATACC	ACATATTCCG	AAATGGAAAG	GAAATAGCTA	CGACAAAGGA	GTGTCTCTAT	1680
	TCGGATGCCA	TCGACGAAAG	TATTATCGGT	AGCGGTATCA	TTGATACGA	AGTAAGCGCA	1740
5	CGCTTCATTT	ATCCCTCGCC	GTTGGATGGA	GTGGAATCTT	ATAAGGATAC	GGACAAGACT	1800
	TCTGCGGACC	TTGCCATAGG	AGACATTGAG	ACCAAGCTGA	AGCGGAGCTG	AACACCTCTC	1860
	CCCGGAGGAG	GAGTATCATT	AAGCTGGAAA	GTTCTTTTCT	TAAGCCAGTT	GGTTCCCGA	1920
	TTTCGAGAAA	GGCCCAATCC	TGTGTTCAAA	ACCTTTGAAG	TGCCCTATGT	TTCTGCCGCA	1980
	GGCCGACAAA	CCCCCAATCC	TCCCGTTGGC	GTAGTCATTG	CAGACAAGTT	TATGGCCGGT	2040
10	ACATATCCCG	AAAAGGCTGC	TATCGCTGCC	GTTTATGTAA	TGCCATCCGC	TCCGGACTCT	2100
	ACTTTCCACC	TCTTCTCTAA	GAGCAACACA	AACAGAAGAT	TGCAGAAGGT	GACAACTCCC	2160
	TCCGATTGGC	AGGCGGGAAC	ATGGTTGAGG	ATCAATTGGG	ATAAGCGGTT	CCCGGTGAAT	2220
	AATGACCATTA	TGCTTTTTCG	CGGTATCAGA	ATGCCTAAAT	AGTACAAGCT	CAATCGTGCT	2280
	ATCGGTTATG	TAAGAAATCC	GGATAACCTT	TTCTCCATTA	CGGTAAGAA	GATTTCATAT	2340
15	AACAACGAG	TCTCTTTTGA	AGGCTACGGA	ATACCTCGCG	TCTTGGGCTA	TATGGCTATC	2400
	AAATATCTGG	TGGTAAATAC	CGATGCTCCG	AAGATCGATA	TGTGCTTGT	ACAGGAGCCT	2460
	TATGCTAAGG	GAACGAATGT	GGCTCCATTG	CCGGAATTGG	TCGGCATATA	TGCTATAAG	2520
	AACGGAACAT	TTATCGGCAC	ACAGGATCCA	TCCGTACAAA	CTTATTCGGT	TTGAGACGGA	2580
	ACAGAGAGCG	ATGAATACGA	AATAAACTG	GTATATAAGG	GATCGGGCAT	TTGGAATGGC	2640
	GTTGCTCAGA	TGAGGAATTA	CAATGCTGTC	GTTGCATATC	CGTCTGTTGT	AACAGATCGT	2700
20	TTGACCATTA	AGAACGCTCA	TATGGTTTAC	GCTGCCGCC	TCTACTCATT	GGATGGCAAG	2760
	CAGGTTCTGT	CTTGGAAACA	CCTCGCAAT	GGCGTGACAT	TCAGTGTTC	AGGACTTAGC	2820
	GCCGTACTT	ATATGCTCGT	TATGCAGACG	GCAACGGCC	CTGTGAGCCA	AAAGATCGTG	2880
	AAGCAG						2886
25	(2) INFORMATION FOR SEQ ID NO:73						
	(i) SEQUENCE CHARACTERISTICS:						
30	(A) LENGTH: 2106 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
35	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
40	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
45	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2106						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73						
50	TGGAAAAA	GTAACTCTCA	ATACCGGGGC	AGGACAGCAA	ATTACCGAGA	TCATTATAAT	60
	ACAGAAAGCT	ATTTAAGCCT	AAGGAGGAAT	CAAACAATGA	AATATCTTAT	CAGACTCTTC	120
	TTATCATTGA	TGTTACTCTC	TCTCTGGACG	GGCTGTACAC	ACGAGGAGCT	CTCTATTTCG	180
	GATGGCGAGA	ATACGCTTGT	TTTACCGGTA	GAGACCGGTA	AAGCCCCAAA	TGCTCGTGCC	240
	ACAGAACCCG	GTCAGGGCAT	ATACAATGAG	AATAAAGTAG	GCTCCATTTC	TGTGCTCTTC	300
55	TATTTACAGG	GACAACCTCG	TTGGCAGGTG	AAGTCTACAG	ACTATCAAA	CCATGAAGGG	360
	GCCTATATCA	TTCCGGTCAA	AGAGCAAATG	CGACCATAT	TCAATGGCAA	CAACAACCTC	420
	AGCATCTATG	TAGTGGCCAA	TCTCGATTTC	AATGCTCCGG	CCACAGAGGC	TGCGCTTTCT	480
	CAATTGTGG	TAGAGAAATC	TATTGAAGTC	TCTTCTACGA	CAGCCCTGCG	CGATTTCGTA	540
	ATGCTTGCTC	ATGGCAATAA	GCAGATCAAT	ATGGCTACGA	CAGAAGGGAA	ACTGTTGGGG	600
60	GATTATAAAC	TCAAACGAGT	GGCAGCAAAG	ATTGCGATGA	TAAACCCAC	CATCAATGTG	660
	CAAGGATATG	AAGTGGTCGG	AAATATACAG	GCAAAGTTTC	GCAATTGCGT	AACGAAGGGG	720
	TTCTTACCA	CAGAAGCTCA	AGAGATCCCA	GCTGCTGCAT	CCTATAAGAC	ATCGGAATAT	780
	CTTGATATTG	CAGAGTCGGC	ACCTGCCAAT	TCTATCCATT	TCTATTCTTA	CTATAACAAA	840
	TGGACACTCT	CCACACCGGA	GAAGCGACCG	GAATTCTTCA	TCATGGTCAA	ATTCAAAAAG	900
65	ACAGGACAGC	CGGACAACAC	AGCCAAACCG	TACTACTACA	GAGTGCCCTC	CGAATCTCAG	960
	GACAATCAGG	TCAAGAGCAA	TGTCTCTAT	AATCTGAATG	TGAAAATCGA	AATCTTGGGT	1020
	TCTTTACAG	AGCCGGAAGC	TGTTTCTGTA	AACGGCACAC	TCGCAATAGA	AGAATGGATT	1080
	CTCCATCAGG	ATGCATTCAA	TCTGCCTGCC	ACCAATTACT	TGATAGTGGA	ACAGCACGAA	1140
	ATCTTCATGA	ATAACGTGAA	CACATACTCG	GTGAAATATC	AAACTTCGCA	GAACCAATC	1200
70	AGCATTAGCA	TACAGTCAGT	TACCTTTAGC	TACGTCTCTT	CTGATGGCAC	TCAGCACAA	1260
	CATCTTGTAG	CAAGTAGTAG	CGACCAAGTAT	CCTACGATTA	CAAGCGATAA	TACAAGCATC	1320
	ATAATCACTT	CCAAGATACC	GGTTAATAAC	GTACCAAAAG	AGATCGTTTT	TGAGGTAAC	1380
	AATGGGGTAG	CCGGTTTGAA	AGAGACTGTC	ACAGTACTCC	AATATCCTCG	ACAATTTATT	1440
	GTCAATACAC	TTGGCACAGC	ATCGGCATGG	AGACCAGACG	GATCTTTGGC	TCCGGGGGCT	1500
75	AACAATAAAG	CGATTTACCA	TGTCGTAGTA	CTGCTTCCAC	CCGAGAATTT	ATTGAAGAT	1560
	GGGACACAGA	CAATCATCGG	TTATCCCCCC	ACTGAACAAA	TTTCTTTTCA	TAAGAAAGAG	1620

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5 AACAATACCT ATCCGATAGT ATGGTCTGAC ACAAATACGA CAAACAGGA CCTTGAGACA 1680  
 TCAAGAATGA TTTCACCTTC CTTTGAGTTA GCCTCCCAAC TTGGGGCTAC TCTCCCGATG 1740  
 CCCTATCTCG AGTATTTGGCC AGGGACATCA TATCTCCTTG ACTATTCGGG AACTATAAT 1800  
 AATAAGAGAT ACCGCTTGTT TAATTGCGCT TTTTACTGGG AGAAAAGAAA AGTTAATAAC 1860  
 GAAGAAATTA AATTCGATGA CTGGCGTTTG CCGACAGAAG CTGAGATCAA ATTGATAGAT 1920  
 AAGCTGCAAC ATAATGAGCA GAGTGTCTGC CAAGCTATCA TGACAGGGAA TTATTATTGG 1980  
 GATAGTTACT CTGCAATGG GTCTTATAAA ATGCAAGGAG GAGGGGGCCA AGGAAATTCC 2040  
 TCCAAAGCCT ATGTTCTGTT CGTGCGGGAT GTGAAAAAGC CGATTCTGA CAAGAAGTCA 2100  
 GGTAA 2106

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## (2) INFORMATION FOR SEQ ID NO:74

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3936 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3936

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

35 AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA 60  
 CAAAATTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG 120  
 TGCTCTCTGC ATTAGGCTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA 180  
 GCGCTACGCT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTTGTT 240  
 TTCCCGGAT TTTATAGTGT GGA AAAACGA GAAGGCAACC AAGTCTTTCA GCGCATTTCC 300  
 40 ATGCGCGGTT GTGGCTCGTT TGGGAATCTG GCGGAAGCTG AATTGCCTGT TTTGAAAAAG 360  
 ATGATAGCCG TTCCGGAAAT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG 420  
 ACATTGACGA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCCTGAG 480  
 GGGGGGACTT ATCTGGTAGA GGCTTTGCGG ATAAACAATG ACTATTATAG CCAAAATGTA 540  
 AGCCTCCCTT CTACTCACTA TGCTATTCT CAAGACGGGT ATTTCCGCTC ACAAAGATT 600  
 45 ATCGAAGTTA CCTGTATCC TTTTCGATAC AACCTGTCC GACAGAAAT TCTATTGCA 660  
 AAAAAATCG AGGTTACAAT AACTTTGAT AATCTCAGC CACCTTTACA AAAAAACACC 720  
 GGCATATTTA ACAAGTAGC CTCCTCTCCA TTTATTAAAT ATGAAGCTGA TGGCAATCG 780  
 GCGATAGAAA ATGATATGGT GTTCAGTCGT GGTACAAACA CGTACATAAG CGGAAATGTT 840  
 GCGACGAACC TCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA 900  
 50 AATCAACAAC CACACGACGA AATCAACGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC 960  
 TTTGATGTAG CTGCTGTAG TATAAGGAC GTATTGAATA GCTTCCATC AAATGCCACC 1020  
 TCATACATCA ACGAACTAA ACTGAAAAAT TTCATTGCT CAGTTTACAA CCAAGCAAT 1080  
 GCGAAGAGGA CTTTAGATGG CAACTGGGA TACGTGCTAC TGATCGGAAA ACCAATGAGC 1140  
 AAATATTGG CTGACACTGA TAATACAAAA GTCCCAACCT CTTTATTACA TAATGTCTCC 1200  
 55 TTAATTCCAA GTCATCCAAC TTTTGGTTCC ATAATGCGCT CCGACTATT TTTAGTTCT 1260  
 GTTTCGCCCC TTGATACTGT CGGCGATTG TTTATCGGTC GATTTAGCGT CACCAATGCT 1320  
 CATGAATTGC ACAATCTGAT TGAAAAGACT ATCAACAAAG AAATCTCTA TAATCCTATT 1380  
 GCACACAAAA ATATTCTTTA CGCAAGGGG AAAGGCTGCG ATGCTCCAAT CTACGTTTA 1440  
 TTCTTAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAATC TAATCAGGTC 1500  
 60 TCTGCAATAG ACTCGATATT TGA CTGCTTG AATAATGTT OCCATCATTT TTATTTTAAC 1560  
 ACTCATGGAA TGCCGACTGT TTGGGGGATA GGGCAGGGAC TCGAGCTCAA TACTCTAACA 1620  
 GCGCGATTGA ACAATACATC TFCGAGGGA TTATGTACGA GTCTATCATG TAGTTGGGCT 1680  
 GTAGCAGATT CAATATTAG ATCGCTTGGA GAAGTCTGA CCAATACGC ACCTAACAG 1740  
 65 GGATTCTCGG CTTTCTTAG AGGAAGCAGA GCCACCCAAT ATGCCGTTTA TTTAGAAGGC 1800  
 CCTGTCTC CGTCAGAAAT TTATGAATAT TTACCTTATT CTTTATATCA CAATCTCTCG 1860  
 ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT 1920  
 TCGAAATCA ACTTCAATTT GCTTGCGAC CCTGCACTAA ACATTATGGC TCATGGCATG 1980  
 GAGGTTAGTA ATTGTATTAC ACTACCAAA AACACCAATTA TAAGCAGTCC GATAACAATA 2040  
 70 AAAATGTTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCAATTTAC TAATATGGC 2100  
 TCCATACAAG TCATGTCCGG AGGAACCTCT GAAATAGGCA ATCAGGCTAA AATATCCGGA 2160  
 GAGACCGGTG CTAACCCAC CTTTATTACC GTTTACGGCG ATGGCTCTGC GATTAACAAG 2220  
 CAGGTAGAGA TAGACAATAT AGACCGACIT AACTTGTITT CTACCGATTC GGTATGCCU 2280  
 AAATTTTATT TTGACAGTGT GAAATTCAAC AGTGCCCGCG TGTATACAAC GAAGTGTATT 2340  
 75 GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTTATTTCAA GAATTGTGAC 2400  
 CTAAGCGTTG AAAACAGTAT GTTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT 2460

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	ACAAGCTCCA	TCACCGGATT	ATCTACAAA	GCAAAGATTA	CCGACAATAC	TTTTTTTGGC	2520
	ACAGGAAACT	TCGCUFACCA	TATCACAAAC	ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	2580
	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	TACATTTCCG	GTAATAAAAT	AGTCAAATGC	2640
	GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	AACAGAACGA	ACAGACTCCA	CAATATCACA	2700
5	CGGAATGTGA	TAAAAAAGTG	TAGGATTGGG	AGCAGCGCTT	ATAATTCCTA	TGGTATTTAC	2760
	AACCGAAATA	AGATCAGTAA	CAATCATATA	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	2820
	TATTTCCGATA	ATGCTCCTGT	AATCAATGAA	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	2880
	ACTTGGGCAGC	TCTATTATC	AAACGGTACA	TTCCCTCTCA	ACTTCATTA	CAACAGCTTG	2940
	CAGGCGGGGAG	ATACAGATAC	ATGGATTTAC	AACGACACGT	ATACGAATCG	CTATATTGAC	3000
10	GTTCACAAATA	ATCACTGGGG	CAACATGAT	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	3060
	CCAGACTTGT	TCATTGGGAT	ACCTTTTGG	GATGGATTGC	CAAAATGGGAG	ATCGGGCAAT	3120
	AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	GCATTGAGCT	GTATTGGCNA	TAGCGATTAT	3180
	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	GTGAAACCT	ACCCGGAATC	CGACTTTGCA	3240
	ATAGCTGCTT	TGAAGGAAT	GTTTCAGGATA	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	3300
15	TTGAAAGATT	ATTTTCAGATC	CAATCCAACC	ATCATCTCTT	CCAGAACTT	GTTCCCGACA	3360
	GCTGATTTC	TGTCTGCGCG	ATGCGATATT	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	3420
	TGGTACGAAA	ATCGCTTGAA	TAGTGAAATC	TCCTATCAGG	ACAGTGTTTT	TGCAGTCATT	3480
	GACCTTGGTG	ACATTTATTG	GAATATGCAG	TTAGACTCAC	TCAGAGGGAG	TGGTATAGAT	3540
	TTGACATATC	TTTCCGTGTA	ACAAAGGAAA	TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	3600
20	TATTTGTTGT	CAACTCTTCC	CGAATCAACA	GGTACTCTCC	TGCCCTCCAT	AGAATGCAAC	3660
	AAATCAAGCC	TTGATAAATC	CAAGATAATC	TCTATTTCGC	CCAATCCGGC	GAAAGCTGTT	3720
	GTAACATAAA	TCYACTATAC	CGATAACCCCT	TCTGTTCCTG	TAATAAAAAAT	ATATGGAATA	3780
	AATGSAGCCT	CGGCTGATAT	AACCGGGTTG	CCCAACATC	TATCCGAAGG	TTATTACAGC	3840
	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	3900
25	CAGAAAATTA	TAGATACGGA	AAAATTACGA	ATCAAA			3936

## (2) INFORMATION FOR SEQ ID NO:75

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2814 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
35	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(v) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION 1...2814
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

	TCAGAAAATT	ATAGATACGG	AAAATTAACG	AATCAAATAA	TGGCTATCAT	GATGAAAAGT	60
	ATTGTTTTTA	GAGCATTCTT	AACGATTTTG	CTCTCGTGGG	CAGCSATCAC	GAATCCGACT	120
	GCTCAAGAGA	TCTCAGGCAT	GAATGCATCC	TGTCTGGCTG	CTCCGGCTCA	ACCGGATACT	180
	ATCTTATATG	AAAGTTTTGA	GAATGGACCT	GTTCCTCAATG	GCTGGCTTGA	GATAGATGCT	240
55	GATGCTGATG	GTGCCACTTG	GGGAAGCCCA	TCAGGCTCTT	TCTCTGTACC	TTACGGACAC	300
	AATGGCCTTT	GCACCTACTC	CCATATACGT	TCCGGTATCT	CAACAGCGGG	CAACTATCTG	360
	ATTACACCCA	ATATAGAAGG	AGCCAAACGG	GTCAAGTACT	GGGTATGCAA	TCAGTATAGT	420
	ACCAATCCGG	AACATTAACG	AGTAATGGTA	TCGACAAACG	GGACTGCCAT	TGAAGACTTT	480
	GTTTGTGTTG	TTGATGATTC	CATAACAGGG	AAACCGACTC	CTCTGTATG	GCGTAGACGA	540
60	ATCGTGGACT	TACCGGAAGG	GACCAATAT	ATTGCATGGC	GACATTACAA	AGTCACCGAC	600
	TCACACACAG	AATTCCTTGA	ATTGGATGAT	GTCACTGTGT	ATAGGTCGAT	CGAAGGGGCC	660
	GAACCTGCTA	CCGACTTCAC	AGTAATCAAT	ATTGGTCAGA	ATGTGGGACG	ATTGACTTGG	720
	AACTATCCGG	AGGATTATCA	ACCGGAAGGA	AAGGGGAATG	AAGAGTTGCA	GCTTAGCGGC	780
	TACACATCT	ATGCGAACGG	TACACTACTG	GCACAAATAA	AAGATGTCTC	CATACTGGAG	840
65	TATGTGGACA	GCACCTACTC	TTTGCGAGAC	AATCCCTTSC	AAGTGGAGTA	CTGCGTTACA	900
	CGCGTTTACG	ATGAAAGCAT	AGAACTTTCG	ACCGTATGTG	CCACGCTGCA	TTACGCCACG	960
	GATGCCATCC	TTTATGAAAA	TTTTGAGAAT	GGACCTGTTC	CCAATGGTTG	GCTTGTGATA	1020
	GACGCTGATG	GAGATGGATT	TAGCTGGGGA	CACTATTTGA	ATGCATACGA	CGCTTTTCCC	1080
	GGCCATATAG	GAGGCCATTG	CTCCTTGTGG	GCTTCTTATG	TTCCGGGTAT	AGGCCCGGTG	1140
70	ACTCCCTACA	ACTATCTGAT	TACCCCAAG	GTGGAAGGAG	CCAAACGTGT	CAAGTACTGG	1200
	GTAASCACCG	AGGATGCCAA	TTGGGCAGCG	GAACATTACG	CGGTGATGGC	TTGACAAACG	1260
	GGGACTGCTG	TCGGAGATTT	CGTCATATTG	TTCCGAAGAA	CCATGACAGC	GAAGCCGACC	1320
	GGCGCATGGT	ATGAAAGAAC	CATCAACTTA	CCTGAAGGGA	CTAAATACAT	CGCATGGCGG	1380
	CATTACAAC	GTACCGATAT	ATATTCTTGG	AAGTTGGACG	ATATCACTGT	ATTCGGGACT	1440
75	CCTGCATCAG	AGCCCGAACC	TGTTACCGAT	TTGCTGTCT	CGCTTATTGA	AAACAACAAG	1500

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	GGACGATTAA	AGTGGAAATTA	TCCTAACGGC	TACGAACCCG	ATAAGACTGA	TGATAAAGAC	1560
	CCATTGCGAGC	TTGCCGGCTA	CAATATCTAT	GCAAACGGCT	CGCTCCTTGT	TCACATACAA	1620
	GACCCGACTG	TTTTGGAGTA	TATCGATGAG	ACTTATCTCT	CACGAGACGA	TCAGGTGGAA	1680
5	GTGGAATATT	GTGTCACTGC	CGTTATAAC	GACAAATATCG	AGTCCCAATC	GGTTTGCAT	1740
	AAGCTGATTT	ATGATTCTCA	ATCGGACATT	ATCTTATATG	AAGGCTTTGA	GGCCGGAAGT	1800
	ATTCTGGAAG	GCTGGTTGTT	GATTGATGCT	GATGGCGACA	ATGTTAATTG	GGACTATTAT	1860
	CCTTGGACTA	TGTATGGACA	TGACAGTGAG	AAGTGTATTG	CATCCCTTC	GTAATTACCG	1920
	ATGATTGGCG	TTTAACTCC	GGATAACTAT	TTGGTTACAC	CCAGACTCGA	AGGAGCCAAG	1980
10	CTTGTCAAGT	ATTGGGTAAG	TGCGCAAGAT	GCTGTTTATT	CGCCTGAGCA	TTATGCTGTG	2040
	ATGGTTTCTA	CTACGGGAAC	TGCTGTTGAA	GATTTTGTCC	TCTTGTTCGA	AGAGACAATG	2100
	ACCGCTAAGG	CTAACGGTGC	ATGGTATGAG	CGAACTATTA	CATTGCCTGC	AGGAACAAAA	2160
	TATATTGCLT	GGCGGCATTA	TGATTGCACC	GATATGTTTT	TCTTGTCTCT	GGATGACATT	2220
	ACGGTTTATC	GTCTACTGA	GACTGTTCCC	GAGCCTGTTA	CTGATTTCGT	TGTCTCGCTT	2280
15	ATTGAGAATA	ACAAGGGTCG	CCTGAAATGG	AATTATCCTA	ACGGCTACGA	ACCCGATAAG	2340
	ACTGATGATA	AAAAACCATT	GCAGCTTACC	GGCTACAACA	TCTATGCAAA	TGGCTCGCTC	2400
	CTTGTTCACA	TACAAGACCC	GACTGTTTTG	GAGTATATCG	ATGAGACTTA	TTCTTCACGA	2460
	GACGGTCAGG	TGGAATGGA	ATATTGTGTC	ACTGCCGTTT	ATAACGACAA	TATCGAGTCC	2520
	CAATCGTTTT	GGGATAAGCT	GAACATATACT	ATCAGATCCT	TGGATAATAT	TCAATCTGAT	2580
20	ACAAGCTTGA	AAATATATCC	TAATCCGGCA	TGATATGTTG	TAAGGATAGA	GGGATTGAGT	2640
	CGGAGCAAGT	CGACAAATCGA	GTGTATTAAT	CGGCTGGGAA	TTTGATATAT	AAGGGAAGAG	2700
	ACTCATTCAG	AGAAAACGGA	AATCGATGTT	TCACGTCTCA	ATGACGGAGT	CTACTTGATT	2760
	AAAGTAGTCG	GTGGAATAAA	AACAACAACC	GAAAAGGTAG	AGATAAAGAG	GCCG	2814
25	(2) INFORMATION FOR SEQ ID NO:76						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 1818 base pairs						
30	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
35	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
40	(A) ORGANISM: PORPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc feature						
45	(B) LOCATION 1...1818						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76						
	ATAATCTTCT	GTACGATTCA	CTACTCTGAG	TTGGAATAAA	TGAACAGCAT	CATGAAATAT	60
50	CAATATATATA	CGGCGCTCAT	AATGGCTCTC	TCTGTATCAT	CGTTTTCGGG	TCAAACCCCA	120
	CGAATATACAG	AAACCAACAG	CCCCGACACG	CTGCGCAGGG	AGCTTACTAT	CGTTAATGAC	180
	CAGACTGTGG	AGATGGAGCA	TGCGGATCCG	CTTCCGGCTG	CATACAAAGC	CATCGAACCT	240
	CGATTAAAC	CTTCCGTTCC	GGAATATAAC	AAGCGTACAT	TCCGATTGTT	CCCTGAAGTT	300
	TCCTCTTCAG	GCAGGAACAA	TCTTCCGAAT	ATCCTGCCGA	CGGAAGGTCA	TATGAAGCAC	360
55	CGGGGGTACC	TGAATATCGG	TATCGGCCAT	ACGCTAAACC	AGCGAATGGA	TGCCGGCTAT	420
	GGTCTGATAG	ATGCAGAGCA	GGAGAGACTG	AATCTTTTCC	TCTCCTATCG	TGGGATGAAA	480
	TCCGCTTTCA	ATACCGGTGA	CTTCGACGGC	GACAGAAVGG	ATAGACGAAT	GATGGCAGGA	540
	GTGGACTACG	AGCAGCGCAG	GCCTTCCTTT	GTGCTTGCTA	CGGCTTGTA	TTATTCGAAC	600
	CATTATTCCA	ATAACTACGG	ACGGGGAGCT	ACCACCAATG	TGGGCAGCAT	CCCTCAGCTA	660
60	TCGACACCTG	TTACTCCTCA	GATGGACAAC	GGGACCCACA	ACGTCCGTGT	ATACTTGGGT	720
	GCAAAAAATG	ATGTGATCGA	TGCCAGGATC	GACTATCGTT	TCTTCCGTTT	TATTCCCTAT	780
	CTGGGTACCG	ATCCGATGAA	GGCTCTCACA	GAACATACGC	CTGAACGTGA	CGTGACGATG	840
	AGTAATGAGT	TGTCGGATGA	TATTAAGCTC	GGTGTGGAAG	TTGCTACGGG	AGGATTGTTT	900
	TTTGCCAAAA	ACAGCGAAAT	GATTCAAACG	GGCGTTCTGT	CCGAAACCGA	CCGCAACCTG	960
65	TATTATGTGG	AGGGCGCGCC	CACAATCGGA	TTTGTGGAG	ACTCGGACAA	TATGCAATGG	1020
	AACATACAGG	CCGGAGTAGG	GATTTCTTCC	CATTTCCGGG	CCAAAGGGAG	GTGTTTTTTC	1080
	TGGCCTAAAC	TGGATGCTTC	GCTTAGTATC	TTCCCTTCAT	GGCGTGTGTA	TGCCAAAGCC	1140
	TTCCGGCGTG	TGATTCGAAA	TGCTCTCGCC	GATGTTATGC	AAGAGGAGAT	GCCCTACCTG	1200
	ATGCCCAATA	CGATTGTACT	CCCTTCGCGC	AATGCTTTGA	CCGCCCAATT	AGGGGTGAAG	1260
70	GGGAATATAG	CCGATGTGAT	ACGTATGGAG	GTTATGGCG	ACTTCTCCAA	GCTGACAGGT	1320
	GTGCTTTTCT	ATACTCCGAC	TCTACCTCTA	TATAATCCAT	CCGACTTGTA	TCAGTATAAT	1380
	GTGAGTTTCT	TGCCGATATA	TGCCGACGGC	AGCCGCTGGC	GCUCAGGTGG	TAAGCTGGAA	1440
	TACTCTTATC	GCGATATGCT	CCGCTTTCTG	GTAGACGCAT	CCTATGGCAA	GTGGAATTGG	1500
	GATGGAGGAC	TTGTCCGCTC	CATGCAGCCC	GATCTTATAT	TGAAGGCAGA	AGTAGGTGTT	1560
75	CATCCCATGG	CCCCATTGGA	TGTACAGCTC	CGGTATACAC	AGCTGAACGG	ACGGTATCGG	1620
	TATTCTTTTC	GCTCGGCTGG	CTCGGAAGCC	TTGGGTATCG	GTAATGTACA	TCTTCTTAGT	1680

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GCGGATGTTT CATAAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG 1740  
 CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800  
 GGTTTTAGCT GGACTTTC 1818

5

(2) INFORMATION FOR SEQ ID NO:77

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1071 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

30 AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60  
 TATCCACATA ACCTTGTGTT CATGATTTCG AAGCATTTCG GTATCATTTT GGGATTTCCT 120  
 TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATT TCTGAACCTT 180  
 CCGGCTACTG CACAGGCTTT GGCTGCCGGA GGCAAAGCTA TCACCATCGT AGACGACAA 240  
 UCCGACTGG CTTTGTAGAA TCCGGCTCTG CTGGATATG AATCCGGTGG CCGCGCCTTT 300  
 CTTTCTTATT TATATTATAT GAGTGGTTCG CATATGGGCA ATGCCTGTTA TGCCTCGTCC 360  
 35 GTGGGAGAGC GTGGCATGTG GGGTGTGGC ATGCGTTTCC TGAAGTACGG GTCTATGCAA 420  
 GGATACGATC AGAATGCGAT TGGCACCAGG TCTTTTAGTG CTTGGGATAT AGCTGTACAA 480  
 GGATTTTACA GCGATGAATC GAGCAACCAC TTCCGCGGTG GAGTCAGCCT AAAAGCATTG 540  
 TATTCTTCTA TCGAGACGTA TAGTTCCCTT GGCCTTGGTG TGGATGTCGG TATCAGTTAT 600  
 TACGACGATG ACAAAGGATA TTCCGCTTCC GCTCTGTTCA AGAAGCTAGG GGCAGCACTG 660  
 40 AAAGGCTATA ATGAAGAAGC GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTCCCGC 720  
 AGTTTATCA ATGCTCGGT TCGCTTGAC ATCACGTTGT TCAATCTGAA TCCGCACTAT 780  
 TTCAAGCGTC TTGTACCACG CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACCTTCTG 840  
 ATAGGAGCAG AATTACTCC TTCCGAGAGG TTTGGGTGCG GGCTGGGATA TACGCCACAG 900  
 ATTGCACAGG ATTTCGAGGT GGAAGGCGGC AACAAATGGG GAGGTCTTC GGCAGGCGTC 960  
 45 GGTTCACCTT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020  
 CTTTCGTTCA TGTGTTCGGT AGGTATCCGT TTGGACGATA AGAGCATCTT C 1071

50

(2) INFORMATION FOR SEQ ID NO:78

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1011 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

70 CCTCAGCCCG TCGGCCTTAA AGAATAAACC ATTAACCCCA TGTGCCTCGA ACCATAAT 60  
 GCTCCGATTT CATCCGAGTT GCTCGAGCAG GAGCTGACTG CCGATCGTTT TCTGCGGATG 120  
 75 ACAACCAAG CCGCAATGA GATCTATGTT TTTACGGCCG AAGAAGCTCC GCATTGCATG 180  
 AAAGAAGTAG GCCGACTGCG AGAAGAAGCC TTTCCGCATT ATGGCGGAGG TACTGGCAAG 240

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5 GCGATCGATA TAGACGAGTT CGACACCATG CCCGGGAGCT ACAAACAGCT GATCGTATGG 300  
 GATCCGCAAA ACAAGGCTAT ACTCGGAGGC TACCGCTTTA TCTATGGGGG GGACGTTGCT 360  
 TTGGATACCG ATGGCAAGCC TTTGCTGGCA ACGGCAGAGA TGTTCGCTT CAGTGATGCT 420  
 TTTTGGCAGG ATTATCTCCC CTACACAGTC GAATTGGGAC GTTCGTTTCGT GTCGCTCCAG 480  
 10 TACCAATCGA CACGGATGGG CACAAAGGCC ATTTTGTGTC TGGACAATCT TTGGGACGGT 540  
 ATCGGAGCAC TCAGTGTAGT CAATCCAGAG GCACTCTATT TCTATGGCAA GGTGACCATG 600  
 TACAAGACT ATGATCGGCG AGCTCGCAAT CTGATCCTGT ATTTTCTTCG CAAGCACTTC 660  
 TCCGATCCGG AAGGCTTGGT CAAGCCTATT CATCCCTAC CGATAGAGAT CAGTGGGAG 720  
 15 GACGAAGCCT TGTCTCTCTC ATCCGACTTT SACACCAATT ACAAGACTCT CAATATAGAA 780  
 GTGGCGAAGC TGGGTATCAA TATCCCTCCT CTCGTGAGTG CATATATAGC TTTGTCTCCG 840  
 GAGATGCGTG TTTTCGGCAC TGCAGTGAAT GAGTCTTTTG GAGAGGTGGA GGAAACCGGC 900  
 ATATTCAATG CTGTGGGTAA GATCCTGGAA GAGAAAAAC AACGGCACAT AGAGAGCTTC 960  
 ATCTCAGCG GGAACGAAAA AAAAGGCTCT GACAGTAGCA ATGGCCGATC A 1011

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(2) INFORMATION FOR SEQ ID NO:79

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

35

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

40 TACCACGGAG CGAGACTGGT CTATACCTTA TTTCCGAATA GAAACGACAT TCACCCATG 60  
 AAAACCATTT TAAGATACAG CCGCTTCCG GTCCGCTCTT TCTTTTGCTT TTTGGGAGCT 120  
 GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180  
 GTCCCTGTCT CCACCGAAGG GCAATACAGG GAGATTGTGT TGCAAACGAA AGAAAAAAGG 240  
 GGGGCCGATC TTTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCTATGT TCGTTTCGGC 300  
 TCGGCCTATG GCGATATTGC GGGCGACTAT CTTCCTTACA ACGGCATTA CTACTCTCTG 360  
 45 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAAC ATGGCACATT GCAGGGCAGT 420  
 GCTTCTACT CACGTGCCAT GCACAAACGC ATCGGCTGGA ATGCTCTGGC CAAGCCCGAA 480  
 GCTTACTATC CCTATTGGT GTCCGATTCG ACGGGCGGAG ACTATCATT CSAAGACTAT 540  
 CGGCTTGGCG GCTACTATT TTTTCGGCGC GCGCGCTTGC CCTCGGTAT AGGCTTCTCA 600  
 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCGTA CGACCAATAC GACCGGTGCA 660  
 50 TTGGAGCTTT CTTGTGCTAC CTCTTTGACG CTGCTCGAG AGAACAGGCT ATCGCTTTCG 720  
 GCTGCTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780  
 GACAAATTCT TCGTCAGCTA CGGTTTCGGT CAGGTGGAATG TCAGCAACAG CCCTATCTGG 840  
 TTCCGTATCT CCAGAATGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900  
 CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAAGAGAGG 960  
 55 TCGTCCATCA ATCTCTTTCG TTTGCTTTAC AATCGCTGCG GACTCTATGG TAGCTGGCAT 1020  
 CTGTGCGACT TCGATTTTTC ATTTTCAGCC GACTATGCTC TGGGCGAAGG GATAGAGCGG 1080  
 ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140  
 ATTCGCGGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACGCTATT 1200  
 CGCACGGATA GAGTTTGTGC CCTGAGAGTG AGTCCCGATA GTGATTICTA CGGCTATGAT 1260  
 60 GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTCCCGGT 1320  
 ATAGCCTATG ACCATGCCGG ATCCAAATTG GATTTTGGAC TTTTCGTTTC GGCTGCTTAT 1380  
 CGAATGGTGC TGACGCATTG GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCGACTAT 1440  
 CAGCTGCGCT ATTTGCCCTA TGCCTATCGT AATAGAGAAG GCGTGGAGGT GCGTCTCTCT 1500  
 CTGTACGTCT CGATTCCGAT GCAGAAATACC CACCGCCTGA TGACAGAGCT GCGGTTGTAT 1560  
 65 GGCGACCTGA TGAAGAGAAA GACGGGTATA GCCTATGGCA AAACGCCCGG TGTCTATCTA 1620  
 CATATCCTGT CCGATCCGCA AGCCGAACGA ACCTCCGSCC ATACCATCGS GCGTATCTGC 1680  
 AATATCTCCT ACCTCTTC 1698

70

(2) INFORMATION FOR SEQ ID NO:80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2457

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

AGGACGAACG	TTTTCTTATC	1TTGTCCCAT	AAAATTGGGA	GAAGGGGTGC	TTCCTGTAGC	60
AATCGGAATG	CGTGGATGGC	TGAGAACAAA	CCCTCATCAC	CTGAACCGGA	TAATACCGGC	120
GTAGGAAACT	CTCCGCTGGA	CTATCTTCAC	GGCGAAGCAA	TCATTCCCCC	TCTCTCTTCT	180
TTGTCCAACT	TCAATGATAA	GAGATTTATG	AAAAAANTTC	ACATGATTGC	CGCCTTAGCC	240
TCTCTGCCIT	TCTGCCGTAC	GGCACAAGCA	CCCGTCTCCA	ACAGCGAGAT	AGATAGTCTT	300
AGCAATGTGC	AGCTCCAGAC	CGTACAGGTC	GTAGCTACTC	GGCCACGGCG	GAANACCCCT	360
GTCCGCTTAG	CCAACGTTTC	CAAGGCGGAA	CTTTCCAAAT	CCAATTATGG	TCGTGACATC	420
CCCTATCTCG	TGATGCTGAC	TCCCTCCGTG	GTAGCCACCA	GGGATGCCGG	TACGGGTATC	480
GGATATTCGG	GCTTTCGGGT	GCGTGGCAOC	GATGCCAATC	GCATCAACAT	AACTACCAAT	540
GGAGTACCCC	TCAAGCACTC	CGAATCTCAG	TCCGTCTTTT	GGGTGAATAT	GCCCGACTTC	600
GCCCTCTTCA	TGGAAGACCT	TCAGGTGCAG	CGAGGTGTGG	GTACTTCCAC	CAATGGTGGC	660
GGAGCTTTTC	GGGCAAGTGT	CAATATGCGT	ACGGATAATT	TGGGACTGGC	TCCCTATGGC	720
CGTGTGCAIT	TGAGCGGAGG	TTGTTTCGGC	ACATTCCGCC	GATCGGTCAA	ACTCGGTAGC	780
GGACGCATCG	GTCCGCAATT	GGCAGTGGAT	GCCCGCCTGT	CCAAAATCGG	TTCCGACGGC	840
TACGTGGATA	GAGGAAGCGT	GGATCTGAAA	TCCTATTTCG	CACAGGTGGG	CTATTTCGGT	900
AGCAACACGG	CTCTCAGGTT	CATCACTTTC	GGAGGAAAAG	AAGTTACGGG	TATCGCATGG	960
AACGGTCTTT	CCAAGGAGGA	TGAAGCCAAA	TATGGCCGCC	GATACACAG	TGCCGCTCTT	1020
ATGTACGTGG	ACGCCGAAGG	AGTACCGCAC	TACTACCACA	ATACCGACAA	TTACGAGCAG	1080
CGTCACTACC	ATGCCATCAT	GACGCACAGC	TTCTCTCCTT	CCGTTATCCT	CAACCTCACG	1140
GCACACTACA	CGGCCGGATA	TGGCTATACG	GACGAATATC	GTACCGGACG	TAAACTAAAG	1200
GAATATGCAC	TGCGCCCTTA	TGTGGAAAAC	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
CGTCAGAAAT	ATCTGGACAA	TGACTTCGGA	GGACTCATCG	GTTCCGTTAA	CTGGCACACC	1320
GGTGCATGGG	ATTTGCAGTT	CGGGGCCCTCG	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
AACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAACTCGCA	GATCACTCCG	1500
GAACGTGAAC	TCTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACACGAT	AAACGGCATC	1560
ACGGACGAAT	ATGATGAGGT	ACAGGGGAAGT	ATGCAGCACA	TCGATTTGGA	CAAGACCTTC	1620
CCCTTCCTCA	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
GCTTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCGGAATA	1740
GGACAGTATC	CTACGCCCTGA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
CCCTCTTGT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGCTG	1860
GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAACA	ACGTCCCCGA	CAGCTACCGT	1920
ATGGGACTGG	AGCTGACTCT	CGGTTGGCAG	ATCCTTCCTC	GTTTGCTGCG	TGGGATGCT	1980
TCTTCACTA	TGAGTCGCAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
GCGGACTACA	ACTGGCTCGA	ACTCAAGGAG	GAGACCCTCG	AAAGCACGGA	TATAGCCTAC	2100
TGCCCCAATG	TCATTGCCGG	CAGCATGCTT	ACCCCTCTCT	ATGCCGGTTT	CGAAATGGCT	2160
TGGACGAGCC	GCITCGTCAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
CTTCTCTCT	ATTGGGTGAA	CGACCTCCGC	CTCGGCTATG	TGCTGCCGGT	TCACTTCGTT	2280
AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCAAT	2340
GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGGAG	AACTAAGTGC	ATATGCCGAT	2400
CTGCGTTATT	ATCCTCAGGC	CGGATTTAAT	GCATGGGTA	GTCTGACAA	CGATTTC	2457

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1596 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

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10 TACAGGCGAT CGGGAAGGGT TTGCTCTCGT ATCCTCCGGA ACAAACGTTT CTACGCAGAT 60
   ACTCGGTTAC AGCCGAGAAAG AGCGGTTTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA 120
   AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG 180
   CGGTTTCCGA TGSTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TGTGCCCAAG 240
   CGTCTTGGC GCGCCATCGG TAAACGATA GCGGTCAATC TGGCGTATG GGGCTTCGAT 300
15 CATTTTCATCA TGAACGAGGA CTTTGACAGC ATCAGTTGGC AGACTATCAA GAGCAATTC 360
   CAAACAGGCT TTGGCTGGGA CAATGACAAAG TTTGTCACCA ACCTCTTCGC ACATCCTTAT 420
   CACGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGTTT TGAGCTTCAG GCACTCTGCT 480
   CCGTTTGCCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT 540
   ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG 600
   CTGTCCGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG 660
20 GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT 720
   TCTGTCCGGA GTCCGAGCGG ACAGATATTT CAGTCTGTCC CCATAAACAT AGTCGTGAT 780
   GCGGCTTTC GCTTTTGGC AGACAAGCGG CATGCCCGAA CCGGTGCCAC GGCTCTGACC 840
   CTGAATCTGA GATTGACTA CCGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT 900
   TTCTTCCAA TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC 960
   AATCTGATCG GAATCCTAAG CCGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG 1020
   GGAGGTCTCT TTCAGCACTT CCACTACTAC AATTCGGAAA AACGAATAAG CAAAATTCG 1080
   ATCTTCCAGC ACCACGGAAA ATTCGACGTA TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT 1140
   CTGAATGTGC TCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC 1200
30 TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG 1260
   TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG 1320
   CCGCACCAGA AAAATACCGA TGTACGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG 1380
   CGCTACTGG TGACGAGTTC CGAGTTCGCA TTTCATCCTG GCCCTGGCA TGTAGCCATC 1440
   GTCCCTCGCC GTTTCATCCG CAAAACAGCC TATCAATTCT ACCCTAAGCT ATCATTGAT 1500
35 ACCGGCGACA TACAGCTGCG TGTCGGATT CACTTC 1560

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(2) INFORMATION FOR SEQ ID NO:82

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40 (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 900 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
   (iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
   (vi) ORIGINAL SOURCE:
   (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
   (A) NAME/KEY: misc_feature
   (B) LOCATION 1...900

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

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60 AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG 60
   TTCACCTTGG CGAACGCACA AGAAGCAAAC ACTGCATCTG ACACTCCCAA AAAGGACTGG 120
   ACTATAAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC 180
   GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA 240
65 GATAAATGGA GTTGGGACAA CGGTTTGGCT ACAGACTTCG GTCTGACCTA CACAACAGCC 300
   AACAAAGTGA ACAAAAGTGT AGACAAGATC GAACCTCTCA CGAAGGCCGG CTATGAGATC 360
   GGCAACATT GTTACGGAAG TGCGCTTTTC ACTTTCCTCT CACACTATGC CAAAGGATAT 420
   GAGAAGCCCT CGSATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA 480
70 TATCTCACTC TCGGTATTGG TCGGCACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC 540
   TCTCCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC 600
   TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTCGAACCTG GTGCTTTGGT AGTGGGTTGG 660
   GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTCTCGGCT 720
   TATACGCACG ACTTTGGCAA CATTGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC 780
75 AACAAATTCC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC 840
   AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC 900

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## (2) INFORMATION FOR SEQ ID NO:83

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 663 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...663

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

25 ACGAGAGAGA GTGTGTTACA TTGTAGRACA AAACCTCAAAA AAGAACGAAA AATGAAGAAA 60  
 ATGATTTTGG CAGCTACTAT GCTGCTCGCA ACAATCGGTT TTGCAAATGC TCAGAGTCGT 120  
 CCTGCTCTTA GACTGGATGC TAACTTTGTC GGTAGTAACT TAATGCAAAA AGTCGCAAAAC 180  
 30 ACGAGCGTGA ACAATAAGAT GATCGTAGGC TTACGTGTTG GTGCTGCTGC TGAGTTGCT 240  
 CTTAGCAATG ATGGATTCTA TCTCGCCCCC GGATTGGCCT ATACGATGAG AGGTGCTAAG 300  
 ATGGAATCAC TAAGTGAAC GACAACTCGC TTGCATTATC TGCAAATACC GGTGAATGCC 360  
 GGTATGAGAT TTAGCTTTGC TGACAACATG GCTATTTCAT TGGGAAGCAGG TCCCTATTTT 420  
 GCATATGGTG TCGCCGGAAC GATTAAGACT AAAGTTGCAG GCGTTACGGC TTCTGTAGAT 480  
 35 GCCTTGGTG ATAACGGATA TAACCGTTTC GACTTGGGCT TGGGCTTGTC TGCTGCCTTG 540  
 AGCTACGACC GTTATTACGT ACAAATTGGA TATGAGCATG GATTGCTTAA TATGTTGAAG 600  
 GATGCTCCGG ATAAGACTTC TTTGCGTAAT CATGACTTCT TTGTGGGTCT CGGTGTTCCG 660  
 TTC 663

## (2) INFORMATION FOR SEQ ID NO:84

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 744 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...744

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

60 ATCAACGAA TAGAAATGAA AAGGATTTT ACTGTAGCCC TTGTGCTACT TGCTTCGGTC 60  
 ACTATGGCCA TCGGACAAAG CCGCCCCGCA CTTGCGCTAG ATGCCAATT CGTAGGCAGC 120  
 65 AATCAGAGCA TGAAAGAGAG CCGATATGTG TGGGACACCA AAATGAATGT CGGCCTGCGG 180  
 GTCGGTGCCG CTGCCGAATT CATGATCGGA TCAAGAGGAT TCTACTTGGC TCCGGGTCTG 240  
 AACTATACGA TGAAGGGCTC CAAAACCGAA TGGGATATAC CCGAATGGT TCCTGGTACC 300  
 TATATTACGA TGGTTTCCAC TCGCTTGCAC TATCTGCAAC TGCCGATCAA TGCCGGCATG 360  
 70 CGGTTCCGAC TGATGAATGA CATGGCGGTT TCGATCGAAG CGGGTCCTTT CCTTGCTATC 420  
 GGTATATATG GTACATATCG GCAGAGTTG GAAGGATGGA AGCCGAACAA CTACAGCACA 480  
 GAGTTTTTTT GCCCAACGCT TGGTGGCCCA ACAATATCC GCTGGGACAT CGGGGCAAAAC 540  
 ATAATAGCCG CATTCACCTA TAAGCGTTAT TATATACAGA TAGGCTATGA ACATGGATTT 600  
 GTGGATATTG TGTCAGGTGG AGGTTCTGAT ATTCCCGAC TGAACGACAA TAGGCAATCC 660  
 75 TCTTCGACGA CCGCTCTAAG AGAAAAGGGA AATAACGAAT ACGCTTATTA TCGTGACTTC 720  
 TTCGTGGGCA TAGGTTACCG CTTT 744



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GAUGACAATC GCTATGGATT TTATTTGAGG AATGGTGGAT ATTATTTTGC CTTACGCGAC 900  
 TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTCAATGGG CATTTCAGCC 960  
 CAATCGAAAT ATAAGAAGAG GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA 1020  
 TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCAACCAG TCTGAATATC 1080  
 5 CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAATGTC 1140  
 AATTTTGCCA CUGGGAGCTA TTTCAGAAAT TCGCTGAATA CCACCTATGA TGTCAATGCC 1200  
 CGTACTGCTA CGACACGAAG TTCGGCCGTG AGCTATTGCG GCAAGTTTCC GGGTACTCCT 1260  
 TTTTCGATTA CCGGTAGCAT GGATATCAGC CAGAACATGC GCGATACGAC GGTGAGCCTT 1320  
 ACCTTGCCGA ATCTTTTCGAT TAATATGTCC ACGCGTTATC CTTCACAGCG GAAGACCCGT 1380  
 10 GTAGGACCGG AGCGATGGTA CGAGAAGTTG AGTGTGGGCI ATTCCGGTCA GCTTCGCAAT 1440  
 AGTATCTTGA CAAAGAGAA AGATTTGCTC CAGAGCAATC TCGTGCAGCA TTGGAAGAAT 1500  
 GGTATGCGTC ATTCGCTACC GATCAGTTTG ACTGTCCCTT TGTGGATTA TATCAATCTG 1560  
 ACTATGGGGG TTAACACAA TGAGTGGTGG TACACGAAAG GCATACGGAA GTCGTGGAAT 1620  
 GAGGATAAGA AAACATTCCCT GCCTTCGGAC ACGACCTATA AATTCCGCGAG ACTGTACGAT 1680  
 15 TACAGTCTGT CGGCAGGCTT ATCTACCACA TTGTACGGTA TGTTCAGGCC TTGGAAACCT 1740  
 TTTTCTTCG GAGGCAATCT CATTATGATC CGTCATCGCT TCACGCCCAC TGTCACTTTC 1800  
 TCCTATATGC CGGACTTAC GAAACGCGAA TATGGCTTTT GGGAGCTTCT TGAGCATACG 1860  
 GATCAGAACG GCAAGCTGCA TACGCTGCTC TACTCTCCTT ATTCGAGCA GATATTCGCT 1920  
 20 GCTCCCTCCA TGGGCAATGC AGGATCTGTC AATTTCTCTT TTGACAACAA CTTAGAGGCC 1980  
 AAGATCAAT CCAATCGGA TTCGACAGGG ATCAAGAAGA TCAGCCTGAT AGATCAGTTC 2040  
 ACATGGTCTA CATCCTATAA TATGTTTSCC GATTCGATCC GATGGAGCAA TATCTCGGCT 2100  
 TCGCTGGCAC TTGCGCTCTC CAAGAGCTTT ACCTTGCGCT TGTCCGGTCT GTTCGATCCC 2160  
 TATTGACGA AGTATTATGA GGGAGAAGAT GGGGAAGATCA TTCCCTATAA GAGCAACGAC 2220  
 25 CTGCGCATTT TTAACGCAA GGGATTGGCA CGCCTGATCA GTACGGGTAC TTCTTTCAGC 2280  
 TATACGCTCA ACAAGAGTC GCTCAGCGGA TTGATAGCTC TTTTCAGTGG CAAAAAGGAG 2340  
 CGGAGAGATG AAAAGAAAAA CACAGGGGCT ACTCCTCATG AAGGAGACGA TGCTGCCGAT 2400  
 ATACTTGAGG GAGGAAGACC GCAAAATGAA AGTGGGGGGT CGCTCCTCGA GCGCAACCGT 2460  
 CAGGGCGGAG CAGTGGATCA GGATGGTTAC TTCGCATATT CGATCCCATG GAGCCTGTCC 2520  
 30 TTCGACTATA GTTGAATAT TGCTACCGAC TACAATAGGT ACAATGTCAA TAAGATGGAG 2580  
 CACTACTACC GGGTAACGCA GAATCTGAGC TTTCGCGCCA ATATCCAGCC TACACCGAAC 2640  
 TGGAGCTTCG GATTCAATGC GAACTACAAT TTCGACTTGA AGAAAATAAC ATCGCTTACC 2700  
 TGCAACGTCA CTCGCGACAT GCATCTCTGG GCTATCTCGG CCAATTTCTAT CCTATAGGA 2760  
 GCATACAAAT CCTATAATTT CGTCATATCG GTGAAGAGTT CACTCTTGCA GGATCTGAAG 2820  
 35 TATCAGCAGA GCAATCGTCC CATCACGAAT ACTTGGTAT 2885

## (2) INFORMATION FOR SEQ ID NO:87

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3753  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

60 AAATGGAAT TGGCATGCGC TTTTGATTGC GCGTGTGTT TCGATCCATT TGTAGTAAC 60  
 AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTT TCTTTTATTC 120  
 TGCACGGTAT TTACCTTTCA AATAAAGCT CGCCCTATG AAAGATTTGC AGATGTAGAG 180  
 AAGCCTTGA TACAGAAACA TTCAATGGAT TCTAAATTGG TGCCCTGCAA TAAGGGTAAC 240  
 65 TTAATTCAG CTGAAATGT ATACCAATCT GTTCTGAAC ATAGTGACTT AGTTATTTC 300  
 CCTGTGAACG AAATAAGGCC TGCAAAATCGT TTCCCTTCGC ATAGGAAGTC TTTTTTGA 360  
 GAAATCTAC GGGCATCTCC CCCCAGTAGT CCGTTGCGG TCGACAAGTA TGCGGTACCG 420  
 GTTGCCATC CAATGGATCC TGAAATCCC AATGCGTGG ATGTGACGCT AAAATCACT 480  
 ACTAAAGCGG TAACAGTACC TGTGATGTG GTGATGGTTA TCGACCAATC TTCGTCAATG 540  
 70 GGAGGGGAAA ACATTGCCAG ATTAAAGTCT GCCATTGCAT CCGGACAGCG TTTTGTGAAA 600  
 AAAATGTTGC CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTGT GAGTTATGAC 660  
 CATGAGCCTC ATGCTTATC TGATTTTACC AAAGACACTG CTTTCTCTG TCAAAAAATC 720  
 CGGGCTTTGA CTCCTATTG GGGAAACCAT ACCCAGGGGG GGCTTAAAT GGCAGAAAC 780  
 ATTATGGCCA CTTCTACTGC TGTGGATAAG CATATCATAT TGATGTCTGA CGGGTTAGCG 840  
 75 ACGGAGCAGT ATCTGTAA AAATGTAAC ACTGCAGACT TCATTGGCAA AACTGAAAT 900  
 GCGAATGATC CCATTGATTT GGTATACAA GGAGCAATTA ATTCCTCTAC AAATTATGTT 960

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TCCACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020  
 CGGAGAAATC TGCCGGAATC CAAATTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080  
 GATGGTGTGG CTGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140  
 TTCCCTTGTA ACCTGTCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200  
 5 CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGCGCA ACAATTCGTT GAAACTAACC 1260  
 GCTACAGACG AGAATCACTT CTTTACGGCG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320  
 AATATTGCCC AAACATTAA TATAGGTATA CAGAGGGGGG AGGTGACGGA CTTTGTAGCT 1380  
 CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATT GCTAAATGTT 1440  
 TCAAAATGGA CGGTGCACTA TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500  
 10 ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATTT ATGCCGATT GGTATATATA 1560  
 CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTC 1620  
 GATACCAATA CCGAGGCAAA ATTGACCTAT ACCAATTCCTA ATGGCGAACC GAATCAGCAG 1680  
 TTAATTTTCC CACGTCCGAC GGTAAAGTTA GGTATGCTG TTATTAAGCG GCACTATGTA 1740  
 TTGGTAAATA AAGACGGTCA ACCCATACAG GCAAAATGGA CAGTTGTCAG TTCCCTAAGC 1800  
 15 GAGGCTCATG TTCTACATGC ACAAGATTTT TTTTTCCTCT CAGGTGGAGG TCATATTGTT 1860  
 CCCAAATGGA TAAAGTTGGA CAAAACGACC GAAGCATTAC AGTACTATT CGTACCGCCG 1920  
 ACTAACACGG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTGGA AGTCCAGGCG 1980  
 TCCACGCCCA ATCCGGGGCA AATCGGTATC AGTTGGAAAA AACCGGACAG AAAGCTTAC 2040  
 TTGCTTACA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100  
 20 GATGTGACGT CCAATTGGAC AGSAGCCCAA GTACCGCTCA CAGGAGAAGA TGTAGAGTTT 2160  
 GCAACGACAG AAAATTTCCG TTCTCCGGCG GTAGCCGATT TGCACTGCC GACAACCAAC 2220  
 CCCAAATATG TCGGTAACTT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280  
 AGTCAATTGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGCTGG TACGATCGTC 2340  
 GTGAAGTCGT CGAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAT 2400  
 25 CAAATGTAG GGGGACCGT CGAGTTTAC AATCAGGAT ATGATTGTGC CGATTGTGGT 2460  
 ATGTATCGCA GGAAGTCGCA GTATTTCGGT ATCCCTGTCA MTGAATCAGG TTTTCCAATT 2520  
 AATGATGTGG GCGGAACGA GACCGTCAAC CAATGGGTTG AGCCTTCAA TGGCGATAAG 2580  
 TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAA AATCAAGGG CTACCAGATC 2640  
 ACGAATGAGC TGCAGGCACA GCCTACGGGA GTTTACAGCT TCAAGGATAT GATTGTGTG 2700  
 30 TGCGATGCCCT TCCTGAATCT GACACGCACG TCCGGTGTCA ACTACTCGGG CGCCAACTTG 2760  
 ATCGGAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGTCTT CCCGCCGGA 2820  
 GTCGAGCAGA CGGTGTATCT GTTCAACACG GGAACACGCG ACCAGTGGCG TAAGCTTAAT 2880  
 GGAAGCAGCG TTTCAGGCTA TCGAGCCGGT CAGTACCTCT CTGTACCTAA GAATACAGCG 2940  
 GGTCAAGACA ATCTTCGGGA TCGTATTCCA TCGATGCATT CCTTCTTGGT GAAGATGCAG 3000  
 35 AACGGAGCGT CTTGTACGTT GCAATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060  
 AACAAACGGTA ATGGTACGCA GATCAGATGG CGATCCGGCA ACTCCGGATC GCGAATATG 3120  
 CGGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCGGCCG ACCGTTTGTG GATCTTTACC 3180  
 GATGGGGGTC TTTCTTTCGG ATTCGACAAC GGCTGGGATG GTCGCAAGCT GACTGAAAA 3240  
 40 GGTTTGTAC AACTTTATGC GATGCTGAC ATCGGTAATG ATAAATTTCCA GGTTCAGGG 3300  
 GTTCCGGAGT TGAATAACCT GCTGATCGGC TTCGATCGCG ATAAGGATGG TCAATACAG 3360  
 TTGGAGTTTG TCCTTTCGGA TCATTTTTCG AAAGGGGCTG TTTACCTGCA CGATCTTCAG 3420  
 TCAGGAGCCA AACACCGTAT TACGAATCT ACCTCGTATT CATTCGATGC CAAGCGGGGA 3480  
 GATTCGGGGC CTCGTTTCCG CTTGTCTAT GGAATGTATG AGAACGTAGA TGATTGCGAT 3540  
 45 GTCTGAGTA CAAATGGCCG TGAATTTATA ATTCTGAATC AAGATGCTCT TGACTGCACT 3600  
 GTAAACCTTAT TCACAATAGA AGTAAGCTT CTTCGCCGCT TGAAGATATT AGCTGGTATC 3660  
 AGAGAAGTCA TGAAGTGCA GACCGGAGGG GCCTATATTG TGCATCTTCA AAATGCTTTC 3720  
 ACTAATGATG TGCATAAGGT GCTTGTGAG TAT 3753

50 (2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

60 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

65 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1278

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ACTATGGAG TGAAGAAAA CACAGTGGTG CTACGCCCTC TGATTGGTT CGTGGGCATT 60  
 CTCTCTTCC ACTCTCACG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA 120  
 75 TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTCTCTCTT TGATTTCATG 180



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5 AGCTCGCGTA CGAGAGTGAG AGGTGAGCTG GAGAGGTCGT TCGGTAATTC GAAAGTAGCC 240  
 GTATCGGTCA ATGCCACCTA CAATGCTCTA CTGAAAGACG AGACCGGCTT ACGTTTACGT 300  
 GAAGCCTTCT TCGAGCATCA GGAAGAGCAT TGGGGCTTGC GCCTCGGACG ACAGATTGTC 360  
 ATTTGGGGGG CTGCGGACGG TGTGCGCATC ACGGATCTGA TCTCCCGGAT GGATATGACC 420  
 GAGTTTCTGG CACAGGATTA CGATGATATT CGTATGCCGG TCAATGCATT GCGTTTCTCT 480  
 GTCTTCAACG AATCGATGAA AGTGGAAATC GTGGTACTGC CTGTATTGCA GGGGTACCGT 540  
 CTGCTGTGG ATCCTCGCAA TCCTTGGAAAT ATCTTCTCCC TTTCGCCCAT TGCTCAGGGG 600  
 ATGAATATCG TCTGGAAGA AGAAGCCGGC AAACCGGCTT TCAAGGTTGC CAATATCGAG 660  
 TACGGTGCGC GATGGAGCAC TACGCTCTCC GGTATCGACT TCGCTTTGGC TGCAATGCA 720  
 10 ACATGGAACA AGATGCCUGT CATCGAAGTA CAGGGCATTG TGCCGACGGA AATCATCGTT 780  
 AGCCCTCGCT ATTATCGTAT GGGATTTGTC GCGGGCGACC TCTCGTACC CGTCGGACAG 840  
 TTGTGTTTCA GGGGAGAGGC TGGGTTCAAT ATCGACAAAC ACTTCACCTA TAAGAGTCAT 900  
 GCGGAGCAAG AGGGTTTCCA AACAAATCAAT TGGTTGGCCG GAGCCGATTG GTATGCTCCC 960  
 GGTGAATGGA TGATCTCAGG ACAATTCTCA ATGGAAGACA TATTGAGTA TAGGGATTTC 1020  
 15 ATCTCCCAAA GACAACATTC TACCCTGATT ACTCTCAATG TTCCAAGAA ATTCTTCGGC 1080  
 AGTACACTCC AACTTTCCGA CTTCACCTAC TACGACCTTA CCGGCAAGG ATGGTTCAGT 1140  
 CGCTTTGCAG CTGACTATGC CTGGAACGAT CAGATACATC TGATGGCCGG ATATGACTGG 1200  
 TTCAGTAGTA AGGGCAGCGG TATATTCGAT CGGTACAAAG ACAATTCCGA ACTCTGGTTC 1260  
 20 AAAGCCCGCT ACAGCTTC 1278

## (2) INFORMATION FOR SEQ ID NO:89

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 40 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1392  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

45 TACGGCAAAA GAAGAAAGCT CGGAACCTCC GTCCGACCTT CCGTTCTAAC CCAATCAGA 60  
 TTTATTTTGG ACTTACACCT TATTACTGAT TTTTGTGAAG GGCTTCGGGT CAATCCTATC 120  
 GGTGCAGAGC CCATAGTGGC TTTCATTATC GACCTGCTTC TTCTTTGCTG TTCGGCTTTT 180  
 ATGTCTCTCT GTGAGGTGCG TTATTTTTC AATAAGCCGA TCGATCTGCA GAACATCCGC 240  
 GAACGGAATC ACTCTTCGGA CATCGCGCTT TCCAAATTTAT TAGACAATTC GAATCAGCTA 300  
 50 TTAGTACTCA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CTTTCCAAAT 360  
 TATGCCATCG AGCAGACATT CTTTTCTCT TCTCCGATCA TTGGATTTCG GATCCAGACG 420  
 ATACTCCTGA CCACTGTTCT TTTGCTGTTT GGAGAGATTC TGCCGAAAGT GTATGCGCGG 480  
 AAGAATCCCG TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCGGTTAT CTATAAGATA 540  
 TTGTCAACGT TTTCAAAATT GCTGGTCAAA AGTACCGGCA TCGTTACCAG AGGTATCAGC 600  
 55 AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CCGTAGCCCT CACCACTACG 660  
 GAGGGAGAGC CGGAGGAGAA AGAAATGATT AACGAAATCA TCAAAATCTA TAATAAGACA 720  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATT 780  
 CGTAAGATGC TTGACTTCGT TGTTCGTCG GGTATTCCA GACTTCCCGT TTCAGAGGGG 840  
 TCAGAAGACA ATATCAAAGG GGTGATTAC ATCAAAGATC TAATCCACA CATGGATAAA 900  
 60 GCGCATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTTGTCCC CGAAAACAAG 960  
 CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCIC CATCGTTGTG 1020  
 GATGAGTTCG GTGGCACTTG CGGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 1080  
 GCGGAGATTA CGGACGAGTA CGATGAGGAA GAACCTCCCT TTAAGGTTTT GGGGGATGGC 1140  
 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCGATGTTT GACACTATCT TGACCTTCCG 1200  
 65 GAAATGCTT TCGGTGAATT GGGGACGAG GTAGATACAC TAAGTGGGCT CTCTTGGAA 1260  
 ATCAAGCAGG AACTCCCCCA TGTGGGCGAT ACAGCAGTGT ACGAGCCATT CCGCTTCAA 1320  
 GTGACCAAAA TGGACRAGCG CCGAATCATC GAAATCAAGA TTTTCCCTTT CGAGCGCACT 1380  
 70 TGGGAGGTG AA 1392

## (2) INFORMATION FOR SEQ ID NO:90

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

20	ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA	60
	TCCCGGATGT ATTGCGCAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC	120
	AAAACCATAC AAGGAACGAT ATTGCCCGTA CTGGATTICA AAACCGAAAA GGAAATGTG	180
	TTCACCTTCA AAAATACTGC CAATCTCAAT CTGCTGATAA AGCACGGTCA AGTAATCAAC	240
	TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT	300
25	TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT	360
	TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATT'TTTCGAA	420
	TTCGAAAAGT GGAACAGGCC AGCCACTAGC CTCTTTGCAG GAACCTATGC ATACAGCCGA	480
	AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT	540
30	ACAATACGG CTATTCACCA GGGAAAGCCT GACAGTTATT TTAAGAAGGC ACGTTTGGGA	600
	GGAGCTATCG ACCTCAAATA CCATATCACA CCTACGATAG GAATACGGGG GGCCTATCGG	660
	ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTTGATGTT	720
	GGTATCGATA TTTCGTTT	780
		798

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

60	ACTATATGCG TTGCCTTCTT ATCCGCTCCG GTTGCGGCAT TGCGCGAGTC GCCGCCAATG	60
	GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTG TGATAAAGGA	120
	AAGGGGTTTC ACTACAGACT ATTCACAAGC AATAAACTTA AAGTGTGTC CACAGGTAAC	180
	AGCCGATACA TACACAATAA ACCAACAATC ATCCAAGCAA TGAACGAAT CGTTTTATCA	240
	TCCTTCTGTG TCGTTCTGTC CATACTTTCT TTGATGGCAC AGAACAATAC CCTCGATGTA	300
	CACATATCCG GTACGATCAA GGATGCTCC TCCGGGGAAC CAGTGCCCTA TGCCACTGTA	360
65	AGCATCCGGC TGACAGGAGC AGATACCACA CAGGTGTTCC GACAAGTGAC TGACGGCAAC	420
	GGCTACTTCG TCATAGGCCT GCCGGCAGCT CCCTCCTATC ACCTGACAGC TTGTTTCGTA	480
	GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCAGCA CATCAATCC	540
	ATCGACATT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA	600
	CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCTCTATA ATATGAAAGA TGACCCCGCA	660
70	GCCAAAGCA ACAACCTGCT CGAAATGCTG CGCAACGTTT CTTTGGTAAC GGTGGATGGT	720
	CAGGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCC	780
	TCGACCATGG TGAGCAGCAA CCGAAGGAG GTCTTTGCTC CCATTCTGTC CCATACGATC	840
	AAACGGGTGG AGGTATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC	900
	ATCCTGGACA TCGTCACGGA AGAAGGTAAG AAGCTGGAAG GATATTGAGG TTCCATCACG	960
75	GCCAGTGACA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC	1020
	AAAGTCGGGC TGACTACCAA CTATAACTAC TACGGTGSCA AAAACAAGGG CTCCTGCTAC	1080

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	TTTACCGAAC	GTA	CTACATC	CAT	GCTCCAA	ACG	ATAGAAG	AAG	GCAAAGG	GCA	AGAAACC	1140
	TTTGGCGGAC	ACT	TCGGCAA	TGC	CTCCTC	TCAT	TCGAGA	TAG	ATTCGCT	CAAT	CTCTTT	1200
	ACGGTGGGCG	GCA	ATGTACG	CCT	TTGGGAG	ATG	ACCACCG	ACC	GGAACAG	CGT	AGAAAAA	1260
	AGCTTTGGCG	GCAG	CAACCT	CAT	GTCTAC	ATAG	CAGAA	AACT	CAAAAC	ACAG	ATGGAT	1320
5	GCCGGATCAT	ACG	AGCTCAA	TGC	CGACTAT	CAG	CACAGCA	CTC	GCCTGCC	GGG	CGAATTG	1380
	CTCACCGTTT	CCT	ACGCTT	CAC	TCACAAT	CCT	AATAATA	GCG	AGACCTT	CATT	GACCAA	1440
	TGGAAGCGCG	ATC	CGCTCAA	CAC	AGCTAAT	ACG	ATCCAGT	ACG	CGGCGCA	GCAT	CTCCAA	1500
	TCCGATGCGG	GCAT	GGACGA	ACAT	ACGGCA	CAAG	TGGACT	ATAC	ACGTCC	CTTA	GGACAA	1560
	GCACATTCTT	TGGA	AGCAGG	GCT	GAAGTAC	ATCT	ATCGTC	ATG	CCACGAG	CGAT	CTCTC	1620
10	TATGAGATAC	GACCA	TCCGA	AGAT	GCTCCG	TGG	CAGCCCG	GCT	CTCTATA	TGC	CAGAAAT	1680
	CCGTGGAACG	GAA	AGTTCCG	CCAC	GATCAA	TAC	ATCGGAG	CAG	CCATATG	CGG	CTACAA	1740
	TATCGTAAGG	ATC	AGTATTC	TTT	GCAAAAC	GGC	CTCCGAG	TGG	AAAGCAG	CAGG	CTGAAA	1800
	GCACCTTTTC	CCG	AAAACGC	AGC	AGCAGAT	TTCT	CCACA	ACT	CGTTCGA	CTGG	TGCCA	1860
	CAGCTCACGC	TCGG	CTATAC	CCC	CTCGCC	ATGA	AGCAGC	TTA	AGCTGGC	CTAT	AACTTC	1920
15	GCAATCCAAC	GTCC	TGCAAT	CGG	CCAACTG	AAT	CCCTACC	GGC	TACAGAC	CAAC	GATTAT	1980
	CAAGTACAGT	ATGG	TAAATCC	CGAC	CTAAAG	TCGG	GAGAAGC	GTCA	CCACGT	CGGT	CTCTCC	2040
	TATAATCAAT	ACG	GAGCCAA	GST	CATGCTT	ACAG	CATGCG	TGCA	CTACGA	CTTC	TGCAAC	2100
	AACGCCATCC	AGA	AATACAC	CTT	CTCCGAC	CCG	GCCAATC	CCA	ATCTGTT	CCAC	CAGACC	2160
	TATGGCAATA	TCGG	ACGAGA	GCAT	TCTTTC	AGCT	TGAATA	CCT	ATGCCAT	GTAC	ACGCCG	2220
20	GCCGTATGGG	TCAG	GATTAT	GCT	CAACGGA	AATAT	CGATC	GCAC	ATTCCA	AAAG	AGCGAA	2280
	GCATCGGCA	TTAT	GTCAA	TTAT	GGTCC	GGCA	TGGTAT	ACT	CAGGCT	GAT	GTCAAC	2340
	CTGCCGAAGG	ATTG	AGCTGT	GAAT	CTCTTC	GGAG	GTTATT	ATCA	TGGGGG	AAGA	AGCTAC	2400
	CAGACGAAGT	ATGA	TGGCAA	TGT	TATCAAC	AATAT	CGGTA	TAG	CCAAACA	GCTT	TTGAC	2460
	AAAAAATTGA	GAGT	CTCGCT	GAG	CGCAAAC	AACAT	TCTATG	CGA	AGTATTC	GACAT	GGAAG	2520
25	AGCCGGACCA	TCGG	CATGG	ATT	TACTATT	TATT	CGGAAA	ATG	CCGGTAT	ACA	ACGGAGT	2580
	GTTTCCCTCA	GCCT	CACCTA	CAG	CTTCGGT	AAGAT	GAAATA	CACA	AGTGGC	CAAG	GTAGAG	2640
	CGTAGCATCG	TCAA	CGACGA	CCT	CAAGCAA	ACCT	CATCCC	AAGG	ACAGCA	GGGT	GCGGA	2700
	CAAGGAAATC	CTAC	CGGCAA	T								2721
30	(2) INFORMATION FOR SEQ ID NO:92											
	(i) SEQUENCE CHARACTERISTICS:											
35	(A) LENGTH: 1350 base pairs											
	(B) TYPE: nucleic acid											
	(C) STRANDEDNESS: double											
	(D) TOPOLOGY: circular											
40	(ii) MOLECULE TYPE: DNA (genomic)											
	(iii) HYPOTHETICAL: NO											
	(iv) ANTI-SENSE: NO											
45	(vi) ORIGINAL SOURCE:											
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS											
	(ix) FEATURE:											
50	(A) NAME/KEY: misc feature											
	(B) LOCATION 1...1350											
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92											
55	TGGTGCCAAAT	CCG	ACCCAAT	ACCT	CATTGC	CAT	GCAATAT	ATC	GAAACGC	TCA	AGGACAT	60
	CAACAAGGGC	GAT	CAGACCA	AGAC	CGTTTA	CCT	CCCGTTC	GAG	GCTACCG	GTAT	GCTCGG	120
	TGCCTTGGGC	GGT	ATGAAGG	ATT	TGGTGAA	AGG	ATGAGAC	TCT	CTGCCAT	TCT	TATCGCT	180
	TTGATTGTGA	TGCT	GCCTGC	TGT	GCTTAGC	GGG	CAGCATT	ATT	TATCCAT	GGC	GGGAGAG	240
	CGACTGGAGA	CGG	ACAGCAT	TCGT	CCGAAC	GAA	CTCTCGS	CAT	CGATCCG	AAG	TGCGCTT	300
	TTCTTTCGGA	ACA	ATGAATA	CAAT	GCAAGT	TCGT	CAAAAG	GTT	TATAGTT	GCG	GGTGCA	360
60	CGGGTTTCCG	CTTT	TGCCTC	TTAT	CTCGCTG	CGG	CAGCAC	ATG	GTGTGAA	GCT	TTGCTC	420
	GGAGTATCTA	CCCT	GAACTA	CTG	GGGGGCA	AGT	CGCTATC	CGG	CCGGTAT	CGCT	TATTCC	480
	GATTACCTT	ATT	GGACGGA	CTAT	AACGAC	TAT	GTACGCT	TGG	TATCCT	GCT	TATGTA	540
	CAGGCCATGC	TGA	AGCCGAC	GGC	CACGACT	GCT	CTCATGC	TGG	GCAATAT	AGC	CGGTGCT	600
	ACGGCTCACG	GACT	GATCGA	ACCG	ATCTAC	AAT	CCTGAGT	TGG	ATTGTAC	GGC	TGATCCT	660
65	GAAGCCCGTG	TGCA	AATTTCG	GGGT	GATTGG	ACAC	GTTTCC	GAAT	TGGATGT	TTG	GGTCAAT	720
	TGGATGAGCA	TGAT	TTTCAA	AAAT	GACAAAT	CAT	CAGGAGT	CGT	TTGTCTT	TGG	CTTGCTC	780
	ACTACTTCGA	AAT	TGTTATC	GGGT	GAAAGGC	AAAT	TGGGAC	TCG	AACCTGCC	CTT	GACGGCT	840
	ATTGCCACGC	ATC	GCGCGCG	GGA	ATACAAAC	TGG	GCGCAGC	AGG	ATACCGT	GCAT	ACATGG	900
	GTCAATGGAG	CTGT	CGGACT	TAAG	CTTTCCG	TAT	CGCCCTC	GTAC	CGACAA	ACCC	ATGCAG	960
70	ATTTGGGGAT	CTG	CTTATGG	TGT	GCGAGCC	TTGT	CAAGCG	GAG	GATACCT	CCCT	TACGAA	1020
	AGAGGGTGGG	GCG	GTTATCT	TTCT	CTCGGA	ATG	GAGCTGG	AGC	ACTTCGC	TTT	TCGTACC	1080
	GACTATTGGT	ACG	GCAGGCA	TTAC	GTTTCT	CCCT	TTGCTG	CAC	CTTTCGC	CAAT	TCCTG	1140
	ACGTATGACA	AAC	AGCCTCT	TAC	GAACGGT	TGG	GCGGATT	ATAT	TCGTCT	CTAT	GCGGAC	1200
	TATTCGTGGC	GGAT	GGCACG	AAG	TGTTTCG	TTG	GCGGCTG	TTG	CTCGGGT	ATG	GTTCAG	1260
75	CCTTCGGATC	GTTT	TGCGAT	GAG	CCACGCC	TTG	GAACTGA	CGAT	GCGTAT	CGAT	CCCAAA	1320

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TTCCCAATAG CTTTCTGAA AGGCAATCAT

1350

## (2) INFORMATION FOR SEQ ID NO:93

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1341

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

30

```

CGGTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC 60
TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG 120
GACTCGTGGC CGGCATATTC GCCCATTTGGC TCTTTGTCTT CATCTCACTC ATTTGATTCT 180
ATACCCGACC AACCTATGAA CAAATCGCTA TTATCATTGG CATCCCTCAT CCTGTGCGGT 240
ATGCCGGCCA TCGCCCAACA GACAGGACCG GCGAAGCACA GCGGCGAGCC TTCTCTGGCC 300
GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG 360
TCGTTCTACG ACCAGCGGCT TGTGATGAC GAATCCATA TCGGACACTT CAAGGTACAG 420
GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGGTTTGA CTGGCGACAA 480
CGTCTCAACC GTGCGGCGGA CGGCACTTCG TTGCGCGACA ATCTCTCCAA TGCCATCGAC 540
ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTCTTCGG ACCTCAGTAC 600
GCGGCTTTCG GAGGGATAGA ATACGACATG AACCCGCTAG AGATCTACCA GTACAGCGAC 660
CTTGTGGATT ACATGACCTG CTATCTTCG GCGGTGAATC TCGCATGGAA CTTCCACCCC 720
GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC 780
CACGTGACAC CCGATGTGCG TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG 840
AACGTATCCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTGATG GGCTCATCAG 900
GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC TGTTCATCC GGGCAAACGG 960
ATCAACGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG 1020
ACTGCTCGCT ACGGCAAGGG CAAGACCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG 1080
AAGTGGAACT TCCGATTTT CGATCAGGTC AATCTCTCC TCAAAGGCAT GTACAGAAAC 1140
GGCTATGCGC CTGCCCAATA CGGCGAGAGC AGCCACAGCG GCCACTCCTA GGGCTATATG 1200
GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTCGTAC CTACATAGGA 1260
CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CCGCGGTCTG 1320
ATCTATCAGA TACCTTTCTT A 1341

```

50

## (2) INFORMATION FOR SEQ ID NO:94

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 681 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

70

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

75

TATAAGCAAG CTATAATGAA ACATTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT 60

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5 TCTTTTCCG GTACCTATAC CTTTGACAAA GAAAATAATA CAGAAAAGTC ACGATTGAT 120  
 TTTTCTGTTA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180  
 TATACATCTG CTAACGATAG ACTTTTGTCT GGTGGAATTT ATCTGGGCTT GACACCAAGT 240  
 AAGAAAGAAA ATGCAACCGG CGTAGCATT CTTTTCTTAT CCCCCCTCC GGGTTATTAT 300  
 10 GTCGATATAT CCGGCAAGA AAATACCTTG AATTATGCGT TTACGTTGT CGGAGCATAT 360  
 AATAGAATAG CCATTCCAT ACGCCCTATC AAAAAATTTA ATTTCTCTT CTCTACAGAA 420  
 GTCGGAATGG CTGGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG 480  
 GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATHC 540  
 CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTCCTG CATGTCGGA 600  
 15 AAAAGGATCA ATGACTACCA GCRAAAGGAT CGAACCTTCA TTGCACCTAT CGACAACAGT 660  
 ATTGGCATAG GATTAAACCT C 681

## (2) INFORMATION FOR SEQ ID NO:95

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1218 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 25 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1218

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

35 ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60  
 ATGCTGAAAA ATAAATTGGC CCCCTGGGCC ATACTGTTC TTTTGTCTCC AAAGGCTATG 120  
 40 AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180  
 GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA 240  
 CAGTATTGGA ATCOGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300  
 TATACACCTT GGCTGTCCAA GCTGGTCAAT GATATTGCC TGATGCAGAT GACCGGTTTC 360  
 TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420  
 45 GGAAAGTTGG AGACTTTCGA CGAATTGGGC GAATCCATCG GAGAGGCCCA ACTTCTCCAT GGCTGTGCA 480  
 TTTGCTGTGC ATTTGGGCTA TAGCCGCCAG TTGTCGGAGA ACTTCTCCAT GGCTGTGCA 540  
 CTGCGTTACA TCCGCTCAGA CCAAGCACT CACAACCCG GAGAGATCA GGCCGGAAAT 600  
 GCCTTTGCGG CGGATATAGC CGGTATTTC CAGAAGTATG TGCTACTGGG TAATGCGGAG 660  
 AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720  
 50 GGTGTACAGA GTTTTTTCAT CCTACTTCG TTGAATCTCG GGACGGGGCT GTTGATCCG 780  
 ATCGATGACT ATAACAGCAT CAATTCAAC CTTGAACCTA GCAAGCTGCT TGACCCACT 840  
 CCTCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900  
 GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG 960  
 GAAGATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAATTT 1020  
 55 TTTGTTCGTG CCGGATATTC ATACCTGCAC CCCACCAVAG GCAATTTGCA GTACTTCAG 1080  
 GCCGGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCTACCT GTTGTCTAG 1140  
 ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA 1200  
 TTGCACAATT TGTCCAC 1218

## (2) INFORMATION FOR SEQ ID NO:96

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1356 base pairs  
 65 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 70 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1356

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

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CTAATAATCG AAAAGGAAAT GAAACAACA GTTCAACAAA TTATTCTGTG CCTGGCTTTA      60
ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGGAAAGAAAT AGCTCCTCCT      120
TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAATTCCCA ATATGGGGAT TGATTCAAAG      180
GGAAACAATCT ATGTAACCGT GACAAAAAGG ATTACGCAGG GAGCAAAATTA TACTTCTGAG      240
CAATTGGCTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG      300
TATTTTGATG ACAAGATAGT TCGGGATATT CAGACAGATG CATATGGCAG AGTTTATGTA      360
TGTACGACTT CTTCTCGAGA TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG      420
AGGTGTATAT TCAAACTTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT      480
TCGACAGGGG TGACTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAATGAT      540
TTGAGTTTCA ACACTATCTA TGAAGACTCT ACACCTATGA GCTGTGCTT TGCAGAGGCT      600
ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACAATGTC TACGACTATC      660
CTTACTTATC AAAACGGTGA GTTCGTGCGAT ATCTCGGAAA GTGAATTGAG TAACTCGATT      720
ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTAC TTCATATACA      780
CGATTATGTA GTGGAACCTT TCGGATCAGA AAAGCAGATG AAGGCAATG GCAACTTGTT      840
GGCGGAGATA TACGAATGTC GATCGTTCAA AATATATGCA TGATGGACGA CAACAAGATT      900
GCTTGTGAAG TCTTCGGGAC TCCTAACGGA GTAGATGGTC GGACAAGGGT TTGTGTTTCT      960
GACGATCTGT TCTTTGATTT TGAGTGGTAT GAAGATGAAA TATACGGAGG CCTGATATTT     1020
GACACTTTCT TCTATAGCCC TTGGGACAAA CTTCTTTATG CGAAATTGGS TGGGATTATG     1080
CTCAGGAGTA AAGAGTCTT TATAACCTCT TTCATTTCTC CGACAGTTGT ACAAGGAGTG     1140
GATGTCATATA CTTTGGCCGG GAAGATAAGG ATCGAAAGTG AAACCTCCGT GTCTGAGGTG     1200
TTGCTTTTCC ACCTGGCTGG CAGGATGGTA CTTGCGCAAA CCATTGATAA TAAATCTAT      1260
TCGACATAG ATACTAACGG ACTAAGCGA AGCGSTATTT ACGTAGTCTC GGTGCGGCTC      1320
TCTCCGGAC AGGTATTGAG TCATAAGGTG CAGGTA      1356

```

## (2) INFORMATION FOR SEQ ID NO:97

35

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 993 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

40

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

45

(1v) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...993

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

```

GGCCTGTACG GTATGCTGT TGIACCTATA ATAAITTTAT TTTGCGGTAT ATCAAATTAT      60
GCAAGACTCA TGATAATCCG GTGTCTTATC CGTCTCCGA GAACCGTCTT GTTCGGGTTG      120
ATATTGCTGG TAGGTCTTTT CTCTGCGATG GCGCAAGAGA AAAAGGATAG TCTCTCTACG      180
GTTACGCCAG TGCCGAATAG CAGCATGGTG GAGCAGACCC CTCTCTCTC CATTGATCAC      240
CCGCTCCTGC CCGCTTCTTT TCAGAATACC CTTACACTGA AAAGGTTTAG AGACAAACAT      300
CTTTCCGATG CTTTCCCTCA TGGATTGAAG CCTCATCGCT CATCTTTGCA ATTGAATGAG      360
GAACCTCACT TCGCGGCAGA GGTGCGGGAT TCGTTTCTC CCCTCTTGA NACTCGCCAC      420
GCTGCGGGTG TCCTTTTCATG GCGACCGACC GATAGGATGC ATTTTATAC ATCGGGCAAT      480
ATCGGTCTTG GCCATGATTT ATTGACCGGT GTGCGCAAGG ACTTCGGATG GAATGCTGGT      540
GCCGACTTCT TGCTGAGTCA AAATCTTACG GCACATGTCC AAGGCGGTTG GCAGCAGAAT      600
TTGCGCTTTA TACCTATGAC GGCTGTCAAT GSCCACTGC GTTGGCAAGC CACCGAGAGA      660
TTGAGTTTAA CCACGGTAT CGATTATCGA CAGGTACAGT GGAATGCTTT CGATAATAGA      720
ACGTTCTCGC TTAAGGAAG TGCTCGATAC GAATGATGS ACAATGTCTT TGTCAATGGA      780
TTTGGCAGCT ATCCTCTCTA CAGCAGTACG CGCTCAGGAC TCAATATGGC TGTTCGATG      840
CATGGATTCTG GCCCTCAGTA CGGTGGATCG CTTGAGCTGA AAGTCTCCGA GCGATTCCGC      900
TTTCCGCTCG GTATGGAGCG CGAATACAAT ATCTGGACTC GTCGGTGGGA AACGCATTAC      960
TTTGCTTATC CTGATTCTA TGGCGATAAG AAG      993

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75

## (2) INFORMATION FOR SEQ ID NO:98

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

25	GAGACGA	ACT	CTTGGGT	ATC	CAGCGAT	TGC	AATTCGA	CGA	CGATGAA	AAC	GAATAGAC	GA	60
	TACCGAT	TTG	TTTTGCC	GCT	TCTGCTAC	TCT	ACCGGAT	TGT	TGGCATG	GGG	GCAGGAT	TCT	120
	TCCACAG	GTA	GCAATAC	CAGC	GTTTGCA	ACT	GATTCCT	CGA	GTAGAGAG	T	CCCCACG	GAG	180
	CAGTCCG	CCT	ACCGCAT	TCA	TTCTGCC	TAT	ATGGTCG	GTG	GTGGCGG	AAG	CATAACG	CGC	240
	GACACCT	ATT	TGTCACG	CCCT	TCGTTAT	GGA	GGATGGAC	CAC	TGAATTT	GTT	GGGAGAG	AAG	300
	ACGTTCC	CTC	TCAAAGC	CTC	CGATTCC	CGT	TGGATGAT	CC	GTACCGG	GCA	TGAGCTG	GGAT	360
30	TTTGCCCT	GTA	TGGACAAT	CC	GGCCAATA	AT	GCTCATTT	CT	ATTCCTGT	CT	GTATAAC	CGGT	420
	TCCGCTG	CGG	CTCTTTAC	CG	CCTTGGCG	CT	AAGCATCT	GC	GAGCGCG	GTG	GATGGACA	AT	480
	CTGCGCT	TGG	CATTGCG	CCC	GGGCTTGG	AA	ATCGGGCT	TTG	GAGGAATT	TA	TAGTACAC	GC	540
	AACGGCA	ATA	ATCTGCG	AC	ATTGAAG	CTC	TACACCA	ATG	CCATCGCC	CA	AGCCTCG	ATA	600
	GGATACT	ACG	TCCCCTCC	GTA	AACTTTTC	CC	CTGTATTT	TC	GGTTGCT	CTC	CCAGATCA	AT	660
35	CTCTCGG	TAT	TAGCCTAT	GG	AAATGGTT	TTT	GGTGAGAG	CT	ATTACGAG	AA	TTTTTTG	CTC	720
	AAATAAC	GGCA	TTGCAGG	CTC	CCTGCATT	TC	ACTTATCC	GG	GCAAGTTT	AC	TCGGTTCA	CG	780
	ACACTCA	TAA	CGGCGGAT	AT	TCCCATTC	CGG	AACCTCTG	TAT	CGCTTCGT	GT	CGGTTAT	CGC	840
	TATTCCCA	T	TGGGCTCT	TC	GCTTAACG	CA	TTGGATACT	C	GAATCCAC	AG	TCATACG	GCT	900
	TTTATCG	GTT	TCGTACCG	GA	GTTTTACC	GTA	TCCGTTGG	GC	GCAAGGCC	AT	GAATACCG	GT	960
40	CGGAGAAC	CA	GTCTTTAC	TACTAT									987

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 957 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

65	TTTACGT	CCG	GTACGAT	ATT	CGTCCGT	TATA	GGCATAT	CCG	GCCGTGT	AGT	GTGCCGT	GAG	60
	GTTGAGG	ATA	ACGGAAG	GAG	AGAAGCT	GTG	CGTCATG	ATG	GATGGT	AGT	GACGCTG	CTC	120
	GTAATTG	TGC	GTATTGT	GGT	AGTAGTG	CGG	TACTCCT	TGC	CGGTCCAC	GT	ACATAAG	ACC	180
	GGCACTG	TTG	TATCGGG	CGGC	CATATTG	GGC	TTTCATC	CTC	TTGGAAAG	AC	CGTTCCAT	GTC	240
70	GATACCG	ATA	ACTTCTTT	TC	CTCCGAA	AGT	GATGAAC	CTG	AGAGCGGT	GT	TGCTACCG	GAA	300
	ATAGCCC	ACC	TGTGCGAA	AT	AGGATTTC	AG	ATCCACG	CTT	CCTCTAT	CCA	CGTAGCCG	TC	360
	CGAACCG	ATT	TTGGACAG	GC	GGGCATCC	AC	TGCCCAAT	GG	CGACCGAT	GC	GTCCGCT	ACC	420
	GAGTTTG	ACC	GATCGCG	CGGA	ATGTGCC	GAA	CGAACCT	CCG	CTCAAAAT	CGA	CACGGCC	ATA	480
	AGGAGCC	AGT	CCCAATT	TAT	CCGTACG	CA	ATTGACAC	TT	GCCCCAA	AG	CTCCGGC	ACC	540
75	ATTGGTG	GA	GTACCCAC	AC	CTCGCTG	CAC	CTGAAGST	CT	TCGATGG	AG	AGGCGAA	CTC	600
	GGGCATAT	TC	ACCCAAA	GAG	CGGACTG	AGA	TTCCGAG	TCG	TTGAGGG	GTA	CTCCATT	GTT	660

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AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC 720  
 CGTACCGGCA TCGCTGGTGG CTACCACGGA GGGAGTCAGC ATCAGCAGAT AGGGGATGTC 780  
 ACGACCATAA TTGGACTTGG AAGTTCCGGC CTTGCCGAACG TTGGTGTAAG CGACAGGGGT 840  
 TTTCCCGGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT 900  
 5 ATCTATCTCG CTGTTGGAGA CGGTGCTTG TGCCGTCAGG CAGAAAGGCA GGACGGC 957

## (2) INFORMATION FOR SEQ ID NO:100

- 10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1842 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 15 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc. feature  
 (B) LOCATION 1...1842

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:100

CCATATAATG TCCAATCTAT TAGCAACAAG ACGATTAAAA AACAAATGGA AACTTAAAG 60  
 AACATTGAGC CCAGAGAGGA TTTCAACTGG GAAGAGTTTG AGGCCGGTGG CGTCCATGCT 120  
 GCGGTGAGTC GTCAGGAGCA GGAAGCTGCT TATGACAAAA CGTCAATAC CATCAAGGAA 180  
 AAGGAAGTGG TAATGGGTAG GGTAACTGCT ATCAACAAGC GTGAAGTGGT TATCAATGTA 240  
 35 GGGTACAAAT CGGAAGGTGT GGTACCTGCA ACAGAATTCC GCTACAATCC CGAACTCAAA 300  
 TTGTCTCACC GCAAGGGTCG TGCCGCTCCG TCTTGGGAGC GCGTGAACGA GGCTCTCGAA 360  
 AAGACGAAAT TCGTAAAGGG CTATGTGAAG TCTCGTACCA AGGGTGGTAT GATCGTCGAT 420  
 GTATTGCGTA TCGAGGCTTT CCTCCCGGGA TCACAGATCG ACGTGCAGCC CATTCGCGAC 480  
 40 TACGATGCAT TCGTTGAGAA GACGATGGAG TTCAAGATTG TGAAATCAA TCAAGAATAT 540  
 AAGAAATGTA TTGTTTCCCA CAAGGTGCTC ATCGAAGCAG AGCTCGAACA ACAGAAGAAA 600  
 GAAATCATCG GCAAGCTCGA AAAAGGGCAG GACTCTGAAG GTATCGTCAA GAATATTACT 660  
 TCTTACGGAG TAATTATCGA CCTCGGTGGA GTGGATGGTC TTATCCATAT CACTGACCTT 720  
 TCATGGGCTC GTGTGGCTCA TCCGGAAGAA ATCGTACAGC TGGATCAGAA GATCAATGTC 780  
 45 GTTATCTCTG ACTTTGATGA AGATCGCAAG CGTATCGCTC TCGGACTCAA ACAGCTGATG 840  
 CCTCATCTCT GGGATGCTCT CGACAGCGAG CTTAAGGTAG GCGATAAGST GAAGGGTAAA 900  
 GTTGTGGTGA TGGCAGATTA CGGTGCTTTC GTTGAGATTG CACAGGGCGT TGAGGGTCTT 960  
 ATCCACGTAA GCGAAATGTC ATGGACACAG CACTTGCGTT CTGCTCAGGA CTTCTGCTAT 1020  
 GTAGGCGAGC AAGTGAAGC CGTGATCTG ACGCTCGACC GCGAAGAACG CAAATATGTC 1080  
 50 CTGCGTCTGA AGCAACTCAA GCCGGATCCT TGGGCTGATA TCGAAACTCG TTTCCCTGTA 1140  
 GGCTCTCTGC ACCATGCTCG TGTTCCGAAC TTCACCAATT TCGGTGTATT CGTTGAGATC 1200  
 GAAGAGGGCG TAGATGGCCT TATCCATATT TCCGACCTTT CTGGACGAA GAAGATCAAA 1260  
 CACCCACAGC AGTTTACGGA AGTAGGTGCT GATATCGAAG TTCAGGTAAT CGAGATCGAC 1320  
 AAGGAAAACC GTCGTCTCAG CTTGGGTGCT AAACAGTTCG AAGAGAATCC TTGGGATGTA 1380  
 55 TCGAGACGGT TATTCACGTG AGGATCTATC CACGAAGGAA CGGTAATCGA AGTGATGGAC 1440  
 AAGGGTGTGT TCGTTTCTCT GCCTTACGGT GTGGAAGGTT TTGCCACTCC GAAGCACATG 1500  
 GTGAAGGAAG ATGGCTCACA GGCTGTACTC GAAGAGAAGT TACCTTTCAA GGTATTAGAG 1560  
 TTCAATAAGG ATGCCAAGCG AATCATTGTA TCTCATAGCC GTGTATTGTA AGATGAGCAG 1620  
 60 AAAATGGCTC AGCGTGAAGC CAATGCAGAG CGTAAGGCTG AAGCCAAAGC GGCTCAGAAA 1680  
 GAAGCTGCTG CCGAAGCTGC CAATCCTGCA CAGGCTGTAG AGAAAGCCAC TCTCGGAGAC 1740  
 CTCGGCGAGC TGGCCGCTTT GAAAGAAAAG CTTTCAGAAA AC 1800  
 1842

## (2) INFORMATION FOR SEQ ID NO:101

- 65 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 75



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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...729
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101
- |             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| TCGACAATAA  | TGAAAAAAGC | TATTCCTTCC | GGAGCGGCCT | TGCTCCTCGG  | CCTATGTGCC | 60  |
| AACGCACAAA  | ACGTGCAGTT | GCACTACGAT | TTGCGTCATT | CCATCTACGA  | CGAACTAGAT | 120 |
| GGACGTCCCA  | AACTGACTAC | CACAGTGGAA | AACTTCACAC | CCGACAAATG  | GGGAAGCACC | 180 |
| TTCTTCTTCA  | TCGACATGGA | TTACACGGGC | AAGGGTATCC | AGTCGGCCTA  | TGGGAGATT  | 240 |
| TCGCGCGAAC  | TGAAGTTTIG | GCAAGCTCCC | GTTTCCATTG | ATTTGGAGTA  | CAACGGAGGC | 300 |
| CTCTCCACAA  | GCTTTACTTT | CGGACACGAT | GCTCTAATCG | GTGCCACCTA  | CACCTACAAC | 360 |
| AACCCCTCCT  | TTACACGTGG | ATTACGATC  | ACGCCCATGT | ACAAGCATCT  | GGGTGCGCAC | 420 |
| GACTTCCACA  | CCTATCAGAT | CACCGGCAT  | TGGTACATGC | ACTTTCIGGA  | CGGTCTGCTT | 480 |
| ACCTTCAACG  | GCTTCTCGA  | TCTTTGGGGT | TTCCCCAAG  | AGAACCCAAAT | CGGGGGCCCT | 540 |
| GTGCTCAAAG  | AAGGGGATAA | GTTCTGATTC | CTGTCCGAAC | CGCAGTTCTG  | GATCAACCTC | 600 |
| AAATCGCATCA | AAGGCATCGA | CAAGGATTTT | AATCTCAGCA | TAGGGACAGA  | GATGGAAATC | 660 |
| AGCAGGAATC  | TCGCTCGCAT | GGACAAATTC | TCCTGCATCC | CTACTCTTGC  | GGTCAAATGG | 720 |
| ACTTTCAAC   |            |            |            |             |            | 729 |
- (2) INFORMATION FOR SEQ ID NO:102
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102
- |            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ATGAAAAACA | TTAGTAAGAA | CCATGCGGCA  | CGGATCTGTG | CCGCCATTGC | TTTGTTTGCA | 60  |
| GTGTGTAACG | GCCGGATAGC | TGCTCAGGAT  | TTTCTCTATG | AAATAGGAGG | AGGTTTGGT  | 120 |
| GCTGCTCAGT | ATTTTGGCGA | TGCAAAACAGA | GGCTTGTTCG | GTTTCATCCG | AGTAGGTTTG | 180 |
| GAGTTGGTGC | GACGTTACAA | TTATAATTTT  | CGCTGGGCTT | TCAGTACCAT | GTTGGATTGG | 240 |
| CGTACATTGA | GAGGGGATAC | CGATAAGTCC  | GGGAATGTCT | TCCCCGATTI | TGCTCAAGCG | 300 |
| GATTTTAAGG | TCGGGCTTGC | TCAGCTCCAC  | GTTAGAAGCG | AAATTAACCT | TCTCCCTTAT | 360 |
| AGCGATGGCT | ATAAGTATCT | TGGTACAGCT  | CGGCTGTCTC | CTTATGTAGC | GGCCGGGTIG | 420 |
| TCTTTGGGTT | TTGCTTCGGG | TGCTAAAGCT  | TCGGCTTTTG | CTCCCGGGAT | TACTGCGGGA | 480 |
| ATGGGAGTGA | AGTATAAGCT | TAAACCGCGG  | ATCAATGTCT | GTATCGAGTA | TTCTTTCACG | 540 |
| GGGTTACTTA | CCGATGCTTT | GGATGCGCTG  | ACGGATAAAA | GTGTTTGGCT | CGAGGATCCA | 600 |
| TATAAGATCA | ATGACTCCTG | GGTCAAAAAC  | AAGGATGCTA | CAGGGGCCTT | AGTGCTTAGG | 660 |
| ATTACGTATG | ACTTCGGCCT | GCGTAAGACT  | TTTTGTAATA | AACAA      |            | 705 |
- (2) INFORMATION FOR SEQ ID NO:103
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

AAATATAATGT	ATAAAGACTA	TAAAGGTTTG	TATGCGTCGC	TTCGGTGGTA	TGCCCTGATC	60
ATTGGGGTTGC	TATTTCGAGC	AGACGGTATA	CAGGCTCAGA	ACAACAACCT	TACCGAGTCG	120
CCTTACACTTC	GCTTCGGCCT	TGGCGGTCCT	GGAGAACGGA	CGACTATTAG	TGGGCATTCC	180
ATGGGAGGAC	TCGGCGTCGG	TCTGCGTCAG	GGCACATACG	TCAATGCCGT	CAATCCTGCT	240
TCATACTCGG	CTGTGGATTC	GATGACGTTT	ATCTTCGATT	TCCGTGCATC	TACCGGAATT	300
ACGTGGTATG	CCGAGAACGG	GAAAAAGGAC	AATAGGAAAA	TGGGAAACAT	TGAGTATTTC	360
GCCATGGTTT	TTCCTATTTC	CAAAATCCAT	CCTATGAGTG	CGGGAGTGCT	TCCTTACTCC	420
GCATCCGGGT	ACCAAGTTCGG	ATCCGTTGAT	CAAGTGGGAG	GAGGCAGCGT	CCAGTACACC	480
CGTAAATACT	TGGGSACAGG	CAATCTGAAC	GATCTCTATG	TCGGTATAGG	TGCACGCCCG	540
TTCAAAAATC	TCTCAATAGG	AGCCAATGCT	TCATCCCTTT	TGGGGCGATT	CACACACAGC	600
AGGCAGGTAA	TCTTCTCCAC	GGAGGCTCCT	TACAATCCCG	TACATCTCTC	GACGCTGTAC	660
TTGAAGGCTG	CCAAGTTCGA	CTTCGGTATG	CAGTATCACC	TTCTTCTCAA	ATCAGATCGT	720
TCGCTCGTTA	TCGGTGCCGT	CTATTCTCCG	CGGGTGAAGA	TGCATAGCGA	GCTGACTCAG	780
ATAAAGATC	AGGTTTCAGAA	CGGTGTAGTA	GTGGAGAGCG	AAACCCCAAGA	ATATATCAAG	840
GGAAATGAC	ATTATACCTT	GCCTCATACA	TTGGGGATAG	GTTTTTCTTA	TGAAAAGAAA	900
GATAAATCTC	TCTTAGGAGC	AGACGTCCTA	TATAGTAAAT	GGAAGGCGGA	GAAATTTTAT	960
AAATCCGATT	GCAAAATCCA	GGACAGAATA	CGGGTATCTC	TCGGCGGAGA	GATCATACCG	1020
GATATAAATG	CCGTTGGGAT	GTCCGCTAAA	GTTTCGCTATC	GCTTCGGTTT	ACATGGTGAA	1080
AATTCTTACC	TGAAAGTGCC	GACTAAAGGC	GGTGTATATC	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTCC	GTATAGGAAT	CCCGCTCAAT	GACAGACGTT	CGTTCGTAAA	TGTCCTCTCT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAA	AAAATGCTCT	GAAATTGACC	1260
TTCCGGCTCA	CGTTCAACGA	GTATGGTTT	AAAAAGCTGA	AACTGAAC		1308

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AAATACCATTT	CGGAGAAATG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCCAAC	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTTCA	CCTGAAAAAG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
TCATATGTAG	GTACACTAC	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAAACATT	360
ACGCTCAAAG	ATATATCCAT	GAAACGAAGT	GCCCCCTCTC	TACAGAGTGT	GACGCTGCAG	420
GCTAAAGCGG	CAGAGGTCGT	GGTACGCAAC	GATACGCTCG	AATTCAATGC	CGGATCTCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
GGATCCGATT	GGAAGATCAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
AATAAAGTAC	AGGTAATGAA	CAAACTGAGC	GAGCTCTCGC	GGATGAGCGG	TTTCGATGAT	720
GGAGAAGAGG	AGACCGTAAT	CAACCTGAGC	GTGAAGCCCG	AAAAAAGAAA	AGGCTCTCTC	780
GGAAACGCTC	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACTCAAT	840
CGGTTTCGATG	GAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAAGGCGGT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTACGCTCTT	CGTCGATGCT	GGCGGCAAC	1020

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5 TTCAGTGTCT AATTCTCTTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATACAAAC 1080  
 GACAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT 1140  
 ATGGACGAAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTCAGGCGCG ATTTAGGATG 1200  
 CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTCGAGC CGGATCTTTC GATATCCAAG 1260  
 ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC 1320  
 AAAGTTCTTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT 1380  
 ATCAGTCACA AGCTCAACGA CGAAGGCCGT ACGATCAGTG CCTCCGTGAG TGGCGGTCTG 1440  
 ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAAGCGTGGG GACGAATCAA 1500  
 AAGCAATTCA ACGACAATC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG 1560  
 10 TTGGGTAAAA ACTACTTCGC ACAAGCGATT CTGAACAGAC GTTTCTCCCG TCGCAATTCTG 1620  
 GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC 1680  
 GGACTCTCCT ACAGTAACGA GTTCACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT 1740  
 GCCAAAACGT GGGACTACAC CGTAGGATTC AATGTGGATC CCAACAGAAC TGTCAGCTAT 1800  
 CGGAGCGTAG CCGGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCG 1860  
 15 ATGCTCGGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGG CTACCGAGGA 1920  
 CGCACGACAC AACCATCCAT CAATCAGATC GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980  
 TTCGTGACCG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAATGT GATGGCCATG 2040  
 TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTTCTT CGGCAACTAT 2100  
 20 ACATTCGACG ACATCGTCCC CAATACGCAC TACGATCGGT CTACAGGGAT ATCGCTTCCA 2160  
 CGTTACGAAA ACGCCTCCGG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA 2220  
 CTCAAGAAAC GGGCATTTTC TTTCAGGATG TCCTTGTTCA ACAGGTTGGC CGAAGGACAA 2280  
 AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTCC GAACAGGGGA ACGCTGACG 2340  
 CTGACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400  
 GCGAATTAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460  
 25 CAAGTTGCCC TAACGCTTCC CTATGGATTG CGTATCGACA GCGATGTGA ATACAATACG 2520  
 AACTCCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGSC TTTGGAATGC TTCGCTTTCA 2580  
 TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCTCGGT 2640  
 CAGCGGTCAA GTATCAGCGG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700  
 30 ACGATCGGAC GCTACGTGAT GGTGGAATT ATCTACCGAT TCAACGCCCT CAGTGGTGGT 2760  
 GGATCTCGCA CGCATCATCA GCGTGGCAAT ATGAATCGTC GGGGCCACC TTTGCGCGGT 2820  
 GGCAGACGAC CGTCC 2835

## (2) INFORMATION FOR SEQ ID NO:105

- 35 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1236 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1236  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GGAGAGTATC CTGCAAAACG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA 60  
 AGTTTGCTCC TGCTTGGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT 120  
 60 GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT 180  
 AAAGACTGGC AAAACCAAGA GGACGGATAC GGGCAGGATA CGGAATATAC AGTGGCTTCC 240  
 GATCGGGACA TTGACGCCA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG 300  
 TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTGCTGA TAGTCGCCGC 360  
 TTGGCTCGAT TCTATAAGCC GAATACGATC GTCAATTCAG GTGCCGACAA TGTATATGTA 420  
 65 ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA 480  
 AACATTTACA TCAACAGTCC TTGGTGCGAT CCGTTCCCTT ATACGTGATG GTATCCATCT 540  
 TTCTCGGGCT GGTACAACATA TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC 600  
 GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC 660  
 TACAATCCCT ATGGAATCGG TATGGGTTGG GGATATCCTT ATGGCTGGGG CAGCTATTAC 720  
 70 GGTGGGGTGG GCTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT 780  
 TCCATGTGT AGCATTCCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT 840  
 GGAACGTCCG GTGCCAAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCGTCTTCC 900  
 CAAAAAATA AGTTGGGATT GCAGTCGAAC AAACCCATA ATAATCTGCA AAATGTCAAG 960  
 TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAAC 1020  
 75 GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGATACAGT CCGCAATGA CCGACCGACC 1080  
 GGACGGAATA TCCGACGCGA GAGACAGGGG GAAAATAACG ATAGGACATT TTCGACTCCT 1140

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TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GTCTTTCTTC CGGCTCTATG 1200  
 AGCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT 1236

5 (2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1803 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

AGTAATAGCA GCTCCACAA GTGGTTAATT TATTATCATA TAGAAAGAC TAAAAGTATT 60  
 ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 120  
 GTACCAACGG ACAGCACGGA ATCGAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 180  
 TCTTTGAATA GGGATGATGC TCCGGATAAA TGGC/ACCTA TGCATGCCAA TTTCAGTATT 240  
 CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 300  
 TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 360  
 TATAAGCCCC TGCCCCGGCA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 420  
 AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 480  
 GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 540  
 GGACGTATAG TACTCACTCC TTTTGATGGA GTSCGTGTCA AGGGTATTGC AGGACACGAG 600  
 CGTAACACT TCGACCGCAC GGGCAAGGTA TTCATTCCG GCCGAGGCTA CCTACTGGGT 660  
 TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCCCGACAA TGACTATCAT 720  
 TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 780  
 GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 840  
 ACCAAGTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 900  
 CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGAACAG CTGCACTCCT CTCTGCCCTCA 960  
 TACTCCAAAA AAGGGATGAG TATCTCTGTTG CAGGCCAAC GTTGTGAGAA CTITGCTTTC 1020  
 CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1080  
 CAAGCTCACA CTTATACGCT GCGGCGCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1140  
 TGGGCTTTCC AAGGTGAAT GCGTTACAA TTTGCTCACC GGACAGCTCT CGGTGGACGC 1200  
 TACGGTACCG GCTTGCATAT CAACGTTTCG CATGTGCTG GTCTGGACAA AAAGATGCTC 1260  
 AAAGAGAATC CCGACGAACT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG 1320  
 GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1380  
 AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1440  
 GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1500  
 AGTAATAAGG TAGCCCTCCG TACCGAAGCT CAATATITGC ACACGAAGCA GGATCAGGGT 1560  
 GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCTCTCG 1620  
 GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1680  
 CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG 1740  
 GGAGGTGTAT GTCGTGTGGT CCTGAGACT CAGGGATTCT ACCTTCTTA TAGCACCAT 1800  
 CTG 1803

60 (2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 756 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

73 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

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10  AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TGCCTTCTTT ATTTTGTAGC      60
    GCGTTGCGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCGGATAAG TTCTTCTGTA      120
    GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CCGTATGCGC CCAAACGCAT      180
    GATCATCTCA TCGAAATCCA CTGGGTGTGC ATCGAATTCT GGGCCATCGA CACAGACGAA      240
    TTTCGTCTGT CCGCCACGCG TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT      300
    AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACCT TTGGTCAGGA GAGAAACGAA      360
    CTTCATCATC ACAGCGGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC      420
    GCTTTCCACT CCATCGTTA CGAGGCCTTT CGTCCCATAA GACCCATCGT CTGTCTATGAT      480
    GATCACTTCA TCGCTATTGG CTCGCATTTC TTCTTCRAGG ATAACCAGAT CTTTAGTTCT      540
    GGCAGCCAAT ACGACAATTA CACCGTTGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG      600
    CAAAGAGGCC ACACCCACAC CGCCTCCGGC ACAAACTACT GTGCCGACCT TTTCGATATG      660
    CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC      720
    CAATTCTTGT GAAGATTTCG CCACGGCCTG AACCCAC      756

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(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

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CTCTGTGTTT CTCTCTCTTT ACCCGGAATG GATCGTCTTA AGCCTTCATA TATTGTTTGA      60
ATAGCAGCCA TTCTCTGCTT GTTTGTGCGG AGGCCTTTGT TTGCGCAGAG CTATGTGGAC      120
TACGTGATCG CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT      180
CCGGTGATCG GTTTACCGTG GGGAAATGAAT AGCTGGACAC CGATGACCGG TGTAACCGGT      240
GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTGCGG GATTCAAACA GACCCACCAA      300
CCGAGTCCTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCTTAC GGCACCGCAG      360
AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCAACT CTTTTCGGAC      420
GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCNACTA TTATAGTGTC      480
TATTTGGCCG ATTACGACAC ACGCGTGAGG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT      540
CGCATACGTT ATTCGGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC      600
TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC      660
AAGAATAGCG GAGGTGTGCC GGCTAACTTC GCCTGTTATT TCATCCTGCA GTCCGATACT      720
CCTATGGCCG ATGCTCTGCT TGAGACAGAT ACGGGCAAGT CAGACGAAGG CACAGGGGCA      780
TGGGCAGCCT GTCGCTTCGA TTCGCAAGAA GTTACCGTCC GGGTGGCATC TTCTTTTATC      840
AGTGTGAGCG AGGCCGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC      900
AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA      960
ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTCTCTGCT TTTTCCCGGT      1020
CGCTTCTATG AGGAGGATGC TTCCGGCAAT TTTGTGCATT ACAGCCCTTA CAATGGAGAG      1080
GTACTTCCCG GTTATCTCTA TACCGATACC GGATTTTGGG AACTTTTTCG AGCCCTTTTC      1140
CCCCTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT      1200
GTATATCGCG AGAGTGGCTT TTCCCGGAA TGGGCCAGTC CGGGCCATCG GGATTGTATG      1260
ATAGGCAACA ACTCTGCTTC TGTCTGGCG GATGCCTACC TCAAGGGTGT TCGGGTAGAA      1320
GATACCGGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAATC      1380
TCCTCCACGG GTCGCAAGG TTGGGAGTGG TACAACCTCT TAGGTTATGT TCCGGCTGAT      1440
GCAGGCATCG ACGAAAGTGC TGCCCGTAGC CTCGAATATG CTTATAACGA TTGGTGATC      1500
CTCCGACTGG GGGGCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT      1560
TCGATGAAC ATCGTCATCT GTTCGATCCG GAAACCAAAC TCATGCGCGG TAGAAATCAG      1620
GATGGTAGTT TCCGGACACC TTTTCCCGT TTCAATGGG GAGATGTATT CACGGAGGGC      1680
AATGCCTGSC ACTACACTTG GTCGGTCTTT CATGATGTG AGGGGCTTAT CGACCTGATG      1740

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SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

74 / 490

5 GGAGGAGATC GCCCGTTTCGT GTCTATGCTC GATTGCGTAT TCAATACTCC TCCTATGTTT 1800  
 GATGAGAGCT ATTACGGATT TGTATCCAC GAAATCAGAG AGATGCAAT AGCGSATATG 1860  
 GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATAIGA TATATCTGTA TAATCATGCC 1920  
 GGTATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980  
 10 ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTT 2040  
 TCTGCTTTAG GCTTCTATCC TGTACACCC GCTACGGATC AGTATGTGCT CGGTTCCGCG 2100  
 ATTTTTCCTCA AGGTAACTCT CTCTTTTCCC GACGGACACA AACGGTGTG GCATGCTCCG 2160  
 15 GCCAACAGTG CCGATACGCC TTACATCCGC TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220  
 TGCAATTACC TGACTCAGCA ACAGCTTCGC TCTTCTGCAT CCAATCAATG GATGATGAGC 2280  
 20 ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTCTCCAGC 2340  
 GAGCAACAGC GTGCGCTAA TCACAGTAAT 2370

## (2) INFORMATION FOR SEQ ID NO:109

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 858 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...858

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

ATTTGTGGCA GTAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG 60  
 CGCAGCGTGC TGTGCTACT CTTCCATTG TCTTGATCA CTGCTTGGG CTGTAGCAAT 120  
 AACAAAGCTG CCGAATCGAA GTCTGTCTCT TTCGATTGGG CCTATCTCGA ACGCTACATC 180  
 40 CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT 240  
 TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG 300  
 GATTCCTCTT CGCCGGAGAA TGCCATGGAA GGCATATGCAC AGATGCTGGG AGAAGACTAT 360  
 CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC 420  
 TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT 480  
 45 ACATATACTT ACGAAGGCGG TGCACATACG GAGAATACAG TCGGTTTTC CAACATCCTT 540  
 CGCACCACCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TSCGSAAGG 600  
 CTGTCCGCAC TCATCATAGG ACAATTTGGT CACGATTTCG GCAAGACCAC ACCTGCCGAA 660  
 TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC 720  
 50 GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT 780  
 GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCCCCA 840  
 CTAAGCGT ACTTGCCG 858

## 55 (2) INFORMATION FOR SEQ ID NO:110

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1134 base pairs  
 (B) TYPE: nucleic acid  
 60 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 65 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1134  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

WO 99/29870

PCT/AU98/01023

75 / 490

5 GGSATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCGAA 60  
 GCTGCTGGCA CGCATAGTGT GTATTGCGATT CTACATCCCT CGCGCGGTAT TATCCGGATC 120  
 AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCGT 180  
 AGCGGTCTGT CGAGGGGCAA TGTAGGTATT CTTTCGTACA ATCCAGAAAA CACGCCCGAG 240  
 AAAAAAGAGAA AACTGCAAGA AAAAAATGTT TTCTCCAAA TCCGGCTCCG TCAATCATT 300  
 AATAATTGA TACCTTCGCT CCCATTAGA ATCGATAACA CAAAAAAT CACTGAAATG 360  
 AAAAAACTA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTGGG TCTCTCGGCC 420  
 AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTTT CAGTTCCGCC 480  
 10 ACGGCCGGAA ATGGTTTGG TGGCAATATC TTGGCATGG ACATGAGCAT ACGGATGAGG 540  
 GTACACCACA GCATTCTGCC CGAAGGGTTG GATTTTTCGG TAGGAATACA TGAAGAAGA 600  
 GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT 660  
 GGTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGAGAAAG ACTTTTGA CAAAAAGCT 720  
 CTGGCGCGCT TCCTCATCAG TTTGGGGATA TCCTATACCA AGCATCTGGG AGCGTATTGG 780  
 15 GGATGGACCA ATGACGCCCA TATTCTTTTC TCACCGATAC CCAAGAGCAA GSTUCCATAT 840  
 GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG 900  
 AGCAATGGCT TTTACCGGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC 960  
 AAGAGCAVAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA 1020  
 TATCCGTATC GTAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCTCGC 1080  
 20 ATGAACCACA TCGGCCATGT GGGCTTCAAC TTTACCGTGG GTCTTTGGAC TAAT 1134

## (2) INFORMATION FOR SEQ ID NO:111

25 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3807  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

45 GTAAAAATGTA TGGGCAAGTA TAAAAGAGCT AAGTACCGCT AITGGCTTTT TCCTTTCTGT 60  
 TCGGATTATT ATACCTTTGA GGGAGTTACT TTTTATGCG CATCTGACGA TATGACAACC 120  
 AAGAAACCCC AAGCCATTTT AGACTTAGAG AAGGCCTATA ACATTGAAAT TCCTGATCTC 180  
 TCCTCACAAAG AAGGGATAAG CTGCTCGGTA AATAGATATT TCAAGCAAGA TTCTCCGGT 240  
 50 GCAGTCCGTT AGCTTTGCTT GCGAGAAATGT CAGATAGAAA GCATGACTTG GCTTATTGAT 300  
 TTTCTGCTC TAAAAAAGCT TGATCTATCG TATAACCAA TCAGTAAGCT AGAGGGTCTA 360  
 GAACGTCTTA CTTCGTTAAC AAAACTTCGT CTAAGAAAGTA ACCAAATCCG TAAACTAGAG 420  
 GGCCTGGATA GTCTACCTC GCTAACAAAA CTTTCTCTCT CCGATAACCA AATCAGTAAG 480  
 CTAGAGGGTC TGGAAAGTCT CACCTCGTTA GCGGAGCTTT ATCTTTTGA TAACCAAATC 540  
 55 AGTAATCTAG AGGGTCTGGA ACCTCTCAGC TCCTTAGCAA CGCTTGAAGT ATCGGGTAAC 600  
 CAAATCCGTA AGCTGGAGGG TCTGGAACGT CTCACGTCCT TAGCAACGCT TGAACCTATCG 660  
 GGTAACCAAA TCCGTAAGCT AGAGGGTCTG GAACGTCTCA CTTCTTTAAC AAAGCTTCGT 720  
 CTAAGAAGTA ACCAAATCAG TAAGCTAGAG GSTCTGGAAC GTCTCAGTC CTAGCAACG 780  
 CTTGAACCTAT CCGGTAACCA AATCCGTAG CTGGAGGCTC TGGAAAGTCT CAGCTCTTA 840  
 60 GCAACGCTTG AACTGTCCGG TAACCAAATC ACTAAGCTAG AGGGTCTGGA ACCTCTCTCT 900  
 TCGTTAACAA AGCTTCCTCT AAGAAGTAAC CAGATCAGTA AACTAGAGGG CCTGGAACGT 960  
 CTCACCTCGC TAACAAACT TTTCTCTCUC GATAACCAA TCAGTAAGCT AGAGGGTCTG 1020  
 GAACGTCTCA CTTCGTTAGC GGAGCTTTAT CTTTGGATA ACCAAATCCG TAAGCTGGAG 1080  
 GGCCTGGAAC GTCTACCTC GTTAACAAAG CTTCTCTAA GAAGTAACCA AATCAGTAAA 1140  
 65 CTAGAGGGCC TGGATAGTCT CACCTCGCTA ACAAACCTTT CTCTCTCGA TAACCAAATC 1200  
 ACTAAACTAG AGGGCTCGA ACCTCTCAGC TCCTTAGCGG AGCTTTATCT TTTGGATAAC 1260  
 CAAATCCGTA AGCTGGAGGG TCTTGATGGT CTTGCTTCCT TAACAGGCT TAGTCTAAGG 1320  
 CGCAACCAAA TCAATAAGCT GGAAGGACTA GACAGACTAA AGGTTTGGAG AAAACTTGAT 1380  
 GTTTCGGGCA ATGATATTCA ATCTATTGAT GATATTAGC TAITGGCTCC GATTCTGGAG 1440  
 70 CAAACTTTAG AAAAAGTGA AATCCATGAC AATCCATTG TTGATCATC AGGCTTGATA 1500  
 CTCTCTCTCT ATGATAATCA TTTGCCGGAG ATTAAGCTC TTCTTGAAA AGAAAAAGAA 1560  
 AALCAGAAAA AGACTTCAGT TGAATATCAC CCATTTTGCA AAGTAATGCT ATTGGGAAT 1620  
 CATTCTCGG GTAAACAAC ATTCTTAGT CAATACGATA CAAATTATAC GTATCAGAAA 1680  
 AATACACATG TGTGTGCGAT ACATCGAAGC AATAACCTTA ATGCGATCTT TTACGACTTT 1740  
 75 GGGGACAGG ACTATTATCA TGGGATTAC CAAGCCTTT TTACCACCA ATCGTTATAC 1800

WO 99/29870

PCT/AU98/01023

76 / 490

CTCTCTTTT GGGATGCTAA GAAGGATCGA AACTTTGTGA GCGTAGATGA TAAAGAATAT 1860  
 CAGACTCTTA ATTTCAATCG CCCCTATTGG TTAGGACAGA TAGCCTATGC CTGCAATCGT 1920  
 TGTATGTCGG TTGGAGGAAA TCCTGATGGC AAGGACACAC CACAGACCAC AGACGATACA 1980  
 ATTATCATTC AGACTCATGC CGATGAAACG GCGGCTAAGC AGCAAACTT AGGCTGTGCA 2040  
 5 GCGGAGAATG GAGTATTGGA AGAAATCTAT GTATCCTTAG AGCCCAAGGC GAATAGTGCC 2100  
 GTACATGCGC TCAACTATCT GAATGAGCGG GTGCGAGAGG TTGTGCAAG CAGGAGTAAA 2160  
 TCAATTGAGA TCACAGAAAA AGATAAGGGA TTGTACGAAG CTCTTCCCAC AATCGCCGT 2220  
 GATAATTAAC ACATCCCTAT CTCTCTCGAA GCTCTTGGCG CTCATTGAA TAAGGGAAGA 2280  
 GCTGAAAAATG ATCTTTACAC CATAGAGTAT CTACAGACCG AATTGAACCA GCTTAGTCTG 2340  
 10 CAGGGGGAGG TGCTTTACTA TCGTGAGMAT GAGAAGCTGA ACAATTATGT CTGGTTAGAT 2400  
 CCGGCAGCTT TTGTCCAAAT GATTCTGGA GAATCCTCC AAAAAGACAA CATCAATAGA 2460  
 GGAACAGTTC CTAAGACAT TTTGAATGC AAATGCATA ATCTAAGTTC CGGAAGTATA 2520  
 TTTGAAGAAG ATGGCCAAAA TGTTAATATG ATCTTGACGC TATTATTGGA AGAGCTGATC 2580  
 GTATATGAAG ATAAGGACTG CTATGTGATA CCGGGCTATC TCCCTTTGCA TTCCGATGAC 2640  
 15 GAAGCCTATA AATGGCTAC TTTGGGATTC GAGAGGCCCA ATTTTGTCTT CAAATTGGA 2700  
 CGTTTATACC CTTTGGGCT GATCAACCG ATTATAGCCT ACTATGGCG GGAAGAAGGT 2760  
 GCTCTAAAGC GGTATTGGCG AGATCAGTTC ATCTTACAG CAGGCGGTGA GATGGATAGG 2820  
 CAAACGCTTG AGCAAGAAGA AGAGAAAGAG GGTTTGCCCA AGACGAATGC CGAGGATTAT 2880  
 CAGATCTGGA TCAAGCTCGA CTTTACCGAC TTGGCCATAT CCATATTCTT CAAAGAGCAG 2940  
 20 AGAAGACAT CAGCTAAGGA TATGCAGCGG AAGAGGCTA CTATCCTCAG TGATATGTTG 3000  
 GATATGTATT GGAACAATAT CCCTCCGAGG GAGCAATAG GAGATAAGGA TACGGAGCAA 3060  
 ACCGAGAAGCA CTATTCTGTA AACAAACAGA AAGAAGAGAC CCATCCAGGA TCTCTACCTC 3120  
 TCCTGTGCCC AAGCGGATAA AGATTGACG GAGTCTCATT ATATCCATTT GGGCAGCTG 3180  
 GACGATGAJA GCAAGACTAC GGCAGGATT GCAGCCTATC CGTTGAAGAA CGGCGTTATC 3240  
 25 GATAAAGAGC GGGTGCGAGA AGTATCGACT CGTCCCTACA AACATCTTTC CGTCAATAAA 3300  
 AATCTGGCTA CTGCAAAACA GATCTTTATT TCCTATTCCA AAGAGGATCA GACTGAAGTG 3360  
 GAGACCTGTC TGCAATTTT CAAACCCCTG GAGAAGAATG GTCAGATCGA GATCTACTAT 3420  
 GATAAGTTGA CTAAGTTTGA AACACCTATT CACCTGAAA TAAGAAAGCG TATTGTGAA 3480  
 CGCGACTGTA TAATCGCTTT GATCAGCCAA CGCTATCTGG CCACGGATTA CATCTGGAT 3540  
 30 CATGAGTTGC CTGTATTTCG GGAGTATAAC AAGACCATAG TGCCGATATT GATCAAGCCT 3600  
 TGTACATTTC AAGACGATGA GTTCTCTCG GAGAAATATT TTGCTCAGAA AGCTCAATA 3660  
 ATCAATCTTG GAAAAGAGGG AAAAACCATT AAAGCTTATG ATAGTATTAC GGCATCAGCC 3720  
 CATCGTGATG AAAATTGGG GGCAGTAGTC AGAGAGTTCA AAGAGAAGAT ATTAAGAATA 3780  
 35 ACAAAACAGG AGGTAAATAC AGATGAA 3807

## (2) INFORMATION FOR SEQ ID NO:112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 693 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...693  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

AAGTTTATGA TGA AAAAAGC ATTGTTTC GTACTACTGG TTTGCCTATT CTCCTCGTTC 60  
 AGCAGTTCOG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTTTACAGG ACGAATCGAG 120  
 AAGGTGAGTT TGAACCTTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT 180  
 GATGCGAAGC GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTCTTTTCAA CAGCAGGGA 240  
 GATATAGCTA CCACTTATTA CATAGCSAAT AGCGAGGCAA CTTTGAATGA ATGGTGGCAG 300  
 65 TATGCACACC CGGGCGGCAT CGTGAGGGTA GAAGTCTGTT TTTGGAAAAAT GACTTACAAC 360  
 ATACCAACCT ACAATGCAGT CTGCACCCGG ATTACATTCTG AAAATCAAGA AATAGAAGGA 420  
 ACGATCGTCT TGATACCCAA GCCCAAAGTC TCGCTGCCTC ATGTGTGCGA ATCGGTGCCT 480  
 TGCATCCGAA CCGAAGCCGG GAGGGAAATT ATCTTTTGGC AAGAAGACGA CACCTTTGTG 540  
 TCTCACGATG GTAACGAAGT AACGATAGGC GGTAAACUTT TCTTGCTCAA TACCAACGTA 600  
 70 AAGATTGTGG GGGACGTATC TCAAAAGTAT GCGTGGGGG TAGGAGAAAT TCGATTCTGT 660  
 CAGATTTGTG CCCAACAGT ATCAACAACA AAA 693

## (2) INFORMATION FOR SEQ ID NO:113

75



WO 99/29870

PCT/AU98/01023

77 / 490

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1689 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

TCGCTAATCA	ACAATTCAAG	AGACTGGAGG	GCTCCTGTCC	GATTGAGTCT	CAAAAAAAG	60
ACAAAAACTA	TGAAGACAAA	AGTTTACGCG	AAATTCGTGG	TGGCGGCTTT	CGCCGTCGCA	120
ACCTCTGTGC	CTCTCGCCCA	AGCGCAGACG	ATGGSAGSAG	ATGATGTCAA	GGTGGTCCAG	180
TACAATCAGG	AAAAACTGGT	ACAAACGAGG	ATGAGTGTGG	CGGACAACGG	ATGGATCTAT	240
GTAAATGACC	ACAGTGGATA	CGACACCGGC	AATAGCAATG	TGAAGATCTT	CCGCTCCAAA	300
GACCAAGGTG	CCACATACCA	AAAGTTGAGG	GATTGGGATC	CATCGGATGA	TTATCAGTTT	360
CAAGACTTCG	ATATCGTGGT	AACGGGTAAG	AATGAATCCG	ACATCAAGAT	TTGGTCGGTA	420
GAGCTCATGA	ATAAGCCCGG	AGGATATAAG	AGTAGAGTTG	CGGTCTTCAG	TCGCGATGCC	480
AACGCCGAGA	ATGCGAAACT	CGTGTATAAG	CAAGACTTCT	CCAATGTGCA	GTGTGACGAT	540
GTGGATATAG	CCTCCAATA	TGTTTCGCCT	TCTTCTCTTA	ACAATGGTGG	CAACCCCTTT	600
GCTTTGGCTT	TCGCTTACAC	CGGCTTCAAC	AATACGCACA	AAATAAGTTT	TGTGGACTAT	660
GTGTTCTCTC	TGAATGGAGG	GCAAAATTTT	AATAAAAACT	TACTCTTCAG	TCAAGATGGA	720
GAGAAGAAAA	TTGACAAGGT	GGATCTCTCA	TTGGGTAGCA	CCTCTGAATC	CATGGGTCAC	780
AATGCCTGGC	CGCTAATGGG	TGTGGTATTC	GAAATGAATA	AACAAGGGGG	AAAAAGCGAT	840
ATCGGTTTCT	TGTCGAACCT	TGTCGACAAAT	GATCCCGAAT	TTCAGTGGTC	AGGCCCTATA	900
AAAGTGAGTG	AAAGCGACAT	GTCTGTCAGC	CCCAAAATCC	AAATGTTGCT	GGACGAGGAT	960
AACAATAAGA	TCAATGGGGA	GAGTTGCCAC	AACCTCATGA	TTACGTACAG	CGATTATGAT	1020
TCTGAATATT	CGGATTGGGA	CATTGCGTAT	GTATATCCCA	AGAAATCGTT	CAAGTATGAA	1080
AAAGGAAAAA	CTCCGACTAT	GGATGATCTG	GTGGAAGCTT	TCCTTACAGC	TTGTTACCAG	1140
AGTGAGACCA	ACTCGGGGCT	GGGGTATGAC	AAGAAGCCCA	ATCACTACCT	GATTACATAT	1200
GCCAAAAAAG	AAGAGAACGG	TACGAAACAG	CTGAAATACC	GCTGGGCCAA	TTATGACAAAG	1260
ATTCAATAAC	AAGATTTGTG	GAGCGACACA	TTTACGTATA	CATCATCTGC	CAATGCTCTC	1320
TACACACCTC	AAGTAGACAT	CAATCCGACC	AAGGGTCTCG	TGTGCTGGTC	ATGGGTGGAA	1380
TATCTGCCGG	GCAACCGGAT	CGTTTGGTCT	GATACGCAGT	GGACCCATGC	CAACGGTGTA	1440
GAAGACATCG	TAATGCAAGA	AGGCAGCATG	AACTCTTACC	CGAATCCGGC	TCAAGAAATAT	1500
GCTGTGATTA	GCCTGCCGAC	GCGACGAAAC	TGCAAGGCTG	TGTGTTACGA	TATGCAGGGC	1560
AGAGTAGTCG	CTGAGGCTTC	TTCTCCGGC	AACGAATACA	GGCTGAACGT	GCAGCACTTG	1620
GCTAAGGGTA	CGTACATACT	CAAGGTCGTA	TCCGATACCG	AGCGTTTCGT	AGAGAAGCTC	1680
ATCGTGGAA						1689

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

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PCT/AU98/01023

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5 ATCGTTTACC TTTGTCACTG TATGAACCAC AGACGATCAA AAACCATGCT GACGATCCGA 60  
 AACTTCCTCC TCTTTTGTG TCTGTGCTG ATAGCGTTTG CTGCCGATGC ACAAAGCTCT 120  
 GTCTCTTCGG GTAGACGACT GACAGAATAT GTCAATCCCT TTATCGGAAC GGCCAATTAC 180  
 GGTACCCACGA ATCCGGGAGC AGTATTGCC AATGGGTIGA TGAGCGTTAC CCCTTTCAAT 240  
 GTCAGCGGAT CGACAGAGAA TCGCTTCGAC AAAGATTCCG GTTGGTGGAG TCGGCCTTAT 300  
 TCGGCCGACA ATAGTTACTG CATCGGTTTC AGCCATGTGA ATCTGAGTGG AGTAGGCTGT 360  
 CCCGAATGA GTGGAATACT GCTGATGGCC ACTTCCGGCA CATTGATCC TGATTACTGC 420  
 TGCTATGGCT CTTCGCTCAG TCGAGAATAT GCGCGCCCGG GAGAATACAA GGCTGTATTG 480  
 10 GACAAATACG GTATAGATGC AGCCGTGACC GTAACCGAGC GGACTGCTTT GACCGAATTT 540  
 GCTTTTCCCG AAGGAGAAGG CCATATCCTG CTGAACCTGG GACAGGCCCT AAGCAATGAA 600  
 TCGGAGAGCT CTGTTCCGATT CTTAAACGAC TCACAGTCC TCGGCAGCAG GCTGATGGGG 660  
 ACCTTCTGCT ACAATCCGCA AGCAGTTTTT CGTCAGTATT TCGTACTTCA GGTGAGTCGG 720  
 CGACCGATCT CTGCCGGCTA TTGGAAGAAG CAGCCTCCTA TGACAGTGA AGCCCAATGG 780  
 15 GATTGCACTG CAGGGAATA TAAGCAGTAC GACGGCTACA AGCGTGAAT GAGCGGTGAT 840  
 GACATCGGTG TCCGATTCTC GTTCAACTGC GATCAGGGGG AAAAGATCTA TGTACGATCG 900  
 GCCGTTTCCT TCGTCAGCGA AGCCAAATGCG CTCTATAATC TGAAGCGGA GCAAGAAGAG 960  
 ATAGAGCGTT GGGAGGAAGC CCTCGGTACG GTGGAAGTGG AAGGAGGCAC ACCGGATGAA 1020  
 20 AAGACGATAT TCTATACCGC ACTCTATCAC CTGCTGATAC ATCCGAATAT CCTACAAGAT 1080  
 GCCAATGGAG AATATCCTAT GATGGGCAGT GGCAAAACGG GTAATACGGC TCACGACCGC 1140  
 TACACCGTGT TCTCTTTG GGACACGTAC CGCAATGTAC ACCCGCTGCT CTGCCTCTC 1200  
 TATCCGGAGA AGCAGTTGGA TATGGTACGG ACACTGATCG ACATGTACCG AGAGAGCGGG 1260  
 TCGCTGCCGA GATGGGAGCT GTACGGACAG GAGACCTGA CGATGGAGGG CGACCCCTCG 1320  
 25 CTATCGTCA TCAATGACAC TTGGCAAAGG GGCCTTCGTG CTTTCGATAC GGCACCGGCC 1380  
 TATGAAGCCA TGAAAAAATA TGCTTCTCG GCAGGAGCGA CCCATCCGAT CCGTCTGAC 1440  
 AACGACGACT ATCTCACCT CGGCTTCGTA CCGCTTCGCG AACAGTACGA CAATTCCGTA 1500  
 TCGCATGCGC TGGAATACTA TCTGGCCGAC TGGAACTGT CCCGTTTGC CCACGCACTT 1560  
 GGGCATAAAG AAGACGAGC TCTATTGCGA AAACGCTCGT TGGGCTACAG ACCTATTAT 1620  
 30 AATAAGGAGT ATGGTATGCT GTGTCCATTG CTGCCGATG GATCATTCC CTCTCTTTC 1680  
 GATCCCAAC AGGGTGAAAA CTTGAGCCTT AATCCCGTT TCCACGAGGG CAGTGCTTAT 1740  
 AACTATGCTT TTTTCGTTCC CCACGATATA CAAGGGCTTG CCCGGCTGAT GGGAGGAGCA 1800  
 AAGGTTTTTT CGGAAGGTT GCAGAAAGTC TTGATGAAG GATATTATGA TCCGACCAAC 1860  
 GAGCCGGACA TCGCCTATCC TTACCTCTTC TCCTATTTC CCAAGGAAGC ATGGCGAAGC 1920  
 35 CAGAAATTGA CCCGGGAGTT GATAGACAAA CATTTTGCA ATGCTCTTAA CGGCTTGCCC 1980  
 GGTAATGACG ATGCCGATAC GATGAGTGT TGGCTTGCT ATTCCATGCT GGGATTCTAC 2040  
 CCTGACTGTC CGGGCAGCCC CACCTATACA CTGACCTCGC CGGTATTCCC CCGAGTTAGG 2100  
 ATTGGGCTCA ATCCGAGTA TTATCCTCAG GGGGAGTTGA TCATTACGAC CAATACAGAG 2160  
 AATCAACCGA CAGATTCCAT TTACATCCAT ACGGTTTCTC TTGGCAATAA AACACTTCCG 2220  
 40 CATGGAACAA GGCATATCAG CCATGCCGAT TTGGTGCCT GCGGTACCT CCGTTACGAA 2280  
 CTAAGCAATC GTCCTCGA 2340  
 2358

## (2) INFORMATION FOR SEQ ID NO:115

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2442 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 50 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 55 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2442  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

70 CCCCCTTTTC ATCCCGGAGG GACACAGCT CAGCTTTGCA GAAATGGGAG AAGAAACCAA 60  
 AAATCAAATC AGTCATCGTG CTTTGGCCGT GGCACAGCTC CGCGATTTT TATTATGTGC 120  
 AAAATAAGAT TCAGCCTCTT GCAGGCTCTT GTCGTCTGCT TATTGTTTCA CTCTTTTCT 180  
 CTCCAGCTC AAGAGGAAGG TATTGGAAT ACCCTCTTGG CTATCCACAA GACGGAAGAA 240  
 GCGGTAGAAA CGCCCAAGAA AGTCTTTGCC GTAGCCAAAG GAGTACTTTA CTCGGTGGGC 300  
 AAAGAAGCTC CCCATGAGGC AAAGATCTTC GACCGTATCA GCGGACTCAG CGATACATCG 360  
 GTAAGCAGCA TAGCCTACTC CGAGCAACTA AAATCCTTGG TCATATACTA TGCAATCAGG 420  
 AATATCGACA TCTGGACGA AGCAGGCCGT GTGACCAACG TACCTGCATT GAAAGACAAT 480  
 75 ATCGATCTGA TAGACAAAAC GCTCAATCGC CTTTGTATCG TAGGCAACAG GGCTTATTG 540  
 GCAGGAGGAT TCGGCCTCTC CGTCTGATG GTCGCCGAAG CTCGCATACC GGCTACCTAC 600

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5 GCCAAGGGAA CTAAGGTGAC CGATGTGGCT AAGTTGGACA ATGATCGCTT GCTGATGCTG 660  
 AAAGAAGGGC AGCTCTTCAT CGGAAAAGAG ACCGATAACC TGCAAGATCC GGCCGCATGG 720  
 ACAGCCTTGT CTTTGAATTT GCCGATGGGC TCGGTCACCG GTCTGGGCAT TGTCGGGGAA 780  
 GACATCTGTT TCCTGCTCGC CGATGGCCGT GTATATGTGC CTGCAAAACCA ATCCTTTGAG 840  
 CCGGAGCTAT TGCTCTCTTC CTCGCCGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG 900  
 TTCATCTGTG CCGAGAATCG AATTATTTTC ATAGAAAAAG GTCGCAAAAC GACACAATTT 960  
 CCTATAGCCG ACGTCCTTGG TGTCCGTGCC ATGAACGAAA GCAATACGGC ATACATAGCA 1020  
 TTGGGAGAAG AAGGTTTGGC TTCACCTTCT CTCGCAGAGG GAAGTACGGC CGAAGCCATG 1080  
 CCTGTAGCAT TCGACGGACC GGGGGACAAT GATTTCTAAG AGATGCGGTT TAGTCACGGA 1140  
 10 CGTCTGTATC CAGCCAGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG 1200  
 AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAGA AGACCGTACA GGAACAGTTG 1260  
 GGGCGCCGAT TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAACGG AGACCCCGAT 1320  
 CACTTTTTTG TCGGTACATG GGGAAACGGT CTGTTGGAAT TCAAGGATGG CAAAGCGATA 1380  
 GCTCGCTATT CCGGAAACGA AACTGCTATC GCAGAAATGA ATCCCGGAGA TGCCCGTGTG 1440  
 15 AAAGCGATTG CTTTGACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG 1500  
 AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCATT CTTTCAGTA TCCGATGTA 1560  
 GCCAATCTGG CCTCTTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAT 1620  
 ATCCTTCAAC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT 1680  
 ACACCGGAAA CGACTTOSGA CGACAGCCAT CTTTACGTGC AGCAGTTTGT CAATCGCCCTC 1740  
 20 TGGGCGAGCA TAGGACATAA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC 1800  
 TGAGTGGGAT CGGATATAGG CATTTTCGGC GTCTACAATG CAGCGGAGT ATTGTCCTCG 1860  
 ACTTCTACCC CTATCGCTGT TCGGCCGGTC GGAGGAGAAG AACCCAATTT GTACTATGTG 1920  
 CTGGACLAGG TGACGGTGAC AGACATCGTC GTGGACAAAC TCAATCACA ATGGGTTGCC 1980  
 ACCCAAGGGA CAGGACTCTA TCTCCTTCG GAAGATTGTA GTAAGATCCT CGCGCAATTT 2040  
 25 ACCGTAGAAA ACAGCCCTTT GCTTCTTAAC AACATACTAT CCCTGGCCTT AAATGACGAT 2100  
 AACGGACTGC TGTACATCGG TACGGCGGAC GGAATGATGA CGTTCCAAAC GGTACGGGG 2160  
 AGTGGATCAG CTTCCGAACG GGACGGCGTC TATGTATACC CCAATCCGCT AAGGCGGGA 2220  
 TATCCCGATG GCGTACCAT TGCCGGACTG CAAGCGGCT GTAGTGTCAA AATCAGCAT 2280  
 30 ACCACCGCA GACTGCTATA CCACACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT 2340  
 CGAGGTGCCG ATGSCAATAG GGTAGCTTCG CGCGTATATG CCGTTGCAGT GTACGATCCG 2400  
 GTATCGAAAA AGTCCAACT AATTCGCTTC GCAGTGATTC GC 2442

## (2) INFORMATION FOR SEQ ID NO:116

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3486 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3486  
  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

60 GCTATTTCTC AGATGAAAG AACTCTCCA ATAGTCGCAT TCCTTCTCT CTCTCTGCC 60  
 CTTGCTTTGC CTGCGAAAGC GCAACGAGCT ATGGGGAAGA GGGCCGACCG TTCGCTAATG 120  
 GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTACGGAC 180  
 GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAAG TAGGTGTGTT CGGTTATGGT 240  
 GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCAGCAGAG ACGATTTGCC TCCGGTACCG 300  
 GTACTCCGTC AGGGCAATGC GCTGTATTC TATGCCGTGG GCCCGGTGAC ATGGTTCTAC 360  
 AATCCGGCCA AAACCACCAT GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC 420  
 65 TTCCTGTCCG ATGCTGCCGG AGCACCTTTG CAGATGTCCG AATATACGGG TGGAGGTGCG 480  
 TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATGC TCCATGAACA GGAATTGTAT 540  
 TCGCCCAAG AATCGGACG AGATCTGTAT GCGAGTCTT TCAGTGCAGT CAATACGCGT 600  
 ACGGTCAAGT TCCCTTTGAG GGGCAACACC CGTTCGTCTG CCGAAGTCCG TACCGTATTC 660  
 TCATACATAG CCAAGGCCAG ATCGGCCGGT GGGGGCCGTG AGATGTCGCT CTCGGCGAAT 720  
 70 GGCATTCTGA TCTTACGCGA TCCTTTTTC ATGACATGSA ATGAAGTCTC CAATTCCTAT 780  
 TTGGCGGCA AGAAGCGTCG TCTCTATCAC AGTACGCCGA TGAACAGCTT GGTCATGAG 840  
 TTGGCTTGG ACGCGAACA TAGCATGACA GGAGATGCCG TCAATCTGGA TTTCATAGAG 900  
 GTGGCTACAC AGAAGGACCT CCGGTACGAT GGGCACCZA TGCATATCAG GCGGTTTCC 960  
 AATTTCGCCG TTTTGGGGGG CGAGTCTGTC CCGTTCTGTA TCAGTAGGTT GCCGGAGTCT 1020  
 75 CTGGTGGTTT TGCAGGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCCGT TAAGACTGTC 1080  
 GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT 1140

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5 ACGTTTATG CCGTGGACTT GTCACAGGCT TCTGCTCCGG AGATCCTCGG AGCGGTACCC 1209  
 AATCAAAACC TGCAATGGAGA GGAATCCCT GATCTGATCA TTGCTCTTAC TCAGGCGGTC 1260  
 CTCCTTGAGG CTGATCGACT GGCCACCTAT CGTAGAGAGA AAAACGGGCT GAAGGTTTTG 1320  
 GTCGTGTGCG AGGAACAGGT GTTCAACGAG TTTTCGGGTG GAACTCCCGA TGCTACAGCA 1380  
 TACCGCCTCT TTGCCAAAT GTTCTACGAC AGATGGAAAG CAAATGCACC TGTGGGAGAC 1440  
 ACCTTCCCGA TGCAAAATGCT TCTCTTGGT GATGGGGCTC ATGACAACAG GAAGGTCTCC 1500  
 GTAGCTTGGC AGAAACCGTA TCTCCAACAA ACGGAGTTCT TGCTGACATT CCAAGCCGTC 1560  
 AATTCGACGA ACGTAAACAG TTATGTGACG GATGATTACT TCGGCTTGCT GGATGATCAG 1620  
 CCGGCCCTCG TCAATATCGG TTGGCGCAAT TATAATATGG CTGTAGGGCG ATTCCCGCTA 1680  
 10 CGTACTCCGG CCGAAGCTCG CATCGCAGTG GACAAGACCA TCCGATATGA GGAGGATCGA 1740  
 GAGAGTCGTG CCTGGCGTAT TCGTGCTGT TTTGCGGCAG ACAACGGGGA CAAGCAOGCA 1800  
 ACCGAGACTT CCGGTTTGT CGATACCGTC AAGCGTTATG CTCCTGCCAT CATGCCGGTA 1860  
 CGCGCCTTTC AGGACGTATA TCCGCATGTC ATCGAGAACG GGTTCACAG CATTCGGGTG 1920  
 GCAAGAAAAA AGATGCTGGA AACCCCTCAG TCGGGTATTA TCCTGCTTAA TTATGCTGGT 1980  
 15 CATGCCGCTC CTGCCGATG GTCGGACGAG CATTGTGCTA CGCTCAACGA TATACACAAA 2040  
 TTCAATATA AGCATATGCC CATTGGATT ACTGCCACCT CGGACTTTGC CAACTATGAC 2100  
 AGTCAGACGA CCTCGGCAGG GGAGGAGGT TTCTCTCATG AGAAGAGTGG CACTCCGATC 2160  
 ATGTTCTCGA CTACGCGTGT CGTTTACAAI ACGCAGAAAG AGAAGATCAA TGGTTTTATG 2220  
 20 CTTCGGCGTA TGTTCGAGAA AGCTAAGGAT GGGCGTTATC GTACGATGGG CGAGATTATC 2280  
 CGATCGGCCA AACAGGGGAT GCTCAGTACT GTTTTCCCGG ATTTCGATCA CCAGTTGAGT 2340  
 TTCTTTCTGA TGGGTGATCC GTCCGTGCGT ATGAATCTTC CTACCCACAA AGTGCAATTG 2400  
 ACCGCAATCA ACGGGCAGGA TCCCGAAGGG CAGTATGGAA CTATTATGCT CAAGTCTTTG 2460  
 GAACGGGTAG CTCTGAAGGG TAAGGTAACC GATGAAAAGG GGACATTGSA CGAGACATTG 2520  
 25 AGTGGCAAGG TTTTCTGAC CGTCTTCGAT GGCAGAAAGA AAATGACAGC TTTGGAAGAG 2580  
 GAGGGAACCG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TGCCGGTATT 2640  
 GCCGAGGTGA AAGACGGACT CTTCGAAACT TCGTTTATCG TACCCAAAGGA TGTGAACAT 2700  
 TCGAGGACCG AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GGCGGAAGCC 2760  
 ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGGTATTC CTGATGAGGT AACGGAAGAT 2820  
 AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCCG ATCGGGAGAT 2880  
 30 GAGGTTAATC CTACTCTCT GTTTATGGCC GAAGTATTCG ACTTGAATGG AATCAATATC 2940  
 ACGGGTAGCG GAGTAGGGCA TGATATTACG CTTTGTATCG ATGCCCTGCG CAGCTTGACC 3000  
 TACAACTCA ATGCATATTT CACAAGTTCC GCTACGGATG CAGGTGTGGG CACTATTCTC 3060  
 TTCATGATAC CGGCTTTGGC CGAAGGAGAT CATACTGCCG GACTGACGGT TTGGGACATT 3120  
 TTCAATATG CCGTCCATCA TGACTTTTCA TTACAGAGTG TAGATGGCAT TGTTCGGAT 3180  
 35 TGCGCGATG TGATTCTATT CCGGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC 3240  
 CACAAATGCC CCGGAAGCGA TTTGAACGTG GCGCTGGAGA TCTATGACTT CACCGGTCTG 3300  
 CTGTGGAACA GTTTGCCAGT CAAGACCTAT TCGTCTTCTT ACGGAGAACCC TATAGAGATC 3360  
 AAGTGGGATC TGACCTCCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT 3420  
 40 TGTGTGCTGA ACTCTCCCGG AGGACAGACG GCCTCCATGG CCAAGAAAAA GATCGTGGTA 3480  
 GGACAA 3486

## (2) INFORMATION FOR SEQ ID NO:117

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2919 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 50  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 55 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2919  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

60 TTTTACACCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTT CCCATTATTA 60  
 TTACTCATAT TGTCGATTTT GGTCCGATGT GGAAAAAAG AAAACACTC TGTAACTGAA 120  
 ATCGCCCGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCACTGAT 180  
 TCTGTTAAAC AGCTTTACGA GAACAGCGTA CAGAACAAGA ACCTGTGGG ACAATGTTA 240  
 70 TTCCGCGATG AGGTCCGGCA ACUGATCGGT AATATGTCCC AATACACAGA TGCGATGCTA 300  
 TATCACCAAA AAGGGTTGAA CGCTGCATTG AATCTAAGGG ACACCATCGT AGCCGCACAA 360  
 GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT 420  
 TATCATTACA AGGCTCTTTC CTTGATAGAA TCTTTAGCG GAAACAGAA TAGGCTTGGC 480  
 ATCAAGCCA GATCGGCGGC CCTGAACGGC ATCGGCAACA TCAATCTTGA GTTAGGATAC 540  
 75 CATGATGAGG CCGAAAAGAA TTTCTGAAA GCACTGCAAG GTGAGAAAG ACTCGACAGT 600

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	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAAAGAA	660
	TACGACAAGG	CTCGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
5	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTGTCCGAT	840
	CGATGGCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCAGCATT	CATTTCTTTG	GCCGAAGGGA	CTGCGAAAGA	AATTAATTCG	960
	ACTTCACAT	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATTCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
10	GCGCACAAGG	TCAGCAGCAT	ACAAGAAACG	CGATTCAACT	ACGAACGAAA	CAACTCCCAA	1140
	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTCG	CCTTTTCATC	TCGATTCTTT	TGATTTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTCGCTCC	1320
	GGCTTTTTC	CCGGTATTAC	ACACGAATTT	CGTACGCCTA	TCACCGTCAT	ACAAGGTTTG	1380
15	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCAG	GCTGCACAAG	1440
	ATAATAGACA	GACAGAGTAG	CCATATGCTG	AATTTGGTGA	ACCAGCTGTT	GGATATTTCG	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCGAA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TCGATTTCGT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGGAGCTA	1620
	CAACCCGAGA	GCAAACTAT	TGTCGTGGAC	TTCGTCCCTT	CCTACTTGCA	AAAAATCATA	1680
20	TCCAATCTTT	TGTCCAATGC	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
	CTGGCAAAAA	CCAAGAATGA	AAAAAATCTG	ATCATACGCG	TTGCAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TCATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAGCATG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCTG	AAACCTTCGA	1920
	GGTACGATCA	AAGTGGAAAG	CCAGCCGGGG	AAAGGAAATG	CCTTCACCAT	CAGTATTCTT	1980
25	ACACA/AAACC	AGTCCTCTTC	GGCAGAGATT	CTTCCTTGGC	TACCTCTCTC	CGATGACATT	2040
	GTCATGCTCT	TCCACATGCG	GCCCGATGAC	TCACCGACAT	CTCCGATGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCLGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACCTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCCG	CGCAACCGGA	2220
	AAAGAGGGTA	TAGCCCTCGC	TACCGAGCAT	ATTCCCGACA	TTATCATTAC	GGATATTATG	2280
30	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
	CACATTCCCA	TTGTCTGCTT	GACGCCCAAG	AGTACCGAAC	AGGACAGATT	GGAGGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TTCTGAAAGA	CCGTGAGTTG	CTCAAGAAGT	TCTATATGCA	AAAACCTCATG	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
35	CTTGCTGCCA	AAGATGCAGT	GTCCGGTGGG	ATCAAAACAA	ATCCGGATTT	TTCCGCTCAA	2640
	GACTTGGCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGAGTGTC	2700
	GTAGTTTGCT	CCACCATCGG	CTACATACAG	CAGATCAAGA	TAAAATTGGC	CTGCAAGCTC	2760
	CTTGCCGATG	AGAGCAAAAA	CATCTCCGAC	ATTAGCATTG	AGGCAGGCTT	TTCGATCCG	2820
	GCTTACTTCT	CTCGCACCTT	CAAACGCTAC	ATGAAGTCTG	CTCCCTCCCA	ATATCGGCCAA	2880
40	AAACTCCTTG	CCATGCCGGG	GAGCGACAAG	GAGACAGTT			2919

## (2) INFORMATION FOR SEQ ID NO:118

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1689 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (D) LOCATION 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

65	CATCATAAAA	CATATCAAAC	AATGAAAAG	CTTTTACAGG	CTAAAGCCTT	GATTCTGGCA	60
	TTGGGACTCT	TCCAACCTGCC	CGCAATCGCC	CAAACGCAAA	TGCAAGCAGA	CCGAACAAAC	120
	GGTCAATTG	CAACAGAAGA	GATGCAACGA	GCATTCCAGG	AAACGAATCC	CCCTGCAGGT	180
	CCTGTGCGTG	CTATCGCTGA	GTACGAACGC	TCTGCAGCCG	TTTGTGACG	CTACCCGTTT	240
70	GGTATCCCGA	TGGAATTGAT	CAAAGAGCTG	GCCAAGAAGC	ACAAGGTGAT	TACCATTTGT	300
	GCGAGTGAAA	GCCAAAAAAA	CACCGTTATA	ACCCAGTACA	CCCAAGCGG	TGTGAATCTC	360
	TCTAATTGCG	ATTTTCATCAT	TGCGAAAAC	GACTCTTACT	GGACACGCGA	CTATACCGGT	420
	TGGTTGCGAA	TGTACGATAC	GAACAAAGTA	GGTCTCGTGG	ACTTTATTTA	TAACCGCCCT	480
	CGTCTTAACG	ATGATGAATT	CCCCAAATAC	GAAGCACAAT	ATCTGGGCAT	CGAGATGTTT	540
75	GGGATGAAGC	TCAAGCAGAC	CGGTGGCAAC	TACATGACGG	ACGGATATGG	ATCCGCTGTG	600
	CAGTCACATA	TCGCATATAC	GGAGAAGTCC	TCTCTGTCTC	AAGTCAAGT	AAATCAAAAG	660

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5 ATGAAGACT ATCTCGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGCGAATAT 720  
 ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACCGA ACAAATCCT CATCAGGAAA 780  
 GTGCCTGACA ATCACCCTCA GCACCAAGCC CTGGAAGATA TGGCAGCCTA CTTCGAGCA 840  
 CAGACCTGCG CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA 900  
 CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTGT TTCCTGTCAM TGGCCCCGCC 960  
 TCCGTGGACA ACGATGCTCT GAACGTCTAT AAGACGGCAA TGCCCCGTTA CGAAATTATA 1020  
 GGTGTCAAAG GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCGTACT 1080  
 CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG 1140  
 GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCATGTC TACTATCTCG 1200  
 10 CCGGTACAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGAG 1260  
 ATGGAATCAA CAGGTCACTA TACTTATAGC TTTACAGTTC TTAACAAGAA TGATAAGGTA 1320  
 GAATACTATA TCTCTGCCGC TGACAATAGT GGTCCGCAAG AGACTTATCC CTTTATCGGC 1380  
 GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCCTG 1440  
 GCTGCCAAAG CTCTTCGTGC ATGGTTCAAC GCCGGTCGTT CAGAACTGGC TGTTCGGTA 1500  
 15 AGTTTGAATA TTGCCGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC 1560  
 GCTGCAATGA CCAAGGAATT AGTAGCAGGG ACGAGTGTCT TCAGTATGGA TGTGTATTCT 1620  
 CAGGCTCCGG GCACATATGT TCTGGTTGTT GAAGGAATG GAATCCGTGA GACAATGAAA 1680  
 ATTCTCAA

20 (2) INFORMATION FOR SEQ ID NO:119  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1311 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 30 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 40 (B) LOCATION 1...1311  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

45 ACCACAAATA GAAAACCAAA TACTAATATG AAACTTTCAT CTAAGAAAAT CTTAGCAATC 60  
 ATTGCATTGC TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCACA 120  
 GGGATTGCGA TGTCTGTAC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATTGTTGGTT 180  
 CATTCCTAG AGAAGAAAG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACAA 240  
 GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAAAAC 300  
 CTCACTATCT ATGGTAATAC GACCCGATTG GGCTGTCTGAT CTACCCGGTG AACGGCTGTC 360  
 50 GATGTAACGA AAAACCTTAA TCTGACCTAT CTGCGATGCC CGAAAAATAA TCTGAAATCA 420  
 TTGGACTTGA CGCAAAACCC AAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA 480  
 AGTTTGGACC TGAGTGGCAA TCCGGCTTTG ATCATCCTCG GCTGTGACAG GAATAAGCTG 540  
 ACTGAGCTGA AGACCGATAA CAACCCCAAG TTGGCCTCTC TTTGGTGTTC TGATAATAAC 600  
 CTGACGGAGT TGGAACTCAG TGCCAACTCT CGTCTCAATG ATCTTTGGTG CTTCGGTAAT 660  
 55 CGGATCACGA AACTCGATCT GAGTGCCAAAT CCTTATTGG TAACTATTG GTGCAATGAC 720  
 AATGAGCTTT CGACCTTGA TCTTCCAAAG AATTCGGACG TTGCTTACCT TTGGTGTTC 780  
 TCGAACAAAC TTACATCCTT GAATCTGTG GGGGTGAAGG GACTGAGTGT TTTGGTTTGT 840  
 CATTCCAATC AGATCGCAGG TGAAGAAATG ACGAAGTGG TGAATGCTTT GCCCACTA 900  
 TCTCCGCGCG CAGGCGCTCA GAGCAAGTTC GTCGTGTAG ACCTCAAGGA CACTGATGAG 960  
 60 AAGAATATCT GTACCGTAAA GGATGTGGAA AAAGCTPAAA GTAAGAACTG GCGAGTATT 1020  
 GACTTCAACG GTGATTCTGA CAATATGCTT CCATACGAAG GAAGTCCGAC ATCGAATTG 1080  
 GCAGTAGATG CTCCCACTGT CAGGATATAT CCAATCCGG TAGGAAGATA TGGCTCGTC 1140  
 GAGATCCCGG AGTCTCTTTT AGGGCAGGAA GCTGCTTTAT ACGATATGAA TGGGGTAAA 1200  
 STCTATAGTT TCGCGGTAGA STCTCTTCGT CAGAACATTG ACCTGACACA TCTTCCGAC 1260  
 65 GGCACCTATT TCTTCCGTCT CGATAACTAT ACCACTAAGC TCATCAAACA G 1311

(2) INFORMATION FOR SEQ ID NO:120  
 70 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 75 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

15 AATCATTTGA AGACAAATAT CAAGATGAGA AAAACAATAA TTTTCTGCTT GTTGCTCGCC 60  
CTATTTGGCT GTTCTTGGGC ACAAGAAAGA GTCGATGAAA AAGTATTCTC CGCAGGAACA 120  
AGTATTTTGA CCGGCATCCT TGAAAAGGTG AAAGCACCGC TTATGTATGG AGATCGTGAG 180  
GTATGGGGTA TGGCTCGTGC GAGCGAGGAT TTCTTTTSTA TACTTCCCGT TACGGATGAC 240  
20 CTCACCTCCG TGCTTTTCTA TAACCGTCTT ACRAACGAAC CCTGCTTTGT GTGAGACCAA 300  
GGAATAACTG AGTATTTCAA ATTCTGCTCA GAGGTGATT ACATTGAAGT CGAAGGAAGC 360  
TGTGTATCCA TGGCGAATCT TTGTACTAT CGTTTTTCC CGACAAGAAAT TACCTCCTAT 420  
AATGCTCCCA TTGAAGGTGT TGTGAGCAAG ACGGAAATC CTGCTTTTAC AATCCCGATG 480  
CTCCCGGGGG TTTCTGATTG CATAGAAATC TCAACAACCC GCAAAGTCTT TCTGACCAAT 540  
25 CAATTAGGGG TTGTAACAT CACTGACGGG ATGGAACTTC CGATTATTGC CGGAGTCTCT 600  
GCTTCCTATG GATCTTCCGT CCGGGTGAT GGTCTGTCT CACAGCGGTG GGACATCATA 660  
GGCCATTGCT ATTTGGATAT CTACCCAACC AATTGCTATC CGCTCAGCAC GAAACCCGTT 720  
GCAGGAGACG ATGAGGTTTT TGTCAAACAA CAAGGCAGGC AAATAGAGAT CGATAGCAAC 780  
AGCCCATAG TCCAAGTGGT CGTATACGAT CTTGAGGGGA AAAGTGTITT TCGCAAAAGA 840  
30 ATGACCGAAA ACGCTTATAC CTTATCTTTT AGAGCACCCA TGCTCGGCTT TATGACCATC 900  
ATGATCGAAA CACAAATTC GATTATCAAT AAAAACTTA ATGTTACACA GCTA 954

(2) INFORMATION FOR SEQ ID NO:121

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1383

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

AGACGGGCGA TTAAATCCG ATCACCCTCC CATATCCACT CATTATTGT ACGTAAATGT 60  
CTTTTTCAG ACTTAAATA CTTATATTTA TCCCGAATAA TTACCCAAGA GAGATTGGGT 120  
CGATTGTGCA TCCGTCTTAA GTCATACAA CCAATAATCA TTATTGAAAT GAAAAAACA 180  
60 ACCATTATTT CTTTGATTGT CTTGGTGCT TTCTTTGAG CCGTGGGCCA AACCAAGGAC 240  
AATTCTTCTT ACNAACTTT TCCGAAAGAA GATATTGCCG GAGGAGTTTA CTCTCTCCG 300  
ACTCAAAATC GTGCGCAGAA GGACAATGCC GAGTGGCTTC TTACAGCGAC CGTCTCCACA 360  
AACCAGTCTG CAGATACTCA CTTTATCTTC GATGAGAACA ACCGCTATAT CGCTCGTGAC 420  
ATAAAGCCA ATGGGGTAAG AAAATCCAG GACTCCATTT ACTACGATGC CAACGGGCGA 480  
65 ATATCGCATG TGGATCTTTA TATCTCGTTC AGTGGCGGAG AGCTGCACT CGACACCGA 540  
TTCAAGTACA CCTATGATGA CGAGGGAAAG ATGACCGTGA GGGAGTATT CATGCTGGTA 600  
ATGGATCGA ATACACCTAT CTCACGCTTG GAATATCATT ATGATGCACA GGGCAGACTG 660  
ACCCACTGGA TTTCTTTTGC TTTCCGGGCA GAATCCCAAA AGAATACGTA TCACTATAAT 720  
GAAAAGGTC TGTGTGTCAG CGAAGTGCTG AGCAATGCAA TGGGGACAAC CTATTGAGAC 780  
70 ACCGGCAAAA CGGAATACAG CTATGACGAT GCAGATAATA TGGTGAAGGC CGAGTACTTC 840  
GTCGTCCAGC AAGGAAGGCC ATGGCAAGTA CTCAAAAGAG AGGAATACAC CTATGAGGAC 900  
AATATCTGCA TACAATATTT GGCTATTAA GGTACCGACA CAAAGGTGTA CAAGCGAGAC 960  
ATCGAGAGCG ATAAGTCCAT CTCGCAAAAT GTCAATTGACA TTCCGTCAAT CCGGGAACAG 1020  
ACCTGGCCTA ATATGTACGG ATTCAACGCA AAGCGACTGA AAGAGACTTA TTCTCTCTAC 1080  
75 GAAGGAGATG TGGCTACTCC TATATTCGAC TATATCTATA CGTACAAGGC TCTTACCTCA 1140

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ATGGCAACAC CTTGCACAGA AGCTCAGGTA GCAGTCTATC TCAATCCGTC AACGGACCGG 1200  
 TTAGTGATTG TGGCCAAACG CATCACACAT CTCAGCATGT ACGACTTGCA GGGTAAGCTT 1260  
 ATCCGTGATT GTGCCTTGAG CGGCGATAAG GTGGAAATGG GTGTCGGATC TTTGACCAAA 1320  
 GGGACATAAC TGCTTAAAGT GAATACGGAT CAGGGAGCCT TTGTGAGAAA AGTCGTGATT 1380  
 CGA 1383

## (2) INFORMATION FOR SEQ ID NO:122

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1353

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

ATGGCAAAAG TTATAAAAC AAAAAAAGG CTTGCACTTA ATCTGAAAGG AAAACCGCTG 60  
 CCCGAGATGC TGGCCGAACC GGCCCAAAGT CCTACTTACG CGCTCGTGCC CGACGATTTT 120  
 GAAGGTGTTA TCCCAAGGT GACGGCTCGT CCGGGGATA AGGTGCGTGC CGGCTCAGCA 180  
 CTGATGCACC ACAAGGCATA TCCGAGATG AAGTTTACAA GTCCGGTTAG CGCGAAGTG 240  
 ATCGCGGTGA ATCGCGGTGC CAAGCGCAAG GTGTTGAGCA TCGAGGTGAA ACCGGACGGA 300  
 CTGAACGAAT ACGAGTCATT CCTGTGCGGG GATCCGTCG CCTCTCTGC CGAACAGATC 360  
 AAGGAGCTTT TACTGTCGAG CGGTATGTGG GGTTTTATTA AGCAACGTCC TTACGACATA 420  
 GTGGCTACAC CGGATATAGC TCCACGCGAC ATTTATATTA CTGCCACTT TACTGCACCA 480  
 TTGGCTCCGG ACTTCGATTT CATCGTTCCA GGAGAAGAAC GCGCCCTGCA GACTGCCATC 540  
 GATGCCCTGG CCAAACTUAC GACAGGAAAG GTGTATGTGG GCCTGAAGCC GGGTTCACTC 600  
 CTGGGCTTGC ACAATGCAGA AATCGTAGAA GTACACGGAC CTCATCCGGC AGGTAACGTG 660  
 GCGGTGCTGA TCAATCATAC GAAGCCAATC AATCGGGGCG AACGGGTGTG GACGCTCAAG 720  
 GCTACCGACC TGATCGTGAT CGGACGTTTC CTGCTTACGG GCAAAGCGGA TTTTACCAGA 780  
 ATGATTGCCA TGACCGGCTC AGACGCTGCA GCTCACGGAT ACGTCCGTAT TATGCCGGGT 840  
 TGCAATGTCT TTGCTTCCTT CCGCGGCCGA CTGACAATA AGGAATCTCA CGAGCGTGTG 900  
 ATCGATGGCA ATGTGCTGAC CGGTAAAGAG CTCTGCGAGA AGGAGCCTTT CCGTGCAGCC 960  
 CGCTGTGACC AGATCACGGT GATCCCCGAA GCGGACGATG TGGACGAAT CTTCGGGTGG 1020  
 GCTGCACCCC GTCTCGATCA GTACAGCATG AGCAGAGCTT ATTTCTCTTG GTTGCAAGGG 1080  
 AAAAACAAG ASTACGTACT CGATGCCCGG ATCAAGGGTG GCGAACGTGC TATGATCATG 1140  
 AGCAACGAGT ATGACCGCGT TTCCCGATG GACATCTATC CGGAGTATTT GCTCAAGGCT 1200  
 ATTATAGCAT TCGACATCGA CAAGATGGAG GACTTAGGCA TATATGAAGT GGCTCCGGAG 1260  
 GACTTTGCCA CTTGCGAATT TGTGGATACA TCCAAGATCG AGCTGCAGCG TATCGTTCGC 1320  
 GAGGGCTTGG ATATGCTCTA TAAGGAAATG AAT 1353

## (2) INFORMATION FOR SEQ ID NO:123

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 585 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...585



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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

5 ATGGATAAAG TGAGCTATGC TCTGGGATTG AGCATCGGTA ATAATITCAA GTCTTCGGGC 60  
 ATCGACAGCG TCGTTATGGA TGATTTCATG CAAGGTCTGT CTGATGTACT GGAAGAAAAA 120  
 CCCCCTCAGC TCTCGTATGA CGAGGCCAAG CGCGAAATAG AGGCGTATTT CATGGATTTG 180  
 CAGCAGAAGG CTGTCAAAC TGAACAAAGAG GCCGGAGAAG AATTCTCTCA GATAAATGCA 240  
 CACAAGGAAG GTGTGACGAC CTACCGAGC GCTTGCAAT ACGAAGTCAT TAAGATGGGA 300  
 GAGGGCCCGA AACCACCCCT TTCGGACACG GTAACCTGTC ATTATCACGG TACGCTCATC 360  
 10 AACGGTATCG TTTTCGATAG CTCTATGGAC AGGGGAGAAC GGGCCAGTTT CCTCTAAGA 420  
 GGAGTTATAG CCGGCTGGAC GSAGATTCTT CAATTAAATGC CTGTAGGATC CAAGTGGAAG 480  
 GTAACATATC CAGCGCATCT GCGTATGGA GATCGTGTG CCGGCGAACA TATCAAACCG 540  
 GGTAGTACGC TCATTTTAT AATCGAATTA TTGAGTATCA ACAA 585

15

## (2) INFORMATION FOR SEQ ID NO:124

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...819  
 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

40 ATGAAAAAAG CATTACTTAT TGGTCTGCT CTITTGGGAG CAGTCAGTTT TGCAAGTGCT 60  
 CAGTCTTTGA GCACAATCAA AGTACAGAAC AATTCAGTAC AGCAACCTCG TGAGGAAGCC 120  
 ACTATTACAGG TTTGTGGAGA ATTGGCAGAG CAAGTTGACT GCATTGGGAC AGGTAATTCT 180  
 GCAATCATAG CCGCTGCAGC GAAATTTGAA AGCGATGATC TCGAAGCTA TGTGCGCTGG 240  
 GAGATCATGA GTGTTGATT CTTCCTGGA TATAAAGCGT GCAAGTACAC ATCTGCAGTC 300  
 TGGGCTGATG ATATGACCAT TTTGGGCCAA TCAGAAAGATA GTGATCCCGA AATGCAGACT 360  
 45 ATCAACAATC TTGCTCTCAA GACTAGTGTC AAGATTGAAG CCGGCAAGAA TTACATAGTT 420  
 GGTTATATTG CTAATACCGC AGGTGGACAT CCTATCGGAT GTGATCAGGG CCCTGCCGTT 480  
 GATCGTTATG GAGATTGGT TTCTATATCA GAAGATGGTG GTGCTACTTT CCCTCCGTTT 540  
 GAATCTCTTC ATCAAGCAGT TCCTACCTTA AATTACAACA TCTATGTCGT TGTTCATTG 600  
 AAGAGGGGTG AAGGTGTTGA GGCTGTTCTT ACCAACGACA AGGCTAATGC TTATGTTTCA 660  
 50 AATGGCGTTA TCTATGTAGC CGGAGCTAAT GGTGTCAGG TATCTCTGTT CGACATGAAC 720  
 GGTAAGGTTG TTTATACCGG CATTAGCGAA ACGATTGCAG CTCTCTAGAA GGGCATGTAT 780  
 ATCTCCGTG TAGGTGCTAA GAGCATCAAG CTGGCTATC 819

55

## (2) INFORMATION FOR SEQ ID NO:125

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1662 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1662  
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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:125

	ATGCCAAGAA	TTATGAAATT	AAAAATTGCA	CTCAGACTGC	TGCTGGCGAC	TTTGGCCATA	60
	GTTTATTTA	GCCCTCTGGC	CAAGGCCAG	ATGGATATTG	GTGGAGACGA	TGTAATTGATC	120
5	GAGACGATGT	CCACCTTATC	AGGATATTCA	GAGGATTTTT	ATTACAAGAT	GGCTGTGGCA	180
	GACAATGGAT	GGATCTATGT	GATGTTGGAT	TTCTCTCGTA	TTTATTTTGA	TGATGTCAGG	240
	CTGTATCGTT	CCAAAGACGG	TGGTGCTACT	TACCAAAAGT	TAGGGTCTTT	GGGGTCTTTG	300
	GTGCCTTATG	ACTTCGATGT	CTCGCAATTGC	GATTTTATTG	TACGGGAAA	GGATGAAGAT	360
	GATATCAATG	TTTGACAGT	CATGACAGCA	TTGCAATATG	TAGGTGGTAC	TATTGGCAAT	420
10	GGCGTTTTGC	TGATGCATCG	CCATGATGCA	GATATCAATA	ATACAGAGTG	TGTGTACAAG	480
	AAGGATTTCC	CTAATAATAG	ACTGATGGGT	GTAGCCATCG	CCTCCAACTA	CGGTGCGCCC	540
	TCTCCTTAGG	GTTTGGGGGG	CGATCCTTTT	GCTCTCGCTG	TCCCGTTAG	TGGCTCGGGA	600
	AGCGATCACA	GCTTCTTGGG	CTATATTTTT	TGCTTAGATG	GTGGAGTACA	CTTTCAGCAA	660
	AAGCGTATT	ACACAAGACC	CCAAAAACTG	ACTATCAATA	GAGTAGACCT	TTCATTAGGC	720
15	AGTACATCTC	CTTCTCTTGG	ATTTAATACT	TGGCCACTAA	TGGGAGTCGT	ATTGCAAAATG	780
	AATAAGAAC	TTGATGGCTT	CGACATTGGT	TTCAATTTCCA	ACTTTGTGGA	CTATGATCCC	840
	CGCTATGGCT	GGTCTGAACC	GATAATAATA	GAAGAAGACT	GTGGATGGAC	TGATTTTAAT	900
	CCTTTGGGAG	CACATAAGTAT	AGAGATCCAA	ATGATGTTGG	ATGACAAATC	GGATAATACC	960
	GTGGGTGGAG	AACGCTCCCA	TAACTTCCTG	ATCACTTACC	CGGGCCATTA	CGTATATCCG	1020
20	AAGCAATCTT	TCAATTATTC	TCCCGGACAT	ACACCGACAA	AGAAAGATCT	GGTCTTTAAA	1080
	CACCTGTATG	GATTTCCGGC	TITGGCATA	GATAAGGAAG	GCGATCGTTA	TCTGACTACT	1140
	TTTCAAGATC	ACAATCTAAT	GAGATACAGA	TGGATCAAAAT	ACGATGACAT	TAACCTTTTT	1200
	TATGGTTGGA	GTTGGCCATA	TGTATATGCA	AAAGAAGCTA	AAGATAAAAA	GAGGCGCCGT	1260
	CCGCAAGTAG	CACCTCAATCC	TACCAATGGA	AAGGCTTGT	GGGTATGGCA	TACTCGCAAG	1320
25	AGCCCATATG	ATGAAACCAA	ACCACATCCT	ACTCCTGTAA	TTATTAACCA	TTTCTATGG	1380
	TCCGATACGG	AGTGGGTACA	TGCTCTGGAC	GTGGGGGACG	TATTGCAGAA	GGAGGGTAGC	1440
	ATGAAGCTCT	ACCCCAATCC	TGCCAAAGAA	TATGTTCTGA	TCAACCTACC	CAAAGAGGG	1500
	GGGCACGAGG	CAGTCGTATA	CGACATGCAG	GGCCGAATCG	TGGAGAAAGT	TTCAATTTCA	1560
	GGGAAAGAAT	ATAAGCTGAA	TGTGCAGTAT	CTGTCCAAAG	GTACGTACAT	GCTGAAAGTT	1620
30	GTAGCGGATA	CGGAGTATTT	CGTGGAAAAA	ATCATTGTAG	AG		1662

(2) INFORMATION FOR SEQ ID NO:126

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1650

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:126

55	ATGAAATTAA	AAATTGCACT	CAGACTGCTG	CTGGCGACTT	TTGCCATAGT	TTTATTTAGC	60
	CCTCTGGCCA	AGGCCAGAT	GGATATTGGT	GGAGACGATG	TATTGATCGA	GACGATGTCC	120
	ACCCATACAG	GATATTCAGA	GGATTTTAT	TACAAGATGG	CTGTGGCAGA	CAATGGATGG	180
	ATCTATGTGA	TGTTGGATT	CTCTCGTATT	TATTTTGATG	ATGTCAGGCT	GTATCGTTC	240
60	AAAGACGGTG	GTGCTACTTA	CCAAAGTTA	GGGTCTTTGG	GSTCTTTGGT	GCCTTATGAC	300
	TTGATGTCT	CGCATTGCGA	TTTTATTGTA	ACGGGAAAGG	ATGAAGATGA	TATCAATGTT	360
	TGGACAGTCA	TGACAGCATT	CGAATATGTA	GGTGGTACTA	TGGCAATGG	CGTTTGTCTG	420
	ATGCATCGCC	ATGATGCAGA	TATCAATAAT	ACAGAGTGTG	TGTACAGAA	GGATTTCCCT	480
	AATAATAGAC	TGATGGGTGT	AGCCATCGCC	TCCAACCTACC	GTGGCCCTC	TCCTTACGGT	540
65	TTGGGGGGCG	ATCCTTTTGC	TCTCGCTGTG	GCCGTTAGTG	GCTCCGGAAG	CGATCACAGC	600
	TTCTTGGACT	ATATTTTTTC	GTTAGATGGT	GGAGTACACT	TTGAGCAAAA	GCGTATTTAC	660
	ACAAAGCCCC	AAAACTGAC	TATCAATAGA	GTAGACCTTT	CATTAGGCAG	TACAICTCCT	720
	TCTCTTGGAT	TTAATACTTG	GCCACTAATG	GGAGTCGTAT	TGAAATGAA	TAAAGAACCTT	780
	GATGGCTTCG	ACATTGGTTT	CATTTCCAAC	TTTGTGGACT	ATGATCCCCC	CTATGCGTGG	840
70	TCTGAACCGA	TAATAATAGA	AGAAGACTGT	GGATGGACTG	ATTTTAATCC	TTTGGGAGCA	900
	CTAAGTATAG	AGATCCAAAT	GATGTTGGAT	GACAATTCGG	ATATACCGT	GGGTGGAGAA	960
	CGCTCCCATG	ACTTCCTGAT	CACCTACCCG	GGCCATTACG	TATATCCGAA	GCAATCTTTC	1020
	AATTATTCTC	CCGGACATAC	ACCGACAAGG	AAAGATCTGG	TCTTTAACA	CTGTATAGGT	1080
	ATTCGGGCTT	TGGCATACGA	TAAGGAAGGC	GATCGTTATC	TGACTACTTT	CTAAGATCAC	1140
75	AATCTAATGA	GATACAGATG	GATCAAAATC	GATGACATTA	ACTCTTTTAA	TGTTTGGACT	1200

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5 TGGCCATATG TATATGCAAA AGAAGCTAAA GATAAAAAA GGCGCCGTCC GCAAGTAGCA 1260  
 CTCATCTCTA CCAATGGAAA GGCTTGTTGG GTATGGCATA CTCGCAAGAG CCCATATGAT 1320  
 GAAACCAAA CACATCCTAC TCCTGTAATT ATTAACATT TCCTATGGTC CGATACGGAG 1380  
 TGGGTACATG CTCTGGACGT GGGGGACGTA TTGCAGAAGG AGGGTAGCAT GAAGCTCTAC 1440  
 10 CCCAATCCTG CCAAGAATA TGTTCGTATC AACCTACCCA AAGAAGGGGG GCACAGGGCA 1500  
 GTCGTATACG ACATGCAGGG CCGAATCGTG GAGVVAAGTTT CATTTCAGG GAAAGAATAT 1560  
 AAGCTGAATG TGCAATATCT GTCCAAAGGT ACGTACATGC TGAAGTGTGT AGCGGATACG 1620  
 GAGTATTTCG TGGAAAAAT CATTGTAGAG 1650

10

(2) INFORMATION FOR SEQ ID NO:127

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1170  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

35 ATGAAACGAT TACTCCCTT TCTCCTTTA GCAGGACTCG TAGCOGTAGG AAACGTGTCT 60  
 GCTCAGTCAC CCGGAATCCC TCAAGTGGAT GTACACACTC GCATCGCAAG AAATGCCCGT 120  
 TATCGACTGG ACAAGATCAG TGTCCCGGAT TCTCGTCAGA TATTGATTA CTTCTATAAA 180  
 GAAGAAACGA TACCCACTAA AATACAAACG ACCACAGGAG GTGCAATTAC AAGCATCGAT 240  
 TCGCTTTTCT ATGAAGAAGA CAGGTGGTT CAGGTGCGCT ATTTTGACAA TAACCTTGAA 300  
 40 TTAAGAACAG CCGAGAAGTA TGTATACGAC GGTCTAAGC TGGTCCTTCG AGAAATTCGC 360  
 AAGTCGCGA CAGACGAAAC GCCAATAAAG AAAGTTAGCT ATCACTATCT CTGTGGCAGC 420  
 GATATGCCCT TTGAGATTAC GACAGAGATG AGCGATGGCT ATTTTGAAAG CCATACGCTT 480  
 AACTATCTGA ATGGAAGAT TGCCCGAATA GATATCATGA CTCACAGAA CCCATCGGCC 540  
 GAATTGATCG AAACGGGTAG AATGGTATAT GAGTTTGATG CCAATAATGA TGCTGTACTG 600  
 45 CTTCTGACG GTGATTTCT TCCTCTTCAA AACAAGTGGG TAGAAATGTT TACTCACCGT 660  
 TATACATACG ACAATAAGCA TAATTGTATT CGTTGGGAAC AAGACGAATT CGGCACCCTC 720  
 ACCCTTGCCA ACAACTTCGA ATACGACACC ACTATCCCTC TGTGCTGTGT ATTGTTCCCC 780  
 ACGCATGAGG AGTTCTTCCG TCCTCTTCTT CCAATTTTA TGAAGCATAT GCGTACGAAG 840  
 CAAACGTATT TCAATAACTC CGCAGAAGGC TTGTCAGAGG TATGCGATTA CAACTACTTC 900  
 50 TATACCGATA TGCAGGGTAA TGCACTGACC GATGTTGCCG TGAACGAATC GATCAAGATT 960  
 TATCCTCGTC CTGCCACGGA TTTCTGCGT ATAGAAGGTT CGCAACTGCT TCGCCTTTCG 1020  
 CTATTCGACA TGAACGGGAA GCTCATCAGA GCTACCGAAT TGACAGGGCA TTTGGCCATT 1080  
 ATCGGAGTTG CATCTCTTCC GAGAGGCAC TACATCGCAG AAATAACTGC TGCAACAGC 1140  
 55 AAAACCATAC GTGCAAAAGT ATCGCTCAGA 1170

55

(2) INFORMATION FOR SEQ ID NO:128

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 75 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1233

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:128

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5  ATGAGACAGC ATTATCTCT ATTCCTTTT ATCTTGTTT TGCTTCTTC CTTCCTTAT    60
   GTCGGTTGCA GAACAGTCCG ACAAACACCT AAGCAGTCGG AACGGTACGT CGTAGTCCTG    120
   TCTTTGGACG GCTTCCGACC GGACTATACC GATCGGGCAC GTACACCGGC GTTGGATCGG    180
   ATGGCACAGG AGGGATTGAG CGGGTCGCTC CAACCATGCT TCCCCTCGCT TACATTCCC    240
   AATCATTACA GCATGGCTAC GGGGCTTTAC CCCGATCATC ACGGTATCGT AGCCAATGAG    300
10  TTGTGGGATT CGCTACTGGG CATCTTTCGT ATATCCGACC GAAAGCCGT GGAGACCCCC    360
   GGATTTTGGG GGGCGGAGCC GGTTTGGAAT ACGGCCGCAC GCCAAGGCAT CCGTACCGGT    420
   GTCTACTTTT GGGTAGGATC CGAAACGGCT GTGAACGGAA ATCGGCCGTG GCGGTGGAAA    480
   AAATTCTCCT CCACCGTTCC GTTTCGTGAC CGTGCCGACT CCGTCATCGC GTGGCTCGGA    540
   CTGCCCGAAA AGGAGCGACC GCGCTTGCTC ATGTGGTACA TCGAGGAGCC GGATATGATC    600
15  GGACACAGCC AAACGCCCGA AAGCCCGCTG ACACTGGCAA TGGTAGAGCG GTTGGACAGT    660
   GTGGTCGGCT ATTTCCGCAA GCGGTTGGAC TCTCTGCCCA TAGCCGCACA GACCGACTTC    720
   ATCATAGTAT CCGATCACGG TATGGCCACG TACGAAATG AGAAATGTGT CAACTGTGTCG    780
   CATTATCTGC CTGCGGACAG TTCTCTCTAC ATGGCCACCG GGGCCTTCAC CCACTTGATC    840
   CCGAAGCCCT CCTATACCGA GCGAGCCTAT GAGATCCTGC GGGCCATTCC ACATATATCG    900
20  GTTTACCGCA AGGGGGAGGT GCCCAAGCGT TTGCGCTGTG GCACCAATCC TCGTTTGGGC    960
   GAACTGGTCC TGATTCGGGA CATAGGCTCC ACCGCTCTTT TCGCAATAAA TGAAGACGTT   1020
   CGTCCGGGAG CGGCACATGG CTATGACAAC CAAGCACCGG AAATGCCGGC TTTACTCCGG   1080
   GCTGTCCGAC CCGATTTCGG TCCGGGCAGT AGGGTGGAAA ACCTGCCGAA TATCACCATC   1140
   TATCCGCTCA TATGCAGGCT GTTGGGTATA GAGCCTGCAC CCAACGATGC GGACGAAACG   1200
25  TTGCTGAACG GCCTGATCCG AGACAAACGA CCA                                1233

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(2) INFORMATION FOR SEQ ID NO:129

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30  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 738 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular

35  (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

40  (iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45  (ix) FEATURE:
     (A) NAME/KEY: misc feature
     (B) LOCATION: 1...738

```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:129

```

50  ATGAAAGTAG GTTGTTCAT CCCCTGTTAT GTCAATGCAG TGTATCCGGA AGTGGGTATC    60
   GCCACGTACA AACTGCTGAA GAGTTTGGAC ATAGATGTCG ACTACCGGAT GGATCAGACA    120
   TGTTCGGGCC AGCCTATGGC CAATGCCGGA TTGCAACAGA AAGCTCAAAA GCTGGCTTTG    180
   CGATTGCAAG AGCTGTTTCA GTCCATATGAT GTAGTCGTAG GGCCATCGGC CAGTTGCGTT    240
55  GCTTTCGTGA AAGAAACTA TGATCATATC CTCAGACCGA CAGGACATGT CTGCAAGTCG    300
   GCAGCCAAGG TTCGGGATAT ATGCGAGTTC TTGCAAGATG ACCTGAAGAT CACCAGCCTC    360
   CCCTCCCGAT TCGCCCATAA GGTGAGCCTG CACAACAGTT GCCAGGTTGT GCGCGAACTG    420
   CATCTGTCCA CCCCGATGA AGTGCAACGA CCGTACCACA ACAAGGTGCG CCGGCTATTG    480
   GAGATGGTGC AGGGCATAGA GGTATTGAG CCGAAGCGAA TAGACGAATG CTGCGGTTTC    540
60  GCGGTTATGT ACTCGGTGGA GGAGCCGGAG GTATCCACCT GTATGGGCA TGACAAGGTG    600
   CTGGATCACA TATCCACAGG TGCGGAGTAC ATCAGAGGCG CGGACAGCTC GTCCCTCATG    660
   CATATGCAGG GAGTGATAGA CAGAGAGAAA TTGCCGATCA AGACAATTCA TGCAAGTAGAA    720
   ATTTTAGCAG CAACCTTA                                738

```

(2) INFORMATION FOR SEQ ID NO:130

```

70  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 738 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular

     (ii) MOLECULE TYPE: DNA (genomic)

75

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...738

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:130

15	ATGGATATTG TAAGTATGGC CGATAAAGCT CTTGTAGTGG AGATGAGAGA TGTGACGCTC	60
	TGTCAGGAGG AAAACGTCAT TTTTCAAAAT TTGAATCTGA CCCTTTCCGC CGGAGACTTC	120
	GTCTATCTGA TAGGCTCAGT GGGATCGGGG AAGAGCACTT TGCTGAMGGC TTTGTATGCT	180
	GAGGTGCCTA TCTCTGCCGG TTATGCCCGC GTGATAGATT ATGATCTGGC AAAGTTGAAA	240
	CGGAAGCAGT TGCCCTATCT GCGCAGGAAT TTGGGCATTG TGTTCAGGA TTTCCAGTTG	300
20	CTGAACGGAC GTACTGTTGC GGAGAATTG GATTTCSTTT TGGGAGCTAC GGACTGAAA	360
	AACCGAGCG ATCGCGAGCA GCGTATCGAG GAGGTTTGA CCCGTGTGGG AATGTCTCGG	420
	AAGGCTTATA AGAGACCGCA CGAAGTGTCC GGAGGGGAGC AACCAACGTGT GGGTATAGCC	480
	ACAGCTTTGC TGGGGAAGCC TGGTTGATC CTGGCCGACG AACCCACAGG CAACCTCGAT	540
	TCCGTGACCG GATTGCAGAT CGCTTCTCTG CTCTACGAAA TCAGTAAGCA GGGCACTGCA	600
25	GTACTTATGA GCACGCACAA CAGCAGCCTG CTGTCCGATC TGCCGGCAGG GACATTGGCC	660
	GTTCGTAAGA ATGGCGATGC CTCCTCTTTG GTCGAGCTGA GTGCAGATGC TGTTCAGAA	720
	AAAAATACGG AATAGAT	738

(2) INFORMATION FOR SEQ ID NO:131

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
45 (B) LOCATION 1...723

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:131

50	ATGGCCGATA AAGCTCTTGT AGTGAGATG AGAGATGTGA CGCTCTGTCA GGAGGAAAAC	60
	GTCAATTTTC AAAATTGAA TCTGACCCCT TCCGCCGAG ACCTCGTCTA TCTGATAGGC	120
55	TCAGTGGGAT CGGGGAAGAG CACTTTGCTG AAGGCTTTGT ATGCTGAGGT GCGTATCTCT	180
	GCCGTTATG CCCGCGTAT AGATTATGAT CTGGCAAAGT TGAAACGGAA GCAGTTGCC	240
	TATCTGCCGA GGAATTTGGG CATGTGTTT CAGGATTTC AGTTGCTGAA CGGACGTACT	300
	GTTCGGGAGA ATTTGSAATT CGTTTTCGCA GCTACGGACT GGAAGAACCG AGCCGATCGC	360
	GAGCAGCGTA TCGAGGAGGT TTTGACCCGT GTGGGAATGT CTCGGAAGGC TTATAAGAGA	420
60	CCGCACGAAC TGTCCGGAGG GGAGCAACAA CGTGTGGGTA TAGCCAGAGC TTGCTGGCG	480
	AAGCCTGCGT TGATCCTGGC CGACGAACCC ACAGGCAACC TCGATTCCGT GACCGGATTG	540
	CAGATCGCTT CTCTGCTCTA CGAAATCAGT AAGCAGGGCA CTGCAGTACT TATGAGCAG	600
	CACAACAGCA GCCTGCTGTC GCATCTGCCG GCACGGACAT TGGCCGTTCC TAAGAATGGC	660
65	GATGCCTCCT CTTGGTTCGA GCTGAGTGCA GATGCTGTTT CAAGAAAAA TACGGAATA	720
	GAT	723

(2) INFORMATION FOR SEQ ID NO:132

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 696 base pairs  
70 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132
- |    |   |     |
|----|---|-----|
| 15 | ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATT TTCAAAATTT GAATCTGACC  | 60  |
|    | CTTCCGCGC GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTGT  | 120 |
|    | CTGAAGGCTT TGTATGCTGA GGTGCCTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT | 180 |
|    | GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCTATCTGC GCAGGAATTT GGGCATTGTG  | 240 |
|    | TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCGG AGAATTGGA TTTCGTTTGT  | 300 |
| 20 | CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CGCGAGCAGC GTATCGAGGA GGTTTTGACC | 360 |
|    | CGTGTGGGAA TGTCTCGGAA GGCTTATAAG AGACCGCAGC AACTGTCCGG AGGGGAGCAA | 420 |
|    | CAACGTGTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GCCCGACGAA | 480 |
|    | CCACAGGCA ACCTCGATTG GGTGACCGGA TTSCAGATCG CTCTCTGCT CTACGAAATC   | 540 |
| 25 | AGTAAGCAGG GCACTGCGAT ACTTATGAGC ACGCACAACA GCAGCCTGCT GTCGCATCTG | 600 |
|    | CCGGCACGGA CATTGGCCGT TCGTAAGAAT GGCATGCGCT CCTTTTGTG CGAGCTGAGT  | 660 |
|    | GCAGATGCTG TTCAAGAAA AATACGGAA ATAGAT                             | 696 |
- (2) INFORMATION FOR SEQ ID NO:133
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 657 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133
- |    |   |     |
|----|---|-----|
| 55 | ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC | 60  |
|    | CTCGATGGCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGGCATAAT GGGGCTTGG  | 120 |
|    | GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCTTC TCGACAATCC CACTTCCGGT | 180 |
|    | ATCTACAAGC TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAGACAG GACTGCCGTC | 240 |
|    | CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA | 300 |
|    | AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA GCGGAAAGAG | 360 |
|    | CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCGCCCA CTTCCTCAAT | 420 |
|    | CAGCTCTCCG GAGGACAACA GCAGCGCGTG GCTATCGCCC GTGCCGTGGT GGCCAATCCG | 480 |
| 60 | AAGCTCATCC TCGCCGATGA ACCCAGGGGT AACCTCGACT CCAGAAACGG AGCCGATGTC | 540 |
|    | ATGGAACTGC TCAGAGGTCT CAATCGCGAA GGTGCAACCA TCGTCATGGT GAGCACTCC  | 600 |
|    | GAGCACGATG CACGTAGTGC CGGCCGATC ATCAATCTGT TCGACGGTAA GATTGCG     | 657 |
- (2) INFORMATION FOR SEQ ID NO:134
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1785

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGAAAGAAT TTTTCAAAT GTTTTTCGCC TCGATCCTCG GGGTTATAAC GGCAGGAATC 60  
ATCTTGTCT GTATCTTCT ATTATCTTT TTCGGCATCG TAGCCGGTAT TGCTCCAAG 120  
15 GCAACGGGAG GAACCATTC GAAGATCGAA GCAAACCTCA TCCTACATAT ANACAATTCT 180  
TCTTTCCTG AGATCGTATC GGCCAATCCC TGGAGCATGC TCACAGGCAA AGACGAGTCC 240  
GTATCGTCT CACAGGCAGT CGAAGCCATC GGCCAACCCA AAAATAATCC CAACATAACC 300  
GGTATCTTCC TCGATCTGGA CAACCTTTCC GTCCGTATGG CATCGGCAGA GGAATTGUGT 360  
CGCCGCTTGC AGGATTTCAG CATGTCGGGC AAGTTCGTCG TATCCTATGC CGACAGATAC 420  
20 ACCUAAAAGG GTTACTACCT CTCAGTATT GCAGACAAAC TCTACCTCAA TCCGAAAGGA 480  
ATGTTGGGCG TTATCGGGAT TGGCAGCCAA ACAATGTTCT ACAAGATGC CCTCGACAAA 540  
TTCGGCGTGA AGATGGAGAT CTTCAGGTA GGCACCTACA AGGCAGCCGT AGAGCCATTC 600  
ATGCTCAACA GGATGAGCGA TGCCAATCGC GAACAAATCA CCACATACAT AAACGGGCTT 660  
TGGGACAAGA TCACATCCGA TATTGCAGAG TCGCGCAAGA CGGCAATGGA TTCCGTGAAA 720  
25 ATGTTTCCCG ACAAAAGCGA AATGTTCCGT CTTCGCCAGA AAGCGGTGGA GATGAAGCTC 780  
GTGGATGAGC TGGCTTACCG TACCGATGTG GAGAAAGAAC TCAAAAGAT GTCCCAACGC 840  
GGAGAGAAAG ATGAACCTCG GTTCGTATCG CTCTCTCAGG TTCTGGCCAA TGGCCCGATG 900  
AACAAAACGA AAGGCAGTCG GATCGCCGTT CTCTTGGCG AAGGTGAAT AACGGAAGAA 960  
ATAATAAGA AGCCGTTCGA CACTGACGGT AGCTCCATCA CACRAGACT CGCCAAAGAA 1020  
30 ATCAAGGCAG CAGCCGATGA CGATGATATC AAAGCCGTAG TACTTCGTGT CAATTCCTCG 1080  
GGAGGTAGTG CTTTCACTTC CGAACAGATA TGGAAAGCAGG TAGCCGATCT CAAGGCCAAA 1140  
AAGCCTATCG TGGTCTCCAT GGGCGACGTA GCAGCCTCGG GCGGATACTA CATAGCCTGC 1200  
GCAGCCAAAC GTATCGTGGC AGAGCATACG ACTCTGACCG GCTCCATCGG CATATTCCGGC 1260  
ATGTTCCCGA ACTTCGGGGG CGTAGCCAAAG AAGATAGGAG TGAATATGGA CGTCGTACAG 1320  
35 ACATCCAAAT ATGCAGACTT GGGCAACACC TTCTCTCCGA TGACGGTCSA AGATCGTGCC 1380  
CTCATCAAC GCTACATAGA GCAGGGCTAC GACCTCTTCC TCACTCGCGT ATCGGAAGGC 1440  
CGCAACCGCA CCAAGGCACA GATCGACAGC ATCGCTCAAG GCCGTGTATG GCTCGGCGAC 1500  
AAAGCTCTTG CACTCGGTTT GGTGGATGAG CTTGGAGGTT TGGACACAGC TATCAAACGG 1560  
GCCCGAAGC TGGCTCAGCT CGGTGGCAAC TACAGCATAG AGTATGGCAA GACCAAGCGC 1620  
40 AACTTCTTCC AAGAGTTGCT CTCCTCATCA GCAGCGGATA TGAAGTCTGC CATCTGAGT 1680  
ACCTTCTCT CCGATCCGGA AATAGAAGTT CTGCGCGAAC TCCGTCCAT GCCGCCCGT 1740  
CCTTCGGGCA TACAGGCAG TCTCCCCTAT TACTTCATGC CGTAC 1785

45 (2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1767 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1767

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

ATGTTTTTCG CCTCGATCCT CGGGGTTATA ACGGCAGGAA TCATCTTGT CTGTATCTTT 60  
CTATTTATCT TTTTCGGCAT CGTAGCCGGT ATTGCCCTCA AGGCAACGGG AGGAACCAAT 120  
70 CCGAAGATCG AAGCAAATC CATCCTACAT ATATACAATT CTCTTTCCC TGAGATCGTA 180  
TCGGCCATTC CTTGGAGCAT GCTCACAGGC AAAGACGAGT CCGTATCGCT CTCACAGGCA 240  
GTCCGAAGCCA TCGGCCAAGC CAAAAAAT CCACACATRA CCGGTATCTT CCTCGATCTG 300  
GACAACTTT CGTCCGGTAT GGCATCGGCA GAGGAATTGC GTCGCGGCTT GCAGGATTTC 360  
AAGATGTCGG GCAAGTTCTG CGTATCTAT GCCGACAGAT ACACCCAAA GGGTTACTAC 420  
75 CTCTCCAGTA TTGCAGACAA ACTCTACCTC AATCCGAAG GAATGTTGGG GCTTATCGG 480

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ATTGCGACCC AACAATGTT CTACAAAGAT GCCCTCGACA AATTCGGCGT GAAGATGGAG 540
ATCTTCAAGG TAGGCACCTA CAAGSCAGCC GTAGAGCCAT TCATGCTCAA CAGGATGAGC 600
GATGCCAATC GCSAACAAAT CACCACATAC ATAAACGGGC TTTGGGACAA GATCAGATCC 660
GATATTGCAG AGTCGGCGCA GACGGCAATG GATTCCGTGA AAATGTTTGC CGACAAAGGC 720
GAAATGTTGG GTCTTGCCGA GAAAGCGGTG GAGATGAAAG TCGTGGATGA GCTGGCTTAC 780
CGTACCGATG TGGAGAAAGA ACTCAAAAAG ATGTCCCAAC GCGGAGAGAA AGATGAACTT 840
CGGTTCTGAT CGCTTTCTCA GGTTCCTGCC AATGGCCCGA TGAACAAAAC GAAAGGCAGT 900
CGGATCGCCG TTCTCTTTGC CGAAGGTGAA ATAACGGAAG AAATAATAAA GAAGCCGTTT 960
GACACTGACG GTAGCTCCAT CACACAAGAA CTGCGCAAAG AAATCAAGGC AGCAGCCGAT 1020
CACATGATA TCRAAGCCGT AGTACTTCGT GTCAATTCTC CGGAGGAGT TGCCTTCACT 1080
TCCGAACAGA TATGGAAGCA GGTAGCCGAT CTCAGGCCA AAAAGCCAT CTGGGTCTCC 1140
ATGGGCGACG TAGCAGCCTC GGGCGGATAC TACATAGCCT GCGCAGCCAA CAGTATCGTG 1200
GCAGAGCATA CGACTCTGAC CGGCTCCATC GGCATATTCT GCATGTTCCG GAACTTCGCG 1260
GGCGTAGCCA AGAAGATAGG AGTGAATATG GACGTCGTAC AGACATCCAA GTATGCAGAC 1320
TTGGGCAACA CCTTCGCTCC GATGACGGTC GAAGATCGTG CCTCATCCA ACGCTACATA 1380
GAGCAGGGCT ACGACCTCTT CCTCACTCGC GTATCGGAAG GCCGCAACCG CACCAAGGCA 1440
CAGATCGACA GCATCGCTCA AGGCGGTGTA TGGCTCGGCG ACAAGGCTCT TGCATCTCGT 1500
TTGGTGGATG AGCTTGGAGG TTTGGACACA GCTATCAAAC GGGCCGCGAA GCTGGCTCAG 1560
CTCGGTGGCA ACTACAGCAT AGAGTATGCG AAGACCAAGC GCAACTTCTT CGAAGAGTTG 1620
TTCTCCTCAT CAGCAGCGGA TATGAAGTCT GCCATCCTGA GTACCATTTT CTCCGATCCG 1680
GAAATAGAAG TTCTGCGGGA ACTCGGCTCC ATGCCGCCCG GTCTTCGGG CATACAGGCA 1740
CGTCTCCCTT ATTACTTCAT GCCGTAC 1767

```

## 25 (2) INFORMATION FOR SEQ ID NO:136

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 939 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

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30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

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  (A) NAME/KEY: misc feature
  (B) LOCATION 1...939

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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

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ATGAGAGCAA ACATTGGCA GATACTTCC GTTTCGGTTC TCTTTTCTT CGGGACAGCG 60
ATCGGACAGG CTCAGAGTCG AAACCGTACA TAGGAGGCTT ATGTGAAACA GTACGCCGAC 120
GAAGCTATCC GACAGATGAG CCGCTACAAT ATACCGGCAA GCATCACCAT AGCAGAGGCT 180
TTGGTGGAGA CAGGAGCCGG AGCCAGTACA CTGGCCAGCG TACACAACAA TCACTTCGGG 240
ATCAAAATGCC ACAAAATCGT GACGGGCAAG CGCACCTATC GTACCGACGA TGGCCGGAAC 300
GAATGCTTCC GCAGCTATTC GGGCGCTCGC GAATCGTATG AAGATCATTG CCGATTCTG 360
CTCCAACCAC GCTATCGTCC CCGTGTCAA CTGACAGAG AAGACTATCG GGGCTGGGCT 420
ACGGGGTTGC AACGCTGTGG CTATGCCACC AATCGGGGCT ATGCCAATCT GCTGATCAAG 480
ATGGTGGAGC TGTATGAGT ATATGCTTTG GATCGGAGAG AGTACCCTC ATGGTTCCAC 540
AAGCTTACC CCGGTCCAA CAAAAAATCC CATCAAACGA CCAAGCAGAA GCAGAGCGGA 600
CTCAAGCAGC AAGCTTACT CAGCTACGGA CTGCTTACA TCATAGCCAA GCAAGCGAT 660
ACCTTCGATT CTTTGGCCGA AGAGTTCGAC ATGAGAGCCT CCAAACTGGC CAAATACAC 720
GATGCTCCCG TGGATTCCC GATCGAAAAG GCGATGTGA TCTATCTGGA GAAAAAGCAC 780
GCATGCTCCA TCTCAAACA CACACAGCAC GTAGTGCCTG TGGGCGATTC GATGCACAGT 840
ATCTCCCAAC GCTATGGCAT CCGGATGAAG AACCTTACA AGCTCAACGA CAAGGATGGC 900
GAATATATAC CCCAAGAGGG CGATATACTG CGCTTGC3C 939

```

65

## (2) INFORMATION FOR SEQ ID NO:137

```

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1569 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

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70

(ii) MOLECULE TYPE: DNA (genomic)

75



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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

15	ATGGACGGAC	GTGATATTC	GGATGGCCTC	CATCAGGCTA	TGGAAGCCAA	AGAGCATGTG	60
	AAAGTAGAGG	CTGCGACACA	GACATTTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
	TATCATAAAC	TGGCAGGGAT	GACCGGTACT	GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	180
	ATCTACAAAC	TGGACGTTGT	AGTTATTCGG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	300
20	CGTCTTGTCG	AAGAGGGCAG	ACCTGTACTT	GTGCGTACTA	CTTCGGTGGA	AATATCCGAA	360
	TTGTTGAGCG	GTATGTTACG	CTGCGTGCGC	ATCCAACACA	ATGTACTCAA	TGCCAAATTG	420
	CATCAGAAGG	AGCCCGAGAT	TGTAGCTCAG	GCCGGTCAGA	AAGGAACTGT	TACCATCGCA	480
	ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	540
	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
25	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
	AAGCAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
	AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TGAGTACGA	TGATGTAATG	840
	AATTGCGAGC	GTGAAGTCAT	TTATACCCGT	CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	900
	GGTATGGATG	TACTCAATAC	CATATACGAC	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	960
30	GAAGCCAATG	ATTTGSAAGG	CTTCAAGGAA	GATCTGATGC	GTGCACTCGC	GATAGAATCT	1020
	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	1080
	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TGCGAGAAGT	GGCCCAACCT	1140
	GTGGTTTATC	AGGTATTGGA	GACCCAAGCC	GCCGTGTACG	AGCGCATTCT	AATCCCCATT	1200
	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTTCG	GTGAAGCGGA	TGAAACTCAA	1260
35	GGGAAAGCA	TCATCAAAGA	ATTGAGAAA	GCTATCGTAC	TGCATACAT	CGATGAGTCT	1320
	TGGAAGAAAC	ATCTGCGTGA	GATGGACGAG	CTTCGTAATT	CCGTTTCAGAA	TGCCAGCTAC	1380
	GAAACAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACTGTT	CCGCAAGATG	1440
	GTAGAAGCCA	TGAACGTA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
40	GAGGCTCCTT	CCCAGAAGA	GCTGGAACAC	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	1560
	CAACAACGCT						1569

(2) INFORMATION FOR SEQ ID NO:138

45 (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

65	ATGAATTTCT	TAAAAAAGA	ACCGTTTAA	ATATTCTCTA	TGATTTATCT	GCTGTTAGAT	60
	ACAATAACAA	ACCGTGCCGG	TACAGAACGC	GCCGTGATCA	ACTTGGCTAA	CAACCTGCAT	120
	GCCAATGTGC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
	CAAGTAGAAA	AAGGAATAGA	AGTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
70	GCCCGCAAAA	CAGTATATTT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
	GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
	AACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATA	TGCCCGCCCT	420
	ATTACAAAAC	GCATAAGGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTTGT	AGCACTGACA	480
75	AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAGC	ATATGTCATA	540
	CCCAATCAAG	TTTCATTTAC	TACAGTCCAA	AGAGATGCTA	CTACTCACA	ACAAATGTTG	600

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5 GCGATTGGCA GGCTTACCTA CCAGAAGGGT TTTGAATTCA TGATAGAAGA TGCATCACGA 660  
 GTGCTGCGAG AAAGGCCCTGA TTGGAAGCTT ATCATAGTCG GAGATGGCGA AAATGAATCG 720  
 ATGCTACGTA AAGAATATGC ATCTCGCAAT ATGGAGTCGC AATAGAAAT ACATCCATCT 780  
 ACACCGGAAA TTGCAATA CTACGAATCA TCTGCTATTT ATCTAATGAC GTCCCGTTTC 840  
 10 GAAGGACTAC CAATGGTACT TCTCGAAGCA GAAGCATATG CACTACCTAT AATCTCATAC 900  
 GATTGTCCGA CCGGCCCGAG GGAAGTATC GAAACGGTC GCAATGGTTT CCTTGTGCCA 960  
 ATGGAAGCAC ATGAAGACTT CGCGGATAAG TTACGCTTAT TGAIGGATGA TGAAACTCTT 1020  
 CGTAAGAAAA TGGGACAAGA ATCAGAGTTG ATGGTCAAAT CCTACTCTCC GGCAAAATATC 1080  
 TATGAATGTT GGAAGAAACT ATTCGTCGAA ATCGGCTACA TGAAT 1125

(2) INFORMATION FOR SEQ ID NO:139

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1086 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1086  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

35 ATGATTATTC TGCTGTTAGA TACAATAACA AACCGTGCCG GTACAGAAGC CGCGGTGATC 60  
 AACTTGGCTA ACAACCTGCA TGCCAATGGT CATCGCGTAT CATTAGTCAG CGTTTGTACA 120  
 AAAGAAGGAG AGCCTTCCTT CCAAGTAGAA AAAGGAATAG AAGTACACCA TCTCGGAATT 180  
 AGGCTTTATG GCAATGCATT AGCCCGCAAA ACAGTATATT TCAAGGCTTA TCGAAGGATA 240  
 AAAGCCCTAT ACAAGAAGCG TGAACCGGTT TTATTGATAG GGAATAATAT TTTTATCAAT 300  
 40 ACAATTTTGT CTCAGATCAG TAACAGAGGC AGAATATTTA CGATCGGATG CGAACATATC 360  
 TCTTATGATA TTGCCCGCCC TATTACAAA CGCATAAGGG GGTTCGTGTA TTCAGGGCTT 420  
 GATGCCGTTG TAGCACTGAC AAAAGAGAT CAGCAATCGT TCGAGGCAAT CTTACGTGGA 480  
 CGCTCTAAG CATATGTCAAT ACCCAATCAA GTTTCATTTA CTACAGTCCA AAGAGATGCT 540  
 ACTACTCACA AACAAATGTT GGCGATTGGC AGGCTTACCT ACCAGAAGGG TTTTGAATTC 600  
 45 ATGATAGAAG ATGCATCACG AGTGCTGCGA GAAAGGCCGT ATTGGAAGCT TATCATAGTC 660  
 GGAGATGGCG AAAATGAATC GATGCTACGT AAAGAAATTG CATCTCGCAA TATGGAGTCG 720  
 CAAATAGAAA TACATCCATC TACACCGGAA ATTGCAAAAT ACTACGAATC ATCTGCTATT 780  
 TATCTAATGA CGTCCCGTTT CGAAGGACTA CCAATGGTAC TTCTCSAAGC AGAAGCATAT 840  
 GCACTACCTA TAATCTCATA CGATTGTCCG ACCGGCCCGA GGGAACTGAT CGAAAACGGT 900  
 50 CGCAATGTTT TCCTTGTGCC AATGGAAGCA CATGAAGACT TCGCGGATAA GTTACGCTTA 960  
 TTGATGGATG ATGAAACTCT TCGTAAGAAA ATGGGACAAG AATCAGAGTT GATGGTCAAA 1020  
 TCCTACTCTC CGGCAAAATAT CTATGAATGT TGGAAAGAAC TATTCGTGCA AATCGGCTAC 1080  
 ATGAAT 1086

(2) INFORMATION FOR SEQ ID NO:140

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1920 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 75 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1920

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:140

5	ATGGGAAAAA	TCATTGGAAT	TGACTTAGGC	ACAACGAACT	CTTGTGCTC	TGTATTGGAA	60
	GGTAACGAAC	CTATCGTTAT	TACAAACAGT	GAGGGCAAGC	GCACAAACGCC	CTCGGTAGTG	120
	GCTTTTGTGG	ATGGTGGCGA	GCCTAAGGTG	GGCGATCCGG	CCAAGCGTCA	GGCCATCAACC	180
	AATCOGACCA	AGACGATATA	CTCTATCAAA	CSCTTCATGG	GCGAAACTTA	GSATCAGGTT	240
	TCCAGAGAAG	TGGAGAGAGT	GCCATTCAAG	GTAGTACGTG	GSGACAATAA	TACTCCGCGC	300
	GTAGATATAG	ACGGTCGTCT	CTATACGCCG	CAGGAAATTT	CGGCCATGAT	CCTTCAGAAG	360
10	ATGAAGAAGA	CGGCCGAAGA	CTACCTCGGT	CAGGAAGTAA	CGGAGGCCGT	GATCACTGTG	420
	CCCGCATACT	TCAACGACGC	TCAACGTCAG	GCAACGAAAG	AAGCAGGAGA	GATCGCCGGC	480
	CTGAAGTTC	GCCGTATTGT	GAACGAGCCT	ACGGCAGCTT	CTCTGGCCTA	CGGTCTGGAC	540
	AAGTCCAATA	AGGATATGAA	GATCGCTGTC	ITCGACTTGG	GTGGCGGTAC	CTTCGATATC	600
	TCTATCTTGG	AATTGGGCGA	CGGCGTTTTC	GAAGTGAAT	CGACCAACGG	TGATACGGAC	660
15	CTCGAGGAG	ACGACTTCSA	CCACGTGATC	ATTGACTGSC	TGGCAGAAGA	GTTCAAGTCT	720
	CAGGAAGGTG	TGGATCTTCG	CCAGGATCCT	ATGGCTATGC	AGCGTCTGAA	AGAAGCTGCC	780
	GAAAAAGCCA	AGATAGAGCT	CTCCAGCACT	TCATCTACGG	AGATCAACCT	CCCTATATC	840
	ATCGCGGTGA	ACGGCATCCC	CAAGCACTTG	GTGATGACCC	TTACAAAGGC	TAAGTTCGAG	900
	CAGTTGGCCG	ATCGTCTGAT	TCAGGCATGT	GTGGCACCCCT	GCGAAACGGC	CTTGAAGAT	960
20	GCCGGTATGT	CACGTGGCGA	TATCGATGAA	GTGATTCTCG	TAGGTGGTTC	CACACGTATT	1020
	CCTCTATTTC	AGGAGATTGT	GGAGAAGATC	TTCGTAAGG	CTCCGTCCAA	GGGTGTGAAT	1080
	CCCGACGAAG	TGCTAGCTGT	GGGTGCCGCT	ATTCAGGCG	GTGTTCTGAC	CGGTGAGSTA	1140
	AAGGATGTCT	TGCTGTTGGA	CGTTACCCCC	TTGTCGCTCG	GTATCGAGAC	TATGGGAGGC	1200
	GTGATGACTC	GCTTGATCGA	TGCCAATACC	ACTATCCCGA	CGAAGAAGAG	CGAAATCTTT	1260
25	ACCACACGAG	TGGACAATCA	ACCTTCGGTA	GAGATTCTAT	TACTTCAGGG	TGAGCGTTCT	1320
	TTGGCTAAGG	ACAATAAGAG	CATCGGCCGT	TTCATCTTGG	ACGGTATTGC	TCCGGCGCCC	1380
	CGTCAGACAC	CGCAGATCGA	AGTAACGTTT	GACATCGATG	CCAACGGTAT	CCTGAATGTA	1440
	ACGGCTCATG	ACAAAGCTAC	CGGCAGAAG	CAGATATCC	GCATCGAAGC	CTCCAGCGGT	1500
	TTGTCCGATG	ATGAGATCAA	GCGCATGAAG	GAAGAGGCGC	AGGCCAATGC	CGAAGCAGAT	1560
30	AAGAAAGAGA	AAGAACGTAT	CGACAAGATC	AATCAGGCCG	ACAGCATGAT	CTTCCAGAGC	1620
	GAAAGCAGT	TGAAGGAGTT	GGGAGACAAA	TTCCCGGCCG	ACAAGAAGGC	TCCGATCGAT	1680
	ACCGCTCTCG	ACAAACTGAA	AGAAGCACAC	AAAGCACAGG	ATGTAGCTCG	TATCGATACA	1740
	GCCATGGCCG	AACTGCAAAAC	CGCTCTTTCC	GCAGCGGGCG	AAGAGCTTTA	CAAGAATGCC	1800
	GGAGCAGCCC	AAGGTGGCGC	ACAACCCGGT	CCGGAATTCC	GCGGTGCTCA	AGGTCCCTCT	1860
35	GCCGGTGATC	AGCCCTCTCA	CGACAAGAAC	GTACAGACG	TAGACTTCGA	GGAAGTGAAG	1920

## (2) INFORMATION FOR SEQ ID NO:141

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1347

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:141

60	ATGCGCTACG	ACTTAGCTAT	CATCGGTGGA	GGGCGGGCCG	GTATACGGC	TGCCGAACGT	60
	GCTGCCAAG	GTGGCCTGAA	AACCTCTCTA	ATTGAGAAGA	ATGCTCTCGG	TGGTGTATGC	120
	CTCAACGAAG	GATGTATACC	GACCAAGACG	CTACTCTACT	CGGCCAAAGT	GCTACATCAA	180
	ATTGCTACCG	CATCTAAATA	TGCAGTAAGT	GGAACGGCCG	ATGGACTTGA	CCTCGGCAAG	240
65	GTGATTGCCA	GAAAGGTAA	AATCATTCGC	AAGCTGACTG	CAGGCATCCG	TTCACGCGTG	300
	ACAGAGGCGC	GAGTAGAGAT	GGTGACGGCA	GAAGCTACCG	TAAAGGGATG	CGATGCAGAC	360
	GSCATCATCG	GCATTACTGC	GGGCGAAGCA	CAGTACAAAG	CTGCCAACCT	GCTACTATGT	420
	ACCGGTTCCG	AGACGTTTAT	TCCACCCATC	CCCGGAGTGG	AGCAGACAGA	GTATTGGACA	480
	AACCGTGAAG	CTCTACAGAA	CAAAGAGATT	CCGACCTCTC	TGCTCATCAT	CGGTGGTGGG	540
70	GTGATCGGAA	TGGAGTTCCG	TTCTTTCTTC	AACGSTATCG	GTACCGAAGT	GCACGTGGTG	600
	GAGATCTGTC	CGGAAATACT	CAACGGTATC	GATCCCGAAC	ATGCAGCTAT	GCTACGCGCT	660
	CACATGTAAG	AAGAAGGAAT	CAATTTCTAC	CTCGGCGACA	AAGTAACTAT	GGTTCGCAAC	720
	GGAGCTGTGA	CGGTAGAATA	CGAAGGAGAA	AGCAAGAGAA	TGCAAGGAGA	ACGTATCCCTG	780
	ATGAGTGTGG	GACGTCGCCC	CGTCTGCAA	GGATTGAGT	CGCTCGGATT	GGTGTCTGCC	840
75	GGCAAGGTTG	TAAAGACTAA	TGAGAGGATG	CAAACTTCCC	TGCCCAATGT	CTATGCTGCA	900

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	GGTGATATTA	CAGGCTTCTC	GCTTTTGGCA	CATACGGCTG	TACGGGAAGC	AGAGGTAGCA	960
	GTAGATCAGA	TTTTGGGCAA	AACAGACGAA	ACGATGAGCT	ACCGTGCCGT	ACCAGGTGTG	1020
	GTGTACACCA	ATCCCGAGGT	CGCCGGTGTG	GGAGAGACGG	AAGATCGCT	TCGCAAGCA	1080
	GGACGTGCT	ACACTGTTCG	TCGCCTTCT	ATGGCTTCT	CCGGTCGATT	TGTAGCAGAA	1140
5	AACGAACAAG	GCAATGGAGA	GTGCAAACTA	CTACTTGATG	AAGAGAACC	CTTGATCGGA	1200
	GCACACCTCA	TTGGCAATCC	GGCCGGCGAA	CTCATCGTAA	CCGCTGCCAT	GGCCATCGAG	1260
	ACCGGCATGA	CGGATCGACA	AATCGAACGA	ATCATATTCC	CTCATCCGAC	TGTAGGCGAA	1320
	ATCCTAAVAG	AAACTCTCCG	CGGAGGT				1347
10	(2) INFORMATION FOR SEQ ID NO:142						
	(1) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2823 base pairs						
15	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
20	(11) MOLECULE TYPE: DNA (genomic)						
	(111) HYPOTHETICAL: NO						
	(1v) ANTI-SENSE: NO						
25	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
30	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2823						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142						
35	ATGGAATTGA	AAAGATTTT	ATCACTTGGT	CTTCTGCTTG	TGGGATTCAT	TCCGATGAAG	60
	CTTCTGCCCC	AACAGGCTCA	GCCACTCCCT	ACAGATCCCG	CTGTTCTGTG	CGGTAAGTTG	120
	GACAACGGAT	TGACTTATTT	CATCCGTCAC	AACGAGAAC	CGAAAGATCG	TGCGGATTTC	180
	TTTATCGCAC	AAAAGGTAGG	TTCTATTCTT	GAAGAAGATA	GCCAGTCCGG	TTTGGCTCAC	240
	TTCTTGGAAC	ACATGGCTTT	CAACGGTACG	AAGAACTTCC	CCGGTAAGAA	CTTGATCAAC	300
	TATCTCGAAA	CGATCGGTGT	ACGTTTCCGT	CAGAACCTGA	ACGCTTCTAC	CGGATTCGAC	360
40	AAGACGGAAT	ATACGATAAT	GGATGTGCGG	ACTACACGTC	AGGGAATCAT	CGACTCCTGC	420
	TTGCTTATCC	TGCATGATTG	GAGTAACAAT	ATTACCTCCG	ACGGGCATGA	GATCGACGAG	480
	GAGCGCGGTG	TGATCCAGGA	AGACTGGCGT	GCTCGTCGCG	ATGCCAACCT	TCGTATGTTT	540
	GAGGCTATAC	TTGCCAAGGC	TATGCCGGGT	AATAAATATG	CAGAACGCAT	GCCCATCGGT	600
	CTGATGGACG	TCGTGCTCAA	CTTCAAGCAT	GATGAGCTGC	GCAACTATTA	TAAGAAATGG	660
45	TATCGTCCCG	ACCTGCAAGG	TCTGGTGAIC	GTGGGAGATA	TCGATGTGGA	CTATGTGGAG	720
	AACAAGATCA	AAGAATCTT	CAAGGACGTT	CCTGCTCCCG	TGAATCCAGC	AGAGCGTATC	780
	TATACGCCGG	TAGAGGACAA	CGATGAGCCT	ATCGTAGCCA	TTGCTACCGA	TGCTGAGGCT	840
	ACTACACGCG	AGCTCTCCAT	CAGCTTCAAG	AGCGAGCCCA	CTCCTCAAGA	AGTGGCAGGA	900
	TCGATATTCG	GACTTGTGGA	AGACTATATG	AAACAGGTGA	TCATACAGC	CGTGAATGAG	960
50	CGTCTGTCCG	AGATTACTCA	CAAGCCTAAC	GCTCCTTTCC	TCAGTGCAGG	AGCTTTCITC	1020
	TCTAACTTCA	TGTACATCAC	CCAGACTAAG	GAGGCATTCA	ATTTTGTGCG	CACGGTTCGT	1080
	GAGGGTGAAG	CGGAGAAAGC	GATGAACGCA	TTGGTGGCAG	AGATAGAAAG	CCTCCGTGAG	1140
	TTCCGTATCA	CCAAAGGCGA	ATACGATCGT	GCACGACGTA	ATGTGCTCAA	GCGATACGAG	1200
	AATCAATACA	ACGAAAGAGA	CAAGCGTAAG	AACAATGCTT	ATGCCAATGA	ATACTCCACC	1260
55	TACTTCCACG	ATGGCGGCTA	TATCCCGGTT	ATTGAGGTGG	AATATCAGAC	GGTGAATGCT	1320
	TTTGCTCCTC	AGGTTCTCTT	GGAAGCATTC	AATCAGGCTA	TTGCCCAAT	GATCGATCCG	1380
	GTGAAGAATG	CTGTGCTTAC	CCTCACCGGT	CCTTCAAAGG	CTGAAGCCAA	GATTCGAGC	1440
	GAAGCAGACT	TCCTCGCTGC	TTTCAAAGCT	GCTCGTCAGC	AGAAAGTAGA	AGCCAAGAAA	1500
	GACGAAGTCT	CCGACCAAAA	ATTGATGGAG	AAAGCTCCTA	AGGCGGAAAA	GATCGTTTCC	1560
60	GAGAAGAAAG	ATCAGAAGTT	CGGTACCCAG	GAACCTACCC	TTAGCAATGG	CATCAAAGTA	1620
	TACCTCAAGA	AGACCGATTT	CAAAATCAAAC	GAAATCCTGA	TGAGTGTCTT	CAGCCCGCGT	1680
	GGTATCTCT	CCGGAAGGCA	TGCTCCCAAC	CAATCTGTGA	TGAATTCGTT	CATGAACGTG	1740
	GGTGGCTTGG	GCAACTTCGA	TGCTATCCAG	CTGGATAAGG	TGCTGACAGG	TCGCTCTGCT	1800
65	TCCGTATCTC	CCTCTTTGTC	TCTGCTCAGT	GAAGGTCTTT	CGGGCAAAAC	GACTGTAGAA	1860
	GATATGAAAA	CTTCTTTCCA	GTTGATCTAT	CTCCAAATGA	CTGCTAACCG	CAAGGATCCC	1920
	GAAGCGTTCA	AGGCCACACA	GGAAAAGTTG	TACAATAACT	TGAAAAATCA	GGAGGCCAAC	1980
	CCGATGGCTG	CGCTTATGGA	CTCTATCCGT	CATACCATGT	ACGGCGATAA	TCCGATGATG	2040
	AAACCCATGA	AACTGCTGA	CGTGGAGAAA	GTAAATTACG	ATCAGGTAAT	GGCTTTCTAC	2100
	AATGAGCGAT	TCGCTGATGC	CGGCCACTTT	ATGTTCTTCT	TTATCGGTAA	TCGGATGAA	2160
70	GCCCAAGATGA	AGCCATTGAT	CGAACTTAT	CTTGCTTCAT	TGCCCAACCT	CAAGCGTGGC	2220
	GATAAGATGA	ATAAGGCTCA	GGTACGGGCT	GCCGTTCCG	GAAAGATCGA	TTGCCAAGTT	2280
	GAGAAGGAAA	TGGATACTCC	TTGACTACT	ATATTGATG	TCGTGTCGGG	AAATGTGGAA	2340
	TATACGCTCA	AGAAGCTCT	CCTGCTGGAA	GTCTTCTCAG	CCGTAATGGA	TCAGGTGTAC	2400
	ACCGCTACCG	TTCCGAGAAA	GGAAGGCGGT	GCATACAGTG	TGGCTGCATT	CGGCGTCTC	2460
75	GAGCAATATC	CTACGCCCAA	GGCTCTGATG	CAGATCTATT	TCCCAACGGA	TGCTGCTCGT	2520

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GCCGAGGAAA TGAATGCTAT CGTTTTGCT GAGTTGGAGA AGCTTGCCAA GGAGGGCCCC 2580  
 AATGTGGAAT ACTTTAAGAA GACTATCGAA AACCTGAATA AGCAGCACAA AGAAAGTCTG 2640  
 CGTGAGAAAT GTTTCCTGGCT CGAAGCCATG AAGGCGTCTT TCTTCGAAGG AAATGACTTC 2700  
 ATCACAGACT ACGAATCCGT ACTGAACGGT CTTACTCCTG CTGAATTCGA AAAGTTTGGC 2760  
 5 GCACACCTCT TGAAGCAGCA GAATCGGGTT GTTGTCATCA TGGCTCCTGT TGCAAAGGCT 2820  
 CAA 2823

## (2) INFORMATION FOR SEQ ID NO:143

10

## (i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 2052 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2052

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

ATGAGTAAGA AAGGAACAAAT CGGGGTAACG AGGACAAATA TATTCCTCGT CATCAAAAAA 60  
 TTCTGTGACA GCGACCATGA GATATTCTTG CGTGAGATCG TCTCCAATGC CGTGGATGCT 120  
 ACGCAGAAAG TGAAACGCTT TACATCCGTC GGCGAATTC AAGGCGAGAC GGGTGAACCTC 180  
 35 CGCGTAACGG TCAGCGTGGG TGAAGTGGCA GCGACGATCA CGGTCAGCGA CCGCGGCGTA 240  
 GGGATGACCG AAGAGGAGGT GGAGAAGTAC ATCAATCAGA TTGCTTTCTC CAGTCCGGAA 300  
 GAGTTTCTTG AAAAGTACAA AGACGACAAG GCCGCCAATA TCGGCCACTT GGGACTCGGA 360  
 TTTTACTCGG CTTTCATGGT GTCCGAGOGA GTGGACGTGA TCACGCGCTC TTTCCGAGAA 420  
 GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCG AATACACGCT CGAACCTGCG 480  
 40 GACAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCGAGTTC 540  
 CTCAAAAAAG AAAAGATAGA GGGGCTCCTC GGCAAACTACT GTAAGTTTCT TACCGTGCCG 600  
 ATCATTTTTC GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC 660  
 AATCAGATCA ACGACACACA TCCTGCTCGG ACCA/AAAGC CTGCCGACCT CAAGGACGAA 720  
 GACTATAAGG AATTTTACCG TTGCTCTAT CCCATGTCCG AAGAGGCTCT CTTCTGGATC 780  
 45 CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCCT GAAGATCAAA 840  
 AACAACTTGG ATCTGCAGCG CAACAAGATT CAGCTCTACT GCAATCAGGT TTACGTCAAC 900  
 GATGAAGTAC AGGGTATCGT GCCGGACTTC CTCACCTCTC TGCAAGGGGT CATCGATTCT 960  
 CCGGATATTC CCGTCAAGCT ATCGCGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG 1020  
 ATCTCGTCTC ATATCACCAA GAAGGTGGCA GACCGTCTGG AAGAAATTTT CAAAAACGAC 1080  
 50 CGCCCCACAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCGAATA CGGTATGCTG 1140  
 ACGGATGAGA AGTTCTATGA GCGTGCAGCC AAATTCCTTC TTTTACCGA TATGGACGGA 1200  
 CACAAGTACA CGTTCCGAGA ATACCGAAGC CTCGTGGAAG GTGTACAGAC GGATAAGGAC 1260  
 GGACAGGTAG TGTATCTCTA TGCTACGGAC AAGCATGGAC AGTACAGCCA CGTGAAACGT 1320  
 GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGCTC AGTTGATCC GCATATCGTG 1380  
 55 AGCCTGCTGG AGCAAAAGT' GGAGAAGACA CACTTTGTCC GTGTGATAG CGATACGATC 1440  
 AACAACTCTG TCCGCAAGGA GGAAAGAGCC GAAGTGAAC TGTCCGATAC GGAGCGCGCC 1500  
 ACTCTGCTGA AGCTGTTGGA AGCAGCCTG CCACGGGACG AGAAGAAGCA CTTCAATGTA 1560  
 GCTTTCGAAT CGCTCGGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG 1620  
 CGCCGTATGC GCGATATGCG ACAGCTGCAG CGGGAATGA GCTTCTACGG CGAACTCCCC 1680  
 60 GATTGCTACA ATCTGGTACT TAATACGGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT 1740  
 GAGAAAGAAAT CGGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAATCGC CGAGCTGAAA 1800  
 GCGGAAGAGG CCAAGCTGCT CGATGAGGAA AAAGGGAAGA AACCGGAGGA AATCCCTGTT 1860  
 GCCACGAAGG AAGCCAAGGA GAACACGCCC GTCGAACAGG CCAAAACCGA AGGCAGTATC 1920  
 AACGATCAAC TGACCAATA TGCTCAGGAC AACGAGCTGA TAGGTGAGCT CATCGACTTG 1980  
 65 GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CCGAATTCAT TCGTCCGAGC 2040  
 CAGGCTCTTC TC 2052

## (2) INFORMATION FOR SEQ ID NO:144

70

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1392 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

75

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGA	AAAAAC	TGATCGATAT	TTTGGTCGTA	GACGATGATG	TGGCAGTCTG	TGCCGCACTG	60
CGTCT	GGTGC	TCAAGCGAGC	GGGCTATAAT	CCCGTATAG	CCAACAGTCC	CGACGAAGCT	120
TTGTCC	ATAA	TGCGGAATCC	TGATGGCGGC	TGTAAGCCGG	CTGTGATTCT	GATGGATATG	180
AATTTC	TCCC	TTTCGACCTC	CGGCAGGGAA	GGATTGGAAC	TACTGGAGAA	GATGCAGATA	240
TTCACTT	CCT	GCCCTGTCTAT	ACTGATGACG	GCTTGGGCTT	CGATTCCACT	GGCACTGGAG	300
GGAA	TGAGGC	TTGGAGCTTT	CGACTTCATA	GGCAAGCCAT	GGGACAACGA	TGGGCTCCTT	360
CGTACCA	TAG	ATACGGCCTT	GCATCTGGCT	GCTCCCTCAG	CTGTGGCGAA	TCCATCGGAA	420
CACTCTG	ACA	GATACACGC	CGCTCAGCCG	AAAGCTACAG	TCCAAGAGAA	TGACCCCTGT	480
GCCCA	TATCA	TAGGCCGGAG	CGATGCCATC	TGTAAGATCA	AGGAACGGAT	ACGCCGCATA	540
GCTCC	ACCC	ATGCCTCTGT	CCTGATCAGC	GGCGAGAGCG	GTACGGGCA	AGAGTTGATA	600
GCCGA	AGCTC	TGCACCGTGG	GAGCAACGA	GCCTCAGCCC	CATTCTGCAA	GGTCAATTTG	660
GGTGG	GATT	CCGAAAGTTT	GTTCGAAAGT	GAGCTGTTCC	GACATAAGAA	AGGAGCTTTT	720
ACCAAT	GTCT	TTTCCGACAG	GAAAGGACGG	TTCCAGCTGG	CTGATGGCGG	CACGATCTTT	780
CTGG	ACGAA	TAGGCGAACT	ACCGGTGCGC	AACCAAGTAA	AACTGCTGCG	AGTGCTACAG	840
GAAC	AGACAT	TGAGCCGCTT	GGCGGAGAGC	GTCTCCACCC	GAGTGGACAT	CCGTGTGGTA	900
TCCG	CTACGA	ATGCTTCCTT	GGAGCGAATG	GTAGCCGAAG	GACGTTTCAG	AGAGGACCTC	960
TACTAT	CGAA	TCAACCTGAT	ACATCTGCAT	CTGCCTCCGC	TGCGTGAGCG	TCAGGAGGAT	1020
ATAC	AGCTGC	TGGTGAAGC	CTTCAGTGAA	GCCTTTGCC	AATCGAACGG	ATTGCCCAT	1080
GCG	TTTGA	GTGCGGAAGC	TATGCGACGT	ATCTGTGCCA	TGCCCTACC	GGGCAATGTA	1140
CGG	AACTGA	AAAAAGTAGT	GGAGCGTAGC	CTATTGTCT	CGGGATCGAG	AGAAATCAGT	1200
GCC	CGGATG	TGGCTGACTT	CGGTTCGCAG	GTGACGGCAG	CAGACCACTC	CGACGAACGG	1260
GCT	TTGACCG	ACATGGAGGA	AGCTGCTATC	CGAGAGACGC	TGACTAAATA	CAACGGCAAC	1320
GTTAG	TCGTG	TGACAGAGC	CTTGGGATTG	AGCGGGCAG	CTCTTTACCG	GCGAATGGAG	1380
AAAT	ACGGAC	TG					1392

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGCT	TAAAG	AAACCT	CCACGCCACA	GTACAGGGCA	AAGAGATATT	GAAAGGAATC	60
AATCT	GGAGA	TCAATGCCGG	AGAGATTCT	GCTATCATCG	GGCCGAACGG	ATCGGGGAAA	120
AGTAC	GCTCT	CTTCGGTTTT	GGTGGGACAT	CCCTCCTTTG	AAGTCACGGA	AGGAGAGGTG	180
ACATT	CAATG	GAATCGACCT	GCTCGAATC	GAACCGGAAG	AACGTGCACA	CCTCGGACTC	240
TTTCT	CAGTT	TCCAATATCC	GGTCGAGATC	CGGGCGTCA	GCATGGTGAA	TTTCATGAGG	300
GCACT	GTGCA	ATGAACATAG	GAAAGCGATC	GGAGCAGAAC	CCGTATCGGC	AAGCGACTTC	360
CTCA	AGATGA	TGCGAGAGAA	GCGTGCCATT	GTGGAGCTGG	ACAACAAATT	GGCCAGCCGT	420
TCTGT	GAACG	AAGGCTTCTC	CGGTGGAGAA	AAAAGAGGCA	ACGAAATCTT	CCAAATGGCT	480
ATGCT	CGAAC	CCAAGCTGGC	TATTTTGGAC	GAAACCGATA	GCGGGCTCGA	TATCGACGCT	540
CTCC	GATCG	TAGCAGGGCG	GTAACCGGA	CTCCGCTCTC	CGGAGATGTC	TGCTATTGTG	600

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ATCACACACT ATCAGCGTTT GCTCGAGTAC ATCAAGCCGG ACTTCGTACA CGTCCTTTAC 660  
 AAGGGGCGCA TCGTCAAGTC GGGAGGAGCC GAGCTGGCTC TCACGCTCGA AGAAAAAGGC 720  
 TACGACTGGA TCAAGGAAGA GATAGGAGAA 750

5

(2) INFORMATION FOR SEQ ID NO:146

(1) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

25

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

30 ATGGCTAAGG AGAAACGAT CTACGTCTGC CGTTCGTGCG GAACCAAATA CGCCAAATGG 60  
 CAAGGCAACT GCAATGCCTG TGGAGAGTGG AACTGCATTG ATGAGGAGAA GGTGCCGGCA 120  
 CCGGCATCGG GCAAGCATGC AGCCAAGAGT TTTATGCCTC GGGAGCAGGA CAACCGGCCA 180  
 AGACTCTTAC AGGATGTGGA GTCCGGCGAT GAAGAGCGTA TTCGCCTCGG CGATGAAGAG 240  
 TTGGACCGCG TACTGGGTGG AGGAATTGTC AAAGGAGCAT TTGCTCTGCT TGGCGGCGAG 300  
 CCGGGAATCG GTAAGTCCAC GCTTATCCTC CAGACGGTGC TGGCTCTGCC GCAGTTGCCG 360  
 35 ACGCTCTATG TGTCCGGCGA AGAAAGTGCC CGACAACTGA AGATGCGCGC CGAACGACTG 420  
 GGGCAAGCCA TGAATGGGTG CTACGTATAC TGGGAAACGA ATATAGAGAG GATACTCTCC 480  
 CGTGCAGAAG AACTCACACC CGATCTCCTC GTGATAGACT CTATACAGAC GGTCTATACC 540  
 GAGGAAATGG AAAGCTCGGC CGGCAGCGTG GGGCAGATCC GCGAATGTGC CGCCTTACTG 600  
 CTCAAACTAC GCAAGACTAC GGGTATCCCC GTCATCGTCA TCGGACACAT CACCAAAGAA 660  
 40 GGTAGCATAG CCGGACCGAA GGTGCTGGAG CATATAGTGG ATACGGTGCT TCTCTTCGAC 720  
 GGGGATAAAG ATCATCTCTA CCGGATACCT CGAGGACAGA AGAACCGCTA TGGCAGTACT 780  
 TCCGAGCTGG GGATATACGA GATGCGGCAG GACGGTCTGC GTGGCGTGA GAATCCGAGC 840  
 GAACATCTCA TCACACGCAA TAGGGAAGAC CTCAGTGGCA TAGCCATAGC CGTAGCGATG 900  
 GAGGGCATTC GCCCGATACT CATCGAAGCG CAGGCTTTGG TCAGCTCGGC CATTATATGCC 960  
 45 AATCCGCGAG GTTCGGCCAC GGGCTTOGAT ATTGGGCGGA TGAACATGCT CTTAGCCGTA 1020  
 CTGGAGAAAC GTGCCGGCTT CAAGCTCATA CAGAAGGATG TGTTTCTGAA CATTGCGGGA 1080  
 GGTATCAAAA TAGCCGATCC GGCTACGGAT CTGGCCGTTA TCTCGGCAGT GCTGGCGTCG 1140  
 AGTCTGGACA TCGTTATCCC GCCGGCGGTA TGCAAGACGG GCGAGGTGCG ACTCTCCGGA 1200  
 GAGATACGTC CCGTGAGCCG CATCGAGCAG CGCATAACGG AAGCGGTCG CATAGGGTTC 1260  
 50 AAAGAGATAT TGGTACCGGC CGATAATTTC CGCCAGGAGG ATGCCGGCCG CTTCGGTATT 1320  
 CGGCTCGTGC CGGTCAAGAA GGTGGAGGAA GCCTTCCGCC ATCTGTTCTC GAAAGGAAGA 1380  
 GAA 1383

55

(2) INFORMATION FOR SEQ ID NO:147

(1) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

75

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...813

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:147

5 ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCTCTT TGIAGTGACA 60  
 TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCAGTGGG CTCTCGGCGG AAAGCTCTTT 120  
 ACTTCGGCGT GGATACAACG TTCGGCGGAA TATCAAGCGC TTTCGATTCA GGCATACAC 180  
 ATCGCTACGG AAAGAGTGGG CGCTCTACCG GCAGAACGTA AACAAAGAGA TAGGCCTTAT 240  
 GCCATCGTAA CGGACATAGA CGAAACCAT TTGGACAATA CGCCTAACTC CGTGATCAG 300  
 GCTCTCAGCG GCAAGGATTA TGATGAAGAG ACTTGGGGSA AATGGTGTGC ACAGGCGGAT 360  
 GCCGACACAC TGGCAGGAGC TTTGTCTTTC TTCTCCATG CAGCGAACAA GGGGATCGAG 420  
 10 GTCTTTTACG TCACCAACCG CAGAGACAAT CTGGCGGAAG CAATCTTTCA GAACCTTCAG 480  
 CGTTACGGAT TCCCTTTTGC CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC 540  
 AAAGAACCOC GTCCGCTCAA AATACAGAA CAGTATGAAA TAGTATTGCT CATAGGAGAC 600  
 AACTTGGGCG ACTTCCACCA CTCTTCAAT ACGAAAGAA AGTCCGGACG CAAACAGGCT 660  
 CTGGGCGTGA CAGCCGGGGA GTTTGGCCGG CACTTCATCA TGCTGCCCAA TCCCAACTAC 720  
 15 GGATCTTGGG AACCGGCATG GTACGGCGGG AAGTATCCGC CACTGCCCGA AAGAGACAAA 780  
 GCACCTTAAC AACTGCACCTC ACAGAACAGC AGA 813

## (2) INFORMATION FOR SEQ ID NO:148

20 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1251

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:148

40 ATGAGCACCA ATATAGATGT ACAACAGATC AACAGCGTT TCGGCATCAT CGGTAGCAGT 60  
 CCGCTGATGG AACATGCCAT ACGAGTGGCA GCACAGGTGG CTCTACCGA CATGTCCGTC 120  
 CTCGTGACGG GGGAGAGCGG TTCGGGAAA GAGTTCTTCC CACAGATAAT CCACTACTAC 180  
 45 AGCGCCCGGA AACATCATAG CTACATTGCA GTCAATTGCG GAGCCATCCC CGAAGGAACC 240  
 ATCGATTCCG AGCTGTTCCG ACACCGCAA GGTTCCTTTA CCGGAGCCGT ATCGGATCGC 300  
 AAGGGGTACT TCGAAGAAGC ATCCGGCGGC ACGATCTTTC TGGACGAAGT GGGCGAAGTG 360  
 CCTTTGCCCA CGCAGGCGAG GCTGCTGAGG GTGCTGGAGA CGGGCGAGTT CATCCCCGTA 420  
 50 GGAGCCAGCG AGTCCGAGAA GACGGATGTC CGTATCGTAG CGGCGACGAA TGTGAACCTC 480  
 AAGGAGGCGG TAGCGAAGCG GAAGTCCCGG GAAGACCTCT TCTTCCGGCT CAATACGGTA 540  
 CUGATCGAGG TGCTTGGCT GCGTATGCGA CCGGACGAG TGCCCTTGCT TTTTCGCGGA 600  
 TTCGCGCCCG ACAGCGCCGA GAAGTATCGG ATGCCTCCGC TCGCCTATC GGACGAAGCC 660  
 CGTACCATAT TAATGCGTTA CCGCTGGCCC GGCAATGTGC GAGAGCTGCG CAATATAACC 720  
 GACAGGCTGA GCATCTTGA GGAGGAGCGG ACGGTATCGG CAGAGACCAT CACTCGCTAC 780  
 55 CTGGACGCTG AAGGGATGCA AGACCTCCAC CCGTCTGTA TCCGACGGA CGAAGCGACC 840  
 GAAGCGGACA AACAAATCCC CCATTACGAG CGCGAAATCA TCTACCGGT GCTATACGAT 900  
 ATGAAGAAAG AGATAGCCGA TTTGAAGGGG ATGATGAACC GCCTGGCGCA CCACGAACAG 960  
 CCCTCATGGC CTGTAGGGTC GGACGTCTGG GGCAACGACG ACAAGCGCAC CGCAGATCCG 1020  
 60 AAGTGGGGCG TCAGACGCA CAAGGCCCCC ATCGCGAAGC CGGCGAACC CGTGGAGCCG 1080  
 ATACAGGAAG CCAGCGAATA CACCGAGGAT CCGGTTTCCG TGGAGGAGGT AGAGAAGAAA 1140  
 ATGATTTCCT TTGATTGGA ACGCCACGGC GGAAGGCGCA AGCAGACAGC CGAGGAAGTG 1200  
 AAGATTTCGG AGCGGACACT ATACCGTAAA ATCAAGGAGT ATGGACTGGA A 1251

## (2) INFORMATION FOR SEQ ID NO:149

65 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1806 base pairs  
 70 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 75 (iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCCTAC	TCTTCGGCGG	TACTACGGAA	GGCCGTGCCG	CAGCTCGCGT	GCTGGATGAA	60
GCGGGAAGTC	CGTTTTTCTA	CTCCACCAAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCGACATGG	TTTCGTTTGG	TCGGAAGAGAA	180
GAGATCCGAC	TGATCGTGGA	CGCCGTCAT	CCTTCGCGG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAATAAGAT	ACGAGAGACA	ATACCCCTCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAAAC	TACGATACGG	CTGCCGAGCG	GATGCTTGCC	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGAATA	CGATCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACCAAC	CTTTTGCCGC	ATATTGAAGC	GAGACGAATC	GGTTGCTTTG	480
GCAGAGAAGA	ACGGCTTTCC	TGCGGAGCGC	ATCGTTTCT	TCGAACCGCA	TGCGGACGAG	540
GAGCTGATGC	AAGCGTTCG	CCCCGATGCC	ATTATCACA	AAGAAAGCGG	AGAGAGCGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTCGTA	660
CGTCCCGCTT	TGCCTCCTTC	ATTCAATCCC	GTAGGCGGCG	CTGTGCTTTT	GAGACCGGCG	720
GTAGAAGCGC	TGCTGCCGGG	ATTCTTTTCA	CTCGGAAGCG	GATTCAGTAC	CGGCACCAAC	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGGCTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCTTTC	GGCGAAATA	GTCACTCTGC	CCATAGCGGA	AATTGAGAG	900
GAAGAAGATG	CTGTCTATC	CGCAGTCTCG	AAAGATGCAG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCGC	TACGATCAGG	CTCAATCCCG	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCCGCGC	TGCGTCTGGA	GGTCGGAGGT	1080
CCGGCTATCA	ACCTCGTACC	TCGACGAATG	ATGACAGCAG	AGGTACGCGG	ACTCTATGCG	1140
CAGGAGGGTC	TGGATATTAC	GATTAGCGTA	CCCGAAGGCC	GAGAGGCTGC	TACCCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCGTG	1260
AAACCTTTTT	CGGCCGAAGC	GTTGCTTGGT	GCCATCGGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCCTCAT	TCCACAGGCC	TTTGTGCACT	ATGGCAATTT	CGTCGGCGAA	1440
TCACTCAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTCGG	TAACGGTAGG	AATCATGCTC	1500
GGCAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCTGCACGGA	ACTGGCTCGT	CAGGCAGGTT	GTTCGGAAGA	CATCCATGCC	1620
ATATATAGCA	GCCTGAATTT	GGCTCGTGAG	CTATGGACTA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTGCCGCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGGAG	CGATTCTGTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTCCGAAT	CGGTGGTATT	CACCCCCCGG	AAAACAAGTT	GTCCGCAGGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCTCA	CAGGTAGTCA	TCCCTCTTGG	TCAGCACATC	120
GGTGACCGGG	CAACTGCCAC	GGTCAAGAAA	GGGGATGAAG	TTAAGGTGGG	GACTATCATT	180
GCTCAGGCGG	GAGGATTCGT	ATCAGCTAAT	ATCCACTCAT	CTGTGTGCGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGCC	TATCCCAAGC	CCGCAGTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGCTCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGCG	TCTTGGCGGT	420

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5 GCTACCTTCC CTACCCATGT GAAGCTGTCC CCTCCTCCGG GCAACAAACC TGAGATCTTG 480  
 ATCATCAACG CCGTAGAGTG CGAGCCTTAT CTGACGAGCG ACCATGTCCT TATGCTGGAG 540  
 CACGGCGAAG AGATCATGAT CGGCGTGAGT ATCCTGATGA AAGCCATTCA GGTAAACAAG 600  
 GCCGTCATCG GAGTTGAGAA TAATAAGAAA GATGCTATTG CTCACCTCAC CAAACTGGCC 660  
 ACTGCATATC CCGGCATAGA GGTAAATGCCG TTGAAGGTGC AATATCTTCA AGGCGGTGAG 720  
 AAGCAGCTGA TCGATGCAGT GATCCGCAAG CAGGTAAAAA GCGGTGCCTT GCCTATCAGC 780  
 ACAGGTGCCG TAGTACAAAA CGTGGGTACG GTATTCCGCG TGTACGAAGC AGTACAGAAG 840  
 AACAGCCCTC TGGTCCGACG CATCGTGACG GTTACAGGAA AAAAAGTCTC TCGTCCGTCT 900  
 AACCTCCTCG TTCGTATAGG TACTCCTATT GCGGCTTTGA TCGAAGCAGC AGGTGGCTTG 960  
 10 CCGGAGAATA CCGGCAAGAT CATCGGCGGA GGTCCGATGA TGGAGCGCGC TCTGCTGTCA 1020  
 CCGGATGTGC CTGTGACCAA AGGCAGCTCC GAGTATTGA TTCTCGATAG AGAAGAGGCA 1080  
 GTTCGCAAGC CTATGCGCGA CTGTATCCGA TCGGCCAAGT GCGTCGGAGT GTGTCCGATG 1140  
 GGACTCAATC CGGCTTTCTT TATGCGCGAC ACCTTATATA AGAGCTGGGA AACAGCGGAA 1200  
 AAAGGCAACG TGGTTGACTG TATCGAATGC GGTTCGTGCA GCTTCACTTG TCCGCGCAAC 1260  
 15 CGTCTCTGCG TGGATTATAT CCGCCAAGCC AAGAAGACTG TGATGGGTAT CCAAGAGACA 1320  
 CGTAAGCAA 1329

## (2) INFORMATION FOR SEQ ID NO:151

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## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1437 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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## (ii) MOLECULE TYPE: DNA (genomic)

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## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

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## (A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1437

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

45 ATGAAAAGAA TACAACAAAC TCCTATCGCT CTCTTCGCGG CTGTTGCCGG TTTGGTGGCT 60  
 CAAAATGCTT ACGAGGGAGT AATTTTCATAT AAAATTTTCGT TGGACAAAAC CGGAACAAG 120  
 GTTGTACTGA ATGGTGGCGG AGATATGAGT AATTAAAGC TCAAGAGCAC TCAGATGATC 180  
 ATTGTTACGC CTATTCTTCG TTCAGAAGAT GGTACCAAGC GGGTGAATT TCCTTCGGTA 240  
 GTCATTACAG GCCGCAATAG AACAAAAGCT CTCAGCGGTG AAATCGCATT TAGTTCGGCT 300  
 TTGCCCAAG CAAAACATGC AGCTCAATAC ATTCGCCGTC ATAATGGGAA GAGCGAGCAG 360  
 TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCAATGGATGA TGGATGCCAA GTTTGTGGTT 420  
 CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCTT 480  
 50 TTTGATCCAC TCTTCAATCC GGCAGAGGCT CCTTATTGT TGGCACATAT TACTCCGGCA 540  
 GAAGAAGTGG AAAACAGCG AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT 600  
 AAGGCAGATG TCCTTCTCGA GTATCGCAAC AATAAGGCGG AGTTAGAGAA AATCAAAGAA 660  
 TTTGTAAGCA CCGTTAAGGC TAATCCAAC TATTCCGGTCA ATAAATGAT CATCGAAGGG 720  
 TTTGCTTCTC CCGAGGCTTC AATAGCCAC AATAAGGCTT TGTGGAGCG CCGTGCTAAA 780  
 55 AGACTCGCGG AAGAATTGGT GCGTAAATAT GGCAAAACAT TGCCGAATAT AACCACTGAA 840  
 TTCGCGGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT 900  
 CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCACTGGAA 960  
 CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTTG 1020  
 60 CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCTCGA AGAAGCTTCGT 1080  
 GAAATCATTA AGACTGCTCC GAAAGAACTT AGTGAGGCCG AAATGTACCG TGTGGCAATG 1140  
 TCTTATCTCG AGGGGACCA AGAGCGTTTG TTTGCTCTGA ATACGACCCT TAAGTATTTT 1200  
 CCTGAAAGTG TAACGGGCCG AATCAATTTG GCTGTAGCCG CTTTAAATGG TGGAGACGTT 1260  
 CAAACAGGCA TTGCTCTGTG GAGTCCGATT CAGACAGAAA AGGGTGTAAG CAATATCCTT 1320  
 65 GGAGCTGCTT ATGCTCGTAC GGGAGATTTT GCTCGTGCCG AAACCTTCTT CCGTAAGGCC 1380  
 GTTGCAAGAG GAGATGCAAA TGCGCAGCGC AACCTCGATA TGCTGCTTGG CAAAAG 1437

## (2) INFORMATION FOR SEQ ID NO:152

70

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 5 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 10 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1149  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ATGGCAGAAA	AAAGAGACTA	TTACGAAGTC	CTCGGTGTAT	CGAAGAATGC	CACCGACGAT	60
GAACTGAAAA	AAGCATATCG	CAAGAAGGCT	ATCCAATACC	ATCCTGATAA	GAACCCCGGT	120
GACAAGGAGG	CGAAGAGCA	CTTCAAAGAG	GTAGCTGAAG	CCTACGACGT	ATTGAGCGAT	180
CCGCAGAAAG	GCAGTCAATA	TGACCAAGTTC	GGCCATGCCG	GATTGGGCGG	AGCTGCCGGT	240
GGAGGTTTCA	GCGGAGGCGG	TATGTCCATG	GAGGATATTT	TCAGTCCGTT	CGGTGATCTA	300
TTCGGTGGGT	TCGGCGGTTT	CGGCGGATTC	TCCGATATGG	GCGGTGGCAG	TCGCAGACGT	360
GTTCGCAGAG	GGTCTGACCT	GCGAGTACGA	GTGAAGCTTT	CTTTGGCCGA	TATAAGTAAA	420
GGTGTGGAGA	AGAAAGTGAA	GGTAAAAAAG	CAGGTAGTGT	GCAGCAAATG	TCGTGGCGAT	480
GGCACGGAAG	AAGCCAATGG	CAAGACTACC	TGCCAGACCT	GCCATGGAAC	CGGCGTGGTT	540
ACACGTGTGA	GCAACACTTT	CCTTGGGGCC	ATGCAGACCC	AGAGCACTTG	TCCCACTTGC	600
CACGGAGAGG	GTGAGATCAT	CACGAAGCCA	TGCTCCAGT	GTAAGGGCGA	AGGTGTGGAG	660
ATCGGCGAAG	AGGTGATCTC	ATTCCACATC	CCTGCCGCTG	TAGCCGAAGG	AATGCAAATG	720
TCCGTGAACG	SCAAGGGAAA	TGCCGCGCCC	CGAGGAGGCG	TGAATGGCGA	CTTGATAGTC	780
GTGATCGCGG	AGGAACCGGA	TCCGAATCTG	ATCCGCAATG	GCAACGATCT	GATATACAAT	840
CTGCTTATAT	CCGTTCCGTT	GGCTATAAAA	GGAGGTAGTG	TGGAAGTGCC	GACGATAGAC	900
GGACGAGCCA	AGATCCGCAT	CGAGGCGGGG	ACACAACCCG	GCAAGATGCT	GCGTTTGGCG	960
AATAAGGGGT	TGCCCAGCGT	AAACGGCTAT	GGCATGGGAG	ACCAACTGGT	GAATGTCAAT	1020
GTCTATATCC	CCGAATCGAT	CGATGCCAAA	GATGAGCAGG	CTATCGCAGC	GATGGAAAC	1080
TCGGACAGCT	TCAAACCTAC	CGATGCTGCT	CGTAAGGATA	TAGACAGAA	ATACAGAGAG	1140
ATGCTGGAT						1149

(2) INFORMATION FOR SEQ ID NO:153  
 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 50 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...879  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

ATGAAAAAAC	TGATTTTAGC	GACTTTGGGA	CTTATGGCCA	TTGCCATGCT	CTCATGTTCA	60
AGCAACAACA	AGGATTTGGA	GAACAAAGGG	GAGGCTACTC	TTTGGTAAC	GTITGGTAGC	120
TCCTATAAAG	CTCCACGCGA	AACCTATGCG	AAGATTGAGA	AGACTTTTGC	CGCAGCTTAT	180
CCCGATCAAA	GGATAAGCTG	GACATACACG	TCTTCTATTA	TCCGAAAGAA	ACTGGCTCAG	240
CAGGGTATTT	ATATCGATGC	TCCGGATGAG	GCTTTGGAGA	AATTGGCTCG	TCTGGGTTAT	300
AAGAAGATCA	ATGTACAGAG	TCTTCATGTG	ATTCCCGGCC	GAGAATATGA	TGAGATGATC	360
GACTTTGTCA	ATAAGTTTAA	GGCAGCACAT	AGTGATATTA	CTGTGAAGGT	AGGGGCTCCG	420
CTTTTCGATA	CCGATGAAGA	TATGCGCGAC	GTGGCAGAGA	TCTTGACAAA	GCGTTTTCAG	480
CAATGAGTAG	AGAAAGGTGA	AGCTATTGTA	TTCATGGGAC	ACGGCACCGA	GCATGCTGCC	540
AATGACAGGT	ATGCCCGTAT	CAATAAGATC	ATGAAGAACT	ATAGCAAGTT	CATGATCGTC	600
GGAACCCGTC	AGTCCGATCC	CTCTATCAAT	GATGTTATTG	CCGAAGTGAA	AGAAACCGGT	660
GCCACGGCGG	TAACAATGAT	GCCGCTGATG	AGTGTGGCAG	GCGACCATGC	TACGAATGAT	720
ATGGCCGGAG	ATGAGGACGA	TAGCTGGAAG	ACGTTGCTGA	CCAATGCCGG	CTACACAGTT	780
TCTATAGACA	AGCTGGACAA	TGGCAATTTT	TCAGCTCTTG	GAGATATAGA	AGAGATCCGG	840
AATATCTGGC	TCAAGCATAT	GAAAGCCACC	TCTGCTCGC			879

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## (2) INFORMATION FOR SEQ ID NO:154

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1060 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

25 ATGACATCCG TCAGCCACTT ACGTACAATT TCTGTCGCAG GTATCCTGGC TCGCTGGGA 60  
 GGGGCTGTAC TCATTCTCTT CCGGGTTAAT CTCTTCCTCG GCTCGGTGGC TATTCGGATG 120  
 AGCGAGATCT TCCGACATCT TTTTTCAGAT CGTCCCGAAG GAGGAGAAGC ACTCGTGCAC 180  
 TACAATATCC TATGGAATC CCGCCTGCCC GAAGCCCTCA CGGCTGCTTT TGCCGGCGCA 240  
 30 GGTATTATCC TTAGTGGCTT GCAGATGCAG ACCGTCTTTC GCAATCCTTT GGCCGGTCCG 300  
 TCCGTTCTCG GCATCAGCTC CGGTGCCAGT TTGGGTGTG CTTTGGTGGT TCTGCTGAGC 360  
 GGCTCGCTCG GAGGAGTGGC ATTGAGTAGC CTGGGTATA TGGGCGAGGT GGCCATGAAT 420  
 ATAGCCGCTG CCGTAGGCTC GCTGGCAGTA ATGGGGCTGA TCGTTTGTGT CAGCACCAAG 480  
 GTCCGCAGCC ACGTTACGCT GCTCATTATC GCGGTTATGA TCGGATATGT AGCCACTGCC 540  
 35 GTCATCGGGG TATTCAAGTT TTTCAGTATC GAAGAAGATA TTCGGGCATA CGTAATTGG 600  
 GGGTTGGGCA GCTTTTCCG TGCCACGGAT TCGCAACTGA GTTCTTTGC CATTCTGATG 660  
 TTGATCTTTA TTCCGGCCCG TATGCTCCTT GTCAGCAGT TGAATCTCT ATTGCTGGGA 720  
 GAAAGCTACG CACGTAATCT GGGACTGAA ACTCGTCGGG CACGGCTGCT CGTGATCTCT 780  
 TCCGCCGGTT TGCTCATCGC TACCGTCACG GCCTATTGCG STCCCATCGG CTTTGTGGG 840  
 40 ATGGCTGTGC CACACTTGGC ACGGGTTATC TTTCACACAT CGGATCATCG GATCCTGATG 900  
 CCTGCTACCT GTTTGATTGG AAGTGCTCTG GCTCTTTCT GCAATATCAT TGCTCGTATG 960  
 CCGGGGTTTG AGGGGGCTTT GCCCGTCAAT TCCGTAACGG CTTTGGTGGG AGCACCTATT 1020  
 ATCGTCACCG TTTTGTCCG GCGCAGACGC TTCAGGAAG AAACCGAC 1060

## (2) INFORMATION FOR SEQ ID NO:155

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

55 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2271

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

70 ATGCGGACAA AAATATCTT TTTTGGGATT ATCTCTTTTA TTGCTCTATT GTCTCTTCT 60  
 CTGTCCGGCTC AGAGCAATGC CGTTTAAACC GGTAGTGTGT CGGATGCCGA AACCGGAGAG 120  
 CTCTTTGCCG GTGCTCGAAT CGAAGTCAA CACACCAACA TAGTAGCCGG TGCCGATGCC 180  
 GCGGGACATT TCGAGATCAA GAACCTGCCG GCAGGGCAGC ATACTATTAT ATGTTCTGTTG 240  
 GGGGGGTATG GACAGAAAGA GGAGGTGTT GCCATCGAAG CCGGACAGAC CAAAACGATC 300  
 TCTTTTGCAT TGCGACTGCG AACGAACAAC TTGGAGGAAG TCGTCGTTAC CGGTACCGGT 360  
 75 ACACGTTACC GCTTGGTCTG TGCTCTCTGT GCAACGGAAG TCCTTACCGC TAAGGACATA 420

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GCCTCTTCT CGGCTCCTAC TTCCGAGGCC TTATTGCAGG GGCTGAGTCC GTCTTTTGAC 480  
 TTCGGCCCCA ATCTGATGGG CTCTTTTCATG CAGCTGAACG GCCTTAGCAG TAAGTATATC 540  
 CTCATCCTTA TCGATGGTAA GCGTGTGTAC GCGGTCAGCG CGATTGAGT 600  
 CGTATTCTCT CTGATCAGAT CGAACGGATC GAAGTGGTGA AAGGTGCTTC GAGTTCGCTC 660  
 TACGGATCCG ATGCCATCGC CGGGTAATC AATGTGATCA CAAAAAGAA TACGAATCGA 720  
 CTGAGTGCAT ATACGTCACT TCGCATATCG AAGTACAACG ATCGGCAAC CAATACTTCG 780  
 CTCGATATAA ACATCGGTAA GTTCAGTAGC AATACCAACT ATTTCTTCTA CCATACGGAT 840  
 GGCCTGGCAGA ATAGTCCGTT CGAAATAAAA AAGAAAAAAG GATCCGGCGA ACCGGTCTTG 900  
 GAGGAAACGT ATAAGAAAAC TTTTCGTGCA CAGGAAAATC AGGGTGTAAG CCAATCGCTT 960  
 TCCTATTATG CAACTAACAA TCTTAGCTTC AGCGSAAATG TGCAGTACAA TAAACGTCAG 1020  
 ATCTTCACTC CGACTTTTTC CGAAAAGAAG GCCTATGACA TGGATTATCG TGCTTTGACG 1080  
 GCTTCACTCG GTACGAACCTA TCTTTTCCCC AATGGTCTGC ATACGCTTTC TTTGATGCC 1140  
 GTCTACGATC GCTTCGTTT CGGATATTTC TATCATGACA AGGACAGCAG TGAGAGCCTG 1200  
 ATCAACAACC AAGGTCAGAC CGAGCAACCC ACATTCTTTC CGGGTCAGCT ACACAATAAA 1260  
 AACTCATCAGA TCCGATACAC GGCAGAGGCT CGCGTGTAT TTACTCTGCC TTATGCGCAG 1320  
 AAAGTCACTG GCGGTTTGGG GTATTTCGCT GAGGAATTGA TCTCTCCCTA TAATTGATT 1380  
 ACCGACAGG CAGATGCTTC CACGCTCTCT GCTTATGTAC AAGATGAATG GAAACCGCTC 1440  
 GATTGGTTCA ATATGACAGC CGGTTTCGCT CTGGTACACC ATCAGGAGTT CGGTACACGA 1500  
 ATGAOAGCTA AGGTATCCAT ACTCGCCAAG TATGGGCGCG TGAACCTCCG CGCTACGTAT 1560  
 GCTAACGGCT ATAAGACTCC CACGCTGAAA GAGCTTTTTC CACGGAACGA ACTCACCACT 1620  
 ATGGGTTCCG ACAATCTCTA TCTCGGCAAT GCGGATCTTA AGCCACAGAT GTCGGATTAT 1680  
 TATGCTTTGG GCTTGGAGTA CAATCAAGGC CCTATCTCGT TCAGTGCAAC GTTTTATGAC 1740  
 AATCAACTTC GCAATCTGAT CTCTTTTATG GATATACGA UCTCACCGGA GCACGAAGCT 1800  
 CAGGGAATCA AGAAAACCA GCAGTATGCC AACATAGAA AAGCTCCGAG CCGCGGCTT 1860  
 GATGTCTCAT GTGATGCCTC TATCGGTTGG GGTATCAAGT TAGGAGCCGG ATACAGCCTC 1920  
 GTGGAAGCTA AGAATCTCCA GACGATGAG TGGCTGGAAG GAGCTGCACG TCATCGTGCC 1980  
 AATGTGCACG CCGATTGGGT TCACTACTGG GTTCAGTATA GACTTGCGCT GAGCCTTTTC 2040  
 GGCCTATTTC AGAGCGAGCG TTAATAACAA GACGGCAATG CTCGGGACTA TACCTTGTGG 2100  
 UGACTGCCCA CATCGCATCG TTTGCTCAT TTCCGCCACA TCATCTGGA TGAACGCTC 2160  
 30 GGTATAGACA ACCTGTTTGA CTAGTGGAT GATCGTCTA TGGGTGTCAA TTATGCTACC 2220  
 GTAACGCCGG GACGTACTTT CTTTGCTCAA ATAGCGATTG GATTCAACAA C 2271

## (2) INFORMATION FOR SEQ ID NO:156

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGACGGACA ACAACAACG TAATATCGTA TTCCCGCGT TTCTCCTCT GCTGGGAGTC 60  
 ATCGCAGTGG TGACGATCGT TGGTTTTTC ATGCTCAGAC CGGCCGAGGA GATTATCCAA 120  
 GGACAGATAG AAGTGACCGA ATACGAGTG TCCAGCAAAG TGCCCGGGCG CATCAAGGAA 180  
 CTTAGGGTAT CCGAGGGACA GCAGGTGCAG GCCGGCGATA CCTCGCTGT CATCGAAGCC 240  
 CCCGACGTAG CGGCTAAGAT GGAGCAGGCA AAGGCTGCCG AAGCAGCTGC ACAGGCTCAG 300  
 AACGCCAAGG CTCTCAAAGG AGCAGCAGC GAACAGATAC AGGCAGCCTA TGAGATGTGG 360  
 CAGAAAGCTC AGGCCGGCGT AGCCATAGCG ACCAAGACAC ACCAGCGGCT GCAGAACCTC 420  
 TATGACCAGG GAGTGGTACC GGCTCAGAAG TTGGACGAAG CCACTGCCCA GCGGATGCG 480  
 65 GCCATCGCTA CGCAAAAAGC GGCCGAAGCT CAGTACAATA TGGCTCGCAA CGGTGCCGAA 540  
 CGGAAAGACA AGCTGGCAGC TTCTGCCCTC GTCGATAGAG CGAGAGGAGC CGTCGCGAG 600  
 GTGGAGTCGT ACATCAACGA AACCTACCTC ATCGCCCGAC GGGCAGGCGA AGTGTGCGAG 660  
 ATATTCCCCA AAGCCGCGCA ACTCGTAGGT ACCGGGCGAC CTATCATGAA TATCGCCGAG 720  
 ATGGGCGATA TGTGGGCGAG CTTTGCCGTT CGTGAGGATT TCCTCAGCAG CATGACCATG 780  
 70 GGAGCCGTTT TGGAGACTGT GGTGCCGGCT CTGAATGAAG AAAAAGTACG CTTCAAGATC 840  
 ACATTATCA AGAACATGGG TACCTATGCT GCCTGGAAG CGACCAAGAC AACAGGGCAG 900  
 TACGACCTGA AGACCTTCGA GGTAAAGGCC ACCCTTGCGG ATAAAGACAA GGCACAAAAG 960  
 CTACGCCCGG GTATGTCGT GATCATACGC AAG 993

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## (2) INFORMATION FOR SEQ ID NO:157

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...801

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

25 ATGCGTATTG TCAGTAATTT TTTGTTTCGTC TCTTTTTCGG TTTTGCTTTT TGCATCATGC 60  
 CGTTCCCGAGC GAGAAAAGGT CGTTTACCTG CAAGATATCC AAACCTTTAA TCGGGAGATT 120  
 ATCGCTAAAC CATATGACGT AAAAATTGAG AAGGACGATG TGCTGAACAT CCTTGTGAGC 180  
 AGTAGAGACC CGGAGCTTTC AACGCCCTAC AACCAAGTGT TGACCACTCG TGGACTGGCC 240  
 CGCAACGGCT ATGGAACGAA CTCGAACGAA GGCTTCCTGG TCGATTGAA AGGGTACATC 300  
 AATTATCCTA TTTTAGGCCA GATCTATGTA GAGGGCCTTA CTCGTACCGA ACTGGAGAAG 360  
 30 GAGATACAGA AGAGGATTAT TTCCAGTGGG TTTATCAAGG ATCCTAGGGT AACGGTGCAG 420  
 CTTCAAAATT TCAAGGTGTC GGTTTTGGGA GAGGTGAATC ATCCGGGTTC GATGTGCGTA 480  
 AAAGGAGAGC GAATAACTCT TTTGGAAGCG ATCGGAATGG CCGGAGACCT GACAATCTAT 540  
 GGTGCGCCCG ATCGGGTTT TGTGATTAGA GAAACCGATG GGCATCGCGA GGTTTTCCAG 600  
 ACGGATCTCA GAAAGGCCGA CTTGCTCGCA AGCCCGGTGT ACTATCTGCA TCAGAACGAC 660  
 35 GTCATCTATG TGGAGCCGAA CGACAAGAAA ACACAGATGA GCGAGATCAA CCAGAATAAT 720  
 AACGTAAACG TATGGCTGAG TGTACCTCC ACTTTGGTAT CCATTTCAC GCTGACGATT 780  
 ACGATAATAG ATAAGACCAA A

## 40 (2) INFORMATION FOR SEQ ID NO:158

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1707

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

65 ATGAAAAAGA CCAATCTGTT TTTATCTCTG CTGGTGATCT TTATCACCAG TAGTTTTATG 60  
 ACTGCCCTGT CACAGAAGTC CAAGACGAAC AAACCTACCG AAGAAGATCG GAGCCGCAAT 120  
 GAGTATGTAC AGTCGATGGA TGTGCTTAGC AATATTATCG GTAACGTCAG GCTGTATTTT 180  
 STCGATACCA TAAGTATCAA ACATATGACT CGGCGTGGTA TAGATGCGAT GTTGGGCGGG 240  
 CTTGACCCCT ATACCGAATA CATTCTTAC GAGGAAATGG ATGAAGTAA ATTGATGACT 300  
 ACGGGAGAGT ATGCCGAGT CGGAGCTATC ATATCGCAGC GCCCGGATAG TGCTGTGATT 360  
 70 ATCCGAGAGC CTATGGAAGG TATGCCCGCA GACGAAGCAG GATTGATAGC AGGCGACCGC 420  
 ATCCTGACTA TCGATGGGAA AGACTTCCGC AAATCCACCA CACCGAAAGT AAGCCAAAGCA 480  
 CTGAAAGGGA TAGCCGGTAC TGTTCGAAG GTGACAGTAA TGGCTATGG CGAAACCAAA 540  
 CCTCGTACTT TTTCGGTAA ACGTCAAAA GTGATTATGA ATTCCGTAC TTACAGCGGA 600  
 ATGCTCGATG GCTCGATAGG ATATATCCGC TTGAACAAC TTACGGACAA AAGTGCAGAA 660  
 75 GAGGTGCGCA CGGCCTTGTG GGATCTCGT GACAAACAAG GAGCGAAAGG TCTCATTTTG 720  
 GATTTAAGAG GCAATGGTGG CGGACTGATG CAGGCTGCTA TCGAGATAGT CAATCTGTTT 780

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5 GTCCCTAAGG GCAAAGAGGT GGTAAACGACC AAAGGTGCGA TTGCAGATC GGCCTCCGTA 840  
 TTTCCGACAT TGAAGTGAAC GATGACACGC AAATCCCGA TAGTAGTCCT GATCGATGGA 900  
 CAATGGGAT CTCTCTCGGA GATTGTAGCC GGAGCACTGC AGGATATGGA CAGGGCTGTA 960  
 CTGATGGGAC AAAAGAGCTA TGGCAAAGGG CTGTACAAA CGACTCGTCA GCTACCATAC 1020  
 AACCGCGTGA TCAAATTGAC TAGCGCCAAG TACTACATCC CAAGCGGACG TTGTATTGAG 1080  
 CGTTTGGACT ACAGCGGCAC CAATCGGACA GGTATGGCAA CGGCCATTCC TGACAGTCTG 1140  
 CACAAATCT TTTACACTGC TGCCGGAAGA CGTGTAGAAG ATGCAGAGAG AATCCTGCCT 1200  
 GACATCGAGG TCAACACAGA TACAGTGCCT ACATTACTTT ATTATATGGC CATCAATAAT 1260  
 GACGTTTTCC ATTTCTGCAC AGGTTATGTC CTCAAGCATA AAACGATTCC CAAGCCGGAG 1320  
 10 GATTTTTCCA TAACGAACGA GGACTATGCA GCTTTCTGCA AGATGATGGA AGAAAGAAA 1380  
 TTTGACTATG ATGCCAGAG TGGCAAGATG CTTGACAAAC TGAGAGGAAT GGCTAAGATA 1440  
 GAAGGCTACC TGCCGGAGAG CAATCGGAG CTTAAGACAC TACGCGAATA GCTAAACCC 1500  
 AACCTGCTGC GTGATCTGCT ACGATTCAAA AAGGAGATAA CAAACTATCT CAACATGAG 1560  
 15 ATTGTCCTC GCTATTATTA TGAGCGAGGC AGTATCCGCC AGAGTTTGCC GGAAGATAAG 1620  
 GTAGTCAAGG AAGCTATTAA GCTGCTGAAG GACCATCCGG AACAAATTCG ACAGATCCTT 1680  
 GCAGCTCCGA AAGCAGAGAA TAAAGGG 1707

## (2) INFORMATION FOR SEQ ID NO:159

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2943 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

45 ATGCAAAACA AAGGATTGT GATTGTTATC ACATGGGCTC TGGCCATCAT CTGTGGSTTT 60  
 TACCTGTCAT TCTCTTTCGT TACGAACCGT TACGAAAAGA AGGCTAAGGC GATGGGCCAT 120  
 GTTCCCGGAA TGGCCTATCT TGATTCCATG TCGAATGAGA AGGTCTGGTT CGGCTACACG 180  
 CTGAAGAAG CTCAAGCCCA GCAAAATGGT CTGGCCCTTG ACTTAAAGGG GGGTATGAAC 240  
 GTTATCTTGA AACTTAACGC AAGCGATCTG CTTCGTAACC TCTCTAACAA AAGTTTGAT 300  
 CCCAATCTCA ACAAGCTCT GGAGATGCTT GCCAAGACA CGGAGCAATC CGACTTCATC 360  
 GATATTTTCG TGAAGGAATA TCGCAAGCTC GATCCCAAG GTGCTTGGC GGTATCTTC 420  
 GGTTCGGGTG ACCTTCGCGA CCAGATTACC GCAAGTCTA CGGATGCAGA CGTAGTGGT 480  
 50 CTGCTCAAAG AAAAATATAA TAGTGTGTA GAAGCTTCT TCAATGTGCT CCGTGTCTGT 540  
 ATCGATGCTT TCGGTGTGTT TGACCTAAT TTGCAGCAT TGGAGGGCA AGGGCTATC 600  
 CTGTGCGAAC TCCCGGAGT GAAAGACCTT GAGCCTGTTT GTACCTTTT GCAACCGAGT 660  
 GCCAACCTAC AGTTCTGGCG TACATACAAA TTGGAAGAGG TCAGCGGAGA CTTGATCGCT 720  
 55 GCCAATGATC GTCTGAGCGA ATTGGCTATG AACAAACGCG ATGCTACCCC GGAACAGAG 780  
 CCTGCAACTA CTGACTCTGT AGCTGCATCA GCGGATTCTG CTGCTGTACA AGCTGTAGCT 840  
 GATTCTGCTA CTGTAGCACA AAAAGAGGCC AAGGATGCTA CTGCTAAGAA CGCACTCTTC 900  
 TCTCTGCTTA CTCCCGTGAA TCGTGGCGGT GCAAGTAGTG GTGTGGCTCG TCGTGTAAAT 960  
 ATGCTCAGA TATCTGAAAT GCTCCAGCAA GCTCAGATC TGAAGGTTAC ACGTGAAGAT 1020  
 60 GTGCTTTTCC TCTGGGGTGC TAAAGCAATC GAAGACCCCG AAACCAAAA GGAGACCGAC 1080  
 CTCTACGAAC TCTATGCTAT TCGTACCAAT CGTACGGGAG ATCCTGATTT GGGAGGTGAT 1140  
 GTAGTGACTT CCGCCAAGAG TGATATCCAA AATGACTTCG GTGCTTCCGA ACCGATCGTT 1200  
 TCGATGACGA TGAATGAAGA AGGTGCTGTT AAATGGGCGC GTATCAAAA GGATAACGTG 1260  
 GGACGGGCAA TCGCTATCGT TTTGGATGGT GTGGTTTATT CTGCTCGMA COTGAATGAT 1320  
 65 GAGATCAGGG GCGGTGCTCT TCAGATCTCC GGGCACTTCA CCGTGGAGGA GCGCGGTGAC 1380  
 CTTGCCAAG TACTCACTC CGGTAAATG GATGCTACGG TAAGCATCGA ACAGGAATAC 1440  
 GTGATTGGTC CTACGCTGGT TSCCGAGTCC ATTAAAGCAG GATTCTGTG GTTCTGTCTC 1500  
 GCTTTGGTTA TCTGTATGTG TTACATGTGT CTGGCTTAAG GTTCTTGGC GGTCTTATC 1560  
 GCAACGGGCG CATTGATTGT AAACAGCTTC TTCACATTGG GCGTATTGGC TTCTTTCCAT 1620  
 70 GCGGTGCTGA CCTCTCGGG TATCGCAGGT TTGGTCTGA CGCTGGGTAT GGCTGTGGAT 1680  
 GCCAAGCTAC TTATCTTGA GCGTATCAA GAAGAGCTTC GTGCGGTAA GACTCCGATT 1740  
 CGTGCCGTTA CGGATGTTA TGGCAACGCT TTCTCTGCCA TCTTCGACTC GAACTTACG 1800  
 ACTATTATTA CCGGTATCAT CCTATTCTC TACGGGACGG GGCCGATTCC CGGTTTGGC 1860  
 ACTAGTTGA TTATCGGTCT TATCGCTTCT TTCATTACGG CTGTCTTCT GACTCGTATC 1920  
 75 GTCTTCGAA AACTGGCGAA AAAAGGTCGT TTGGATAAGA TTACATTAC TACGAGCAT 1980  
 ACTCGCAATC TCCTTGTCAA TCCTCATAC ATCATCTGG GTAAGCGCAA GACCGGCTT 2040

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5 ATCATTCGGG TGATTATCAT CGTTTGGGA CTTATAGCTT CATTACAAAT CGGTCTCAAT 2100  
 AGGGGTATTG AATTCTCCGG AGGACGTAAC TACGTAGTTA AATTGACCA GCCTGTATCT 2160  
 TCCGAAGCCG TCCGTTCCGG CTGTCTTCT CCCCTGCAGG AAAAGGTATT GGTACCTCC 2220  
 ATCGTACTG AAGGGACAGA GGTGCGTATA TCTACGAACT ATAAGATCCA GGAGGAAAGC 2280  
 GAAGAACTG AAGCAGAGAT TACTGACAAA TTGTATCAGA GCCTGAAAGG TTTCTACACC 2340  
 CAGCAGCCTA CTGCTGATCA GTTCTTGAC AATATCATT GCTCTCAGAA AGTAAGTCCC 2400  
 AGTATGTGCA GTGACATCAC GAGAGGTGCT ATTTGGGCTG TGCTGTTATC GATGATCTTC 2460  
 ATGGCCATT ATATTCTGAT TCGCTTCCGT GACATTTCTT TCTCTGCCGG GGTATTCTGA 2520  
 10 TCTGTGGCCG CTACTACATT CTGCATTATT GCTCTGTATG CGTTGCTGTG GAAGATTCTG 2580  
 CCCTTCACCA TGGAGATCGA TCAGAACTTC ATCGCTGCTA TTCTGGCTAT CATCGGTTAC 2640  
 TCGCTCAATG ACACCGTGGT TGTATTGAC CGTATCCGAG AGACGATGAA ATTGTACCCC 2700  
 AACAGAGATC GCTATCAGGT GATCAACGAT GCCCTTAATT CAACATTGGG TCGAACATTA 2760  
 AATACGTCTT TCACTACGTT TATCGTTATG TTGGTAATCT TCATCTTTGG AGGTGCTACG 2820  
 15 ATGCGTAGTT TCACGTTCTC GATCTGCTC GGTATCGTTA TCGGTACATA CTCTACGCTC 2880  
 TTTGTGCTA CACCCCTTGC CTACGAGATC CAAAAGCGCA AGCTCAACAA AGCAGCTAAG 2940  
 AAA 2943

## (2) INFORMATION FOR SEQ ID NO:160

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3051 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: FORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...3051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGAAAGAA TGACGCTATT CTTCTTTGCG TTGCTGACGA GCATTGGGTG GGCTATGGCC 60  
 CAGAAATAGAA CCGTGAAAGG TACAGTTATC TCCTCCGAGG ATAATGAGCC CCTGATCGGC 120  
 45 GCGAATGTCG TGGTTGTCCG AAACACCACT ATCGGTGCTG CAACCGACTT GGATGGCAAC 180  
 TTCACGCTTA GCGTGCCATG CAATGCCAAA ATGTTGAGAG TGCTCTATTC CGGTATGACT 240  
 ACCAAAGAGG TCGCCATCGC TAATGTGATG AAGATCGTAC TGGATCCGGA CTCTAAGGTT 300  
 CTGGAGCAGG TAGTTGTATT GGGTTACGGT ACGGGACAGA AACTCAGCAC TGTTCGGGT 360  
 TCTGTGGCCA AAGTGTCCAG CGAAAAGCTC GCGGAAAAGC CCGTTGCCAA TATCATGGAT 420  
 50 GCCCTCCAAG CTCAGGTAGC CGGTATGCAG GTTATGACTA CATCCGGTGA CCTACTGCC 480  
 GTCGTTCTG TGGAGATCCA TGGTACAGGG TCGTTGGGGG CAAGCTCTGC ACCATTGTAT 540  
 ATCGTGGATG GTATGCAAAAC TTCTTTGGAT GTTGTGGCTA CGATGAATCC GAATGATTTT 600  
 GAATCTATGT CCGTTTGAAG AGATGCTTCT GCAACATCTA TTTATGGAGC TCGTGCTGCA 660  
 AACGGAGTCG TTTTCATTCA AACGAAGAAA GGTAATATGA GCGAGAGAGG TCGTATTACC 720  
 55 TTTAATGCCA GTTACGGGAT TTCTCAATC CTGAATACTA AGCCCCCTGA TAATATGATG 780  
 ACTGGAGATG AATTGCTGGA TTTTCAGGTG AAGGCAGGTT TTTGGGGGAA CAATCAAAAC 840  
 GTTCAGAAAG TTAAGATAT GATCCTTGCC GGAGCTGAAG ATTTGTATGG CAATTATGAT 900  
 TCTTTGAAAG ATGAGTATGG TAAGACATTG TTCCCACTGG ATTTTAATCA TGATGAGAC 960  
 TGGCTCAAGG CTTTGTAA AACAGCACC ACCAGTCAAG GTGATATTTC TTTCTCGGA 1020  
 60 GGGTCTCAGG GAACCTCATA TTATGCCTCT ATAGGCTACT TCGATCAGGA AGGTATGGCT 1080  
 CGTGAACCGG CAAATTTTAA GCGCTATAGT GGCCGGCTCA ACTTCGAAAG TCGTATCAAT 1140  
 GAATGGCTGA AAGTTGGTGC AAATTGTCT GGTGCGATAG CGAATAGACG ATCTGCGGAC 1200  
 TATTTTGGAAG AGTATTATAT GGGGTCAAGT ACTTCCGCTG TGTTAACGAT GCCTCGTTAT 1260  
 TATAACCCCT TTGATGTGAA TGGGGATTTA GCAGATGTCT ATTACATGTA TGGAGCTACC 1320  
 65 AGACCTTCTA TGACAGAACC GTACTTCGCA AAAATGAGAC CGTTCAGTTC CGAATCACAT 1380  
 CAGGCCAATG TAAATGGTTT CGCCAGATT ACTCCGATCA AAGGCCTTAC TTTAAAGGCA 1440  
 CAGGCTGGTG TTGATATTAC TAATACTGCG ACTTCTTCTA AGAGAATGCC CAATAATCCG 1500  
 TATGATTCTA CTCCTCTTGG GGAAGAAGA GAAAGAGCTT ATCGAGATGT TAGCAAGTCT 1560  
 TTTACAAATA CCGCTGAATA TAAGTTTCTA ATTGATGAAA AACATGATCT TACAGCATTG 1620  
 70 ATGGGGCATG AATATATTGA ATATGAAGGG GATGTTATTG GGGCATCTTC TAAAGGATTT 1680  
 GAAAGTGATA AGTTGATGTT ACTGAGCCAG GGAAGAACCG GAAATAGTTT GTCTTTCCT 1740  
 GAACACAGAG TCGCTGAATA TGCCTATTG TCTTTCTTAA TCGGTTTAA TTACGGTTT 1800  
 GACAAATGGA TGTATATAGA TTTCTCTGTT CGTAATGACC AATCCTCTCG ATTCGGATCC 1860  
 AATAATAGAA GCGGTGGTT CTATTCTGTC GGTGGAATGT TTGACATATA TAATAAATTC 1920  
 75 ATTCAGAAA STAATTGGCT CAGTGATCTT CGACTGAAAA TGAGTTATGG TACAACGGGT 1980  
 AACTCGGAGA TTGTAATTA CAACACCAAA GCATCTGTTA CTGTGAACAA TTATCTGAA 2040



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5 GATGCTATGG GGCTTAGCAT TTCTACAGCA GGCAATCCCG ACCTCTCGTG GGAAAAGCAG 2100  
 TCTCAGTTCA ACTTCGGTTT GGCTGCAGGG GCTTTCATA ATCCGTTATC TGCAGAGGTA 2160  
 GATTTCATAT TCCGCACTAC GAATGATATG TTGATTGATG TCCCGATGCC TTATATCAGT 2220  
 GGTTTCTTCT CACAGTATCA GAATGTAGGC TCTATGAAAA ATACGGGTGT AGACCTTTCT 2280  
 CTTAAGGGGA CGATCTACCA AAATAAGGAC TCGAATGTAT ATGCTTCTGC GAATTTCAAC 2340  
 TACAATAGAC AGGAAATAAC AAAGCTTTTC TTCGGTCTCA ATAAGTACAT GTTGCTTAAT 2400  
 ACCGGTACTA TATGGGAAAT TGGGTACCCC AATTGCTTCT ATATGGCTGA ATATGCTGGA 2460  
 ATCGACAAAA AAACCGGTAA GCAGTTGTGG TATGTTCTCG GTCAAGTCA TCGGGATGGT 2520  
 AATAAAGTTA CAACAAGCCA GTACTCAGCT GACTTGGAGA CAAGAATTGA TAAGTCTGTT 2580  
 10 ACTCCTCCTA TTACAGGTGG TTTCTCCTTA GGTGCTTCTT GGAAAGGACT TTCTTTAGAT 2640  
 GCTGATTTCG CCTACATCGT TGGTAAATGG ATGATCAATA ATGACCGTTA CTTTACAGAG 2700  
 AATGCAGGTG GATTGATGCA ATTAATAAAA GATAAAATGC TATTGAATGC CTGGACAGAG 2760  
 GATAATAAAG AAACAGATGT TCCAAATTTG GGACAGTCTC CTCAGTTTGA TACGCATTGG 2820  
 TTGGAGAAATG CTTCTTTCTT GCGTTTGAAG AATCTCAAAC TCACCTATGT ACTCCCAAT 2880  
 15 AGTCTTTTGG CTGGGCAGAA TGTGATTGGT GGAGCTCGTG TCTATTGAT GGCAGCGCAAT 2940  
 CTGTTAAGTG TTACGAAGTA TAAAGGCTTT GACCTGAAG CAGGGGGGAA TGTGGGAAAA 3000  
 AATCAATATC CTAATTCTAA GCAGTACGTT GCGGGTATTC AGTTGTCTTT C 3051

20 (2) INFORMATION FOR SEQ ID NO:161

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3042 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...3042

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

ATGACGCTAT TCTTCCTTGG CTTGCTGACG AGCATTGCGT GGGCTATGGC CCAGAATAGA 60  
 ACCGTAAGAG GTACAGTTAT CTCCTCCGAG GATAATGAGC CCCTGATCGG CGCGAATGTC 120  
 45 GTGGTTGTTCG GAAACACCAC TATCGGTGCT GCAACCGACT TGGATGGCAA CTTACGCTT 180  
 AGCGTGCCTG CCAATGCCAA AATGTTGAGA GTGTCCTATT CCGGTATGAC TACCAAAGAG 240  
 GTCGCCATCG CTAATGTGAT GAAGATCGTA CTGGATCCGG ACTCTAAGGT TCTGGAGCAG 300  
 GTAGTTGTAT TGGGTTACGG TACGGGACAG AAACCTCAGCA CTGTTCCGGT TTCTGTGGCC 360  
 AAAGTGTCCA CGGAAAAGCT CGCGGAAAAG CCCGTTGCCA ATATCATGGA TGCCCTCCAA 420  
 50 GGTCAAGTAG CCGGTATGCA GGTATGACT ACATCCGGTG ACCCTACTGC CGTCCGTTCT 480  
 GTGGAGATCC ATGGTACAGG GTCGTTGGGG GCAAGCTCTG CACCATTGTA TATCGTGGAT 540  
 GGTATGCAAA CTTCTTTGGA TGTGTGGGCT ACGATGAATC CGAATGATT TGAATCTATG 600  
 TCCGTTTGA AAGATGCTTC TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC 660  
 GTTTTCATTC AAACGAAGAA AGGTAAATG AGCGAGAGAG GTCGTATTAC CTTTATGCC 720  
 55 AGTTACGGGA TTTCTCAAAT CCTGAATACT AAGCCCCTTG ATAATATGAT GACTGGAGAT 780  
 GAATTGCTGG ATTTTCAGGT GAAGGCAGGT TTTTGGGGGA ACAATCAAAC CGTTCAGAAG 840  
 GTTAAGATA TGATCCTTGC CCGAGCTGAA GATTTGTATG GCAATTATGA TTCTTTGAAA 900  
 GATGAGTATG GTAAGACATT GTTCCAGTGC GATTTTAATC ATGATGCAGA CTGGCTCAAG 960  
 GCTTTGTTTA AAACAGCACC CACCAGTCAA GGTGATATTT CTTTCTCCGG AGGGTCTCAG 1020  
 60 GGAACCTCAT ATTATGCCCT TATAGGCTAC TTAGATCAGG AAGGTATGGC TCGTGAACCG 1080  
 GCAAAATTTA AGCGCTATAG TGGCOGGCTC AACTTCGAAA GTCGTATCAA TGAATGGCTG 1140  
 AAAGTTGGTG CAAATTGTC TGGTGCGATA GCGAATAGAC GATCTGCCGA CTATTTTGGGA 1200  
 AAGTATTATA TGGGGTCAGG TACTTTCGGT GTGTTAACGA TGCTCTGTTA TTATAACCT 1260  
 TTTGATGTGA ATGGGGATTT AGCAGATGTC TATTACATGT ATGGAGCTAC CAGACCTTCT 1320  
 65 ATGACAGAAC CGTACTTCGC AAAAAAGAGA CCGTTCAAGT CCGAATCACA TCAGGCCAAT 1380  
 GTAAATGGTT TCGCCAGAT TACTCCGATC AAAGGCCTTA CTTTAAAGGC ACAGGCTGGT 1440  
 GTTGATATTA CTAATACTCG CACTTCTTCT AAGAGAATGC CCAATAATCC GTATGATTCT 1500  
 ACTCCTCTTG GGGAAAGAAG AGAAAGAGCT TATCGAGATG TTAGCAAGTC TTTTACAAAT 1560  
 ACCGGTGAAT ATAAGTTTTC AATTGATGAA AAACATGATC TTACAGCAT GATGGGGCAT 1620  
 70 GAATATATTG AATATGAAGG GGATGTTATT GGGGCATCTT CTAAGGATT TGAAGTGAT 1680  
 AAGTTGATGT TACTGAGCCA GGGAAAAACC GGAATAGATT TGTCTTTGCC TGAACACAGA 1740  
 GTCGCTGAAT ATGCCTATTT GTCTTTCTTT AGTCGTTTTA ATTACGGTT TGAACAAATGG 1800  
 ATGTATATAG ATTTCTCTGT TCGTAATGAC CAATCCTCTC GATTCGGATC CAATAATAGA 1860  
 AGCGCGTGGT TCTATTCTGT CCGTGGAAAT TTTGACATAT ATAATAAAT CATTCAAGAA 1920  
 75 AGTAATTGGC TCAGTGATCT TCGACTGAAA ATCAGTTATG GTACAAACGG TAACTCGGAG 1980

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5 ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG 2040  
 GGGCTTAGCA TTTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC 2100  
 AACTTCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTTCTAT 2160  
 10 GTCCGCACTA CGAATGATAT GTTGATTGAT GTCCCGATGC CTTATATCAG TGGTTTCTTC 2220  
 TCACAGTATC AGAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAGGGG 2280  
 ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG GSAATTTCAA CTACAATAGA 2340  
 CAGGAAATAA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTTCCTTAA TACCGGTACT 2400  
 ATATGGGAAA TTGGGTACCC CAATTCGTTT TATATGGCTG AATATGCTGG AATCGACAAA 2460  
 15 AAAACCGGTA AGCAGTTGTG GTATGTTTCT GGTCAAGTCG ATGCGGATGG TAATAAAGTT 2520  
 ACAACAAGCC AGTACTCAGC TGACTTGGAG ACACGAATTG ATAAGTCTGT TACTCCTCCT 2580  
 ATTACAGTGG GTTTCTCCTT AGGTGCTTCT TGGAAAGGAC TTTCTTTAGA TGCTGATTTT 2640  
 GCCTACATCG TTGTTAAATG GATGATCAAT AATGACCGTT ACTTTACAGA CAATGCAGGT 2700  
 GGATTGATGC AATTAAATAA AGATAAATG CTATTGAATG CCTGGACAGA GGATAATAAA 2760  
 20 GAAACAGATG TTCCAAAATT GGGACAGTCT CCTCAGTTTG ATACGCATTI GTTGAGAAAT 2820  
 GCTTCTTTCC TGGCTTTGAA GAATCTCAAA CTCACCTATG TACTCCCCAA TAGTCTTTTT 2880  
 15 GCTGGCGACA ATGTGATTGG TGGAGCTCGT GTCTATTGTA TGGCGCGCAA TCTGTAACT 2940  
 GTTACGAAGT ATAAAGGCTT TGACCCTGAA GCAGGGGGGA ATGTGGGAAA AATCAATAT 3000  
 CCTAATTCTA AGCASTACGT TGGGGGTATT CAGTTGTCTT TC 3042

## (2) INFORMATION FOR SEQ ID NO:162

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2463

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:162

45 ATGAAGAAAA AGAATTTTTT GCTTCTTGCG ATTTTCGTTG CTTTGCTGAC TTTTCATCGGC 60  
 AGCATGCAGG CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCCCTAC 120  
 TTCTCAITTA AAGTGCCTGA TAGGGCCGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC 180  
 GACGAGTTTG ACCCGGTAAC CAATGAAGCC ATTGCCTATG CCAGCGAAGA GGAGTTCGAG 240  
 GCATTCTGCG GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT GCAGCGCGCT 300  
 50 GTCUAGATGT TCGACTACCG CTCAGGAGAA AAATACGAAT GGAATGCTTA CCCCACTAT 360  
 GAAGCCTATA TCAGCATGAT GGAAGAGTTC CAAACAAAGT ATCCATCACT TTGTACTACT 420  
 TCCGTCATTG GCAAGTCCGT AAAGGATCGT AAATCTGATG TTTGCAAGCT GACGTCCTCT 480  
 GCCAATACAG GGAAAAAGCC TCGCGTGCTC TATACTTCTA CGATGCACGG AGACGAAACG 540  
 ACCGGATATG TGGTACTGCT CCGACTCATA GACCATCTGC TGTGAACTA CGAATCCGAT 600  
 55 CCGAGGATTA AGAATCTTCT GGATAAAACG GAAGTATGGA TCTGCCCTTT GACCAATCCG 660  
 GACGGAGCAT ACAGAGCCGG AAACCACACC GTACAAGGAG CTACTCGCTA CAATGCCAAC 720  
 AATGTCGATT TGAACCGTAA CTTCAAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA 780  
 CCTTGGCAGC CGGAGGCAAC TGCAATCATG GATTGGGAAG GAAACACCTC TTTCTGTCTC 840  
 GGTGCCAATA TACATGGAGG AACAGAGGTG GTGAACATC CATGGGATAA TAAAAAAGAA 900  
 60 AGACATGCAG ACGATGAGTG GTACAACTG ATCACTCGCA ACTACGCAGC CGCTTGTCTC 960  
 AGTATTTCCG CCGCTACAT GACCTCGGAA ACCAATTCCG GAATCATCAA CGGTTGAGAC 1020  
 TGGTATGTAA TTGCGGGAAG TCGTCAGGAC AATGCAAAAT ATTTCCATCG TCTGCGAGAA 1080  
 ATTACCTTTG AAATCAGCAA CACGAAAGTT GTGCGGCGCT CTCAACTTCC AAAGTATTGG 1140  
 AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAT CCTTATACGG CATCCATGGT 1200  
 65 ACAGTGACTT CCGCTGCGAA CGGACAGCCT CTCAAATGCC AGATCTTGAT AGAAAAACCAT 1260  
 GACAAGCGCA ACTCCGATGT TTAATCCGAT GCTACCACAG GCTACTACGT ACGTCTTATC 1320  
 AAAGCCCGCA CTTATACGGT GAAATACAAA GCCGAGGGTT ATCCTGAGGC AACTCGTACC 1380  
 ATTACGATCA AGGACAAAGA AACCGTCATC ATGGACATTG CATTTGGGCA CTCGGTTCTT 1440  
 CTGCGGTGAC CCGATTTCAC AGCTTCTCCT ATGACCATCT CAGTAGGCGA AAGCGTCCAA 1500  
 70 TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GGACGTTTGA AGGCGGACAG 1560  
 CCGTCCATGA GTACAGAGCA GAATCCGCTC GTATCCTATA GTCATCCCGG TCAGTACGAC 1620  
 GTTACGCTCA AAGTGTGGAA TGCAAGTGGT TCCAACACGA TTACGAAAGA AAAATTCATC 1680  
 ACTGTCAATG CCGTTATGCC TGTAGCTGAA TTGTCGGGTA CCGCGACGGA AATAGAAAGAG 1740  
 GCGCAGACGG TATCTTTCCA AAACCAATCC ACCAATGCCA CCAACTACGT ATGGATATTC 1800  
 75 GATGSCGGCA CTCGCCCTAC CAGTGAAGAC GAAAAACCGA CTGTGCTTTA CAGCAAAGCC 1860  
 GGCCAATACG ATGTCACGCT CAAGGCGATC AGTGTCTCCG GTGAAACGGT GAAGACGAAA 1920

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5 GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTCGAAGGA 1980  
 ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACRAAT 2040  
 CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC 2100  
 CCGGTGGTCA CCTACAATGA AACAGGCAAG TACGATGTCC AGCTGACTGC CACCAACGAG 2160  
 GGCGGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC 2220  
 GAGGACATAG TGGCACAGAC GGGTATCGTC ATTGCTCCGC AAAACGGAAC GAAGCAGATC 2280  
 CTCATAGAA CCAACGCTGC TATCAAAGCG ATCGTTCTCT ATGACATCAA TGGACGGGTC 2340  
 GTACTCAAAA CTACTCCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CCGCCCCGAA 2400  
 10 GGAATCTACA CCATCAATAT CAAACCGGAA AAATCCGCTC GCACGGGAAA GATCCATATC 2460  
 GGG 2463

## (2) INFORMATION FOR SEQ ID NO:163

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...228
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

ATCGGACTGA TCAAGGCTTT TCTCGTGCAA CTCTTACTGC TCCCCATTTT CTTCTACAAG 60  
 CGGTTTATAT CGCCGCTTAC ACCGCCTTCA TGCCGGTTTA CCCCCTCATG TCGTCCTAT 120  
 GCCATCGAAG CCTTACGTAA ATATGGCCCG GGCAAAGGAC TATTGCTGAG CATCAAGCGT 180  
 40 ATTCTCCGCT GTCACCCCTG GGGTGAAGT GGCTATGACC CCGTTCCG 228

## (2) INFORMATION FOR SEQ ID NO:164

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

65 ATGGCATACG ACTTTACACA AACATTCCGC AACAGCCTGG AGTACAGCTA TCAGGAAGCA 60  
 ACCCGTCTCG GCGTCGTAGC CGTGACGCAA GATATGCTGG TACTCGGTAT CATTCGCGAC 120  
 GGAGACAATG GCGCATCGA CATCATGCGG CACTATGGGA TCAACTTGT ACGAATCAAA 180  
 CGGTTGATCG AGTTGGAAGC CATCGCCGAG AGTTTGCCTG CTTGCGCTGA GGGATCGCCC 240  
 ATCTTCAACC CTTCGGCTCG GGAGGCTATC GATGATGCCA CAGACATCTG TGCCGACATG 300  
 70 GAGGACGAGG CCGTCAGCCC GGTCCATCTG TTGCTGAGTA TCCTCAACTC GACACAGGAG 360  
 AGCTTAGTAC AAAAGATATT TATGAAACAA GGTATAAAAT ACGACACCAT CCGTCCGGAT 420  
 TACTTCGGAC AGCGCAACCC CTCGGAAGGG AAGTCTCCCT CCGAAATGGA GATCCTCGAC 480  
 GGGTACCAAG ACAACGACTT CGACGACGAA GAGGACGAAT CCTCTCCGCC TTCGGGAAT 540  
 AGCGGGACAG GCGGAGGCTC CGGCGACGCC CCCGAACAGA ATACCGGCGG AGGCGATATC 600  
 75 ACCACCACGA CACGGAGTGG AGGCGACACG CCTGCACTGG ACACCTTCGG CACCGACATC 660

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ACTGCCATGG CGGCAGCAGG CAAGCTCGAC CCGGTAGTGG GTCCGGAGCA GGAGATCGAA 720  
 AGGGTGATAC AGATACTCAG CCGGCGCAAA AAGAACAATC CGGTGCTCAT CGGCGAACC 780  
 GGTGTAGGCA AGAGTGCCAT CGTGGAAGGA CTGGCCGAAC GCATCGTGAA CAGGAAGGTG 840  
 AGCCGTATTG TTTTCGACAA GCGGATCATC AGCCTCGATT TGGCTCAGAT GGTAGCCGGC 900  
 5 ACCAATATATC GCGACAGTT CGAAGAGCGG TTGAAAGCCG TGCTCGATGA GCTGAAGAAG 960  
 AATCCGCAGA TCATCCTCTT CATCGACGAG ATACATACCA TCGTGGGAGC AGGCTCTGCA 1020  
 GCCGGATCGA TGGATACGGC CAATATGCTC AAACCCGCTC TTGCCCGTGG ACAGGTACAG 1080  
 TGCATCGGAG CCATACGCT GGATGAGTAT CGTAAGAACA TAGAAAAGGA CGGAGCACTC 1140  
 10 GAACGCGCTG TCCAGAAGGT GCCGATAGCC CCTCGACTG CAGAAGAAAC GCTGACCATC 1200  
 CTGCAAAACA TCAAAGAGAA ATACGAGGAC TATCAGGTG TACGCTATAC GGACGAAGCG 1260  
 ATCAAAGCGG CAGTGGAACT GACCGATCGC TATGTATCCG ATCGTTTCTT CCCAGATAAG 1320  
 GCGATAGATG CCATGGACGA GGCCGGCGCG AGCGTCCATA TCACCAATGT GGTGGCTCCG 1380  
 AAAGAAATCG AGATACTGGA GGCCGAATTG GCATCGGTGC GAGAGAACAA GCTCTCGGCC 1440  
 15 GTAAAGGCTC AGAATACGA ACTGGCTGCC TCCTTCGCGG ATCAGGAGCG GCGCACTCAG 1500  
 CAGCAGATAG CGGAAGAGAA GAAAAAATGG GAAGAGCAGA TGTCCAAGCA CCGCGAGACG 1560  
 GTGGACGAGA ATGTAGTGGC GCATGTAGTG GCGTTGATGA CAGGCGTTCC GGCTGAGCGG 1620  
 CTGAGCACGG GCGAAGGCGA ACGTCTGCGC ACGATGGCAG ATGATCTCAA GACCAAAGTA 1680  
 TTAGGTGAGG ACACAGCCAT CGAAAAGATG GTGATGCCA TCCAGCGCAA TCGTCTGGGA 1740  
 20 CTTGCGCAATG AAAAGAAACC GATCGGTTCT TTCTTTTTC TCGGCCCCAC GGGGGTAGGC 1800  
 AAGACCTATT TGGCCAGAA GCTCGCCGAA TACCTGTTCC AGGATGAGAA TGCCATGATC 1860  
 AGGTGGATA TGAGCGAGTA TATGGAGAAG TTCTCCGTTT CCGCTCTCGT GGGTGCCCTT 1920  
 CCGGGATATG TGGGCTATGA AGAAGGCGGC CAACTGACGG AGCGCGTAAG ACGCAAACCC 1980  
 TATTCCGTGG TTCTCTTGA TGAGATCGAA AAGGCGCATG CCGATGTCTT CAATCTGCTC 2040  
 25 TTACAGGTGA TGGACGAAGG TCAGCTGACC GACAGTCTGG GACGCGCGGT GAATTTCAAG 2100  
 AACACCGTGA TCATCTACAC CTCCAACGTG GGTACACGCC AGCTCAAAGA CTTCGGGCG 2160  
 GGTATCGGGT TCCGTTCGGA AAAAGACGAG GAAGCGAACA AGGAGCATAG CCGTTCGGTG 2220  
 ATCCAAAAG CTCTGAACAA GACGTTACG CCGGAATTTT TCAACCGTTT GGACGATATC 2280  
 ATCCTCTTGG ACCAACTGGG CAAGACGGAG ATTGCGCGGA TGGTGACAT AGAGCTTAAA 2340  
 30 GCCCTCTTGG CGCGCATCCA TCGTGCCGGA TACGACCTCG TCCTTACCGA TGAAGCCAAG 2400  
 GATGTGATAG CGACGAAGGG ATACGACCTC CATTACGGAG CACGACCGCT CAAGCGCACA 2460  
 CTCAGAAAG AAGTGGAGGA TCGCTCACG GATCTTATCC TCTCCGACA GATCGAGAAA 2520  
 GGCAGACGC TTACGCTCTC TGCTCGCAT GCGAGATCA TCGTACAAGA ACAAGCA 2577

- 35 (2) INFORMATION FOR SEQ ID NO:165  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 55 (B) LOCATION 1...1251  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAATTACC TGTACATACT GATTACACTT TTACTCTCCG GCTTTTTTTC CGGTGCTGAG 60  
 ATTGCTTTCC TTTCTTCGGA CAAACTGCGT CTGAGTTGG ACAGGAATAG AGGCGATCTC 120  
 ACAGGCGAGG CGTTAAACTT GCTGTATCGA CATCCGGACC AACTGGTGAC TACTCTCCTT 180  
 GTGGGTAATA ATATCGTTTT GGTAGTCTAT GGTCTGCTGA TGGCGGGATT GCTGGCGCA 240  
 CCTTTGGCGC AATGGATTGA TAACGATGCT ATGATCGTGG TTCTCCAATC TGTCTTATCC 300  
 ACTATCATCA TACTGTTTAC CGGGGAATTT CTACCCAAAG CCATTTTCAA GACCAATGCC 360  
 65 AATATGATGA TGAAGGTATT CGCCTCCCT ATCGTAGCGA TCTATTATCT GCTTTATCTT 420  
 CTGTCTAAAC TCTTACCGG TTTATCTCGC TCTTTTATTC GTCTGGTGGG CAAGAATTAT 480  
 GTGCCTACAA CAGTAGGGTT GGGGCGCGTA GATCTCGATC ATTATTTGGC AGAAAATATG 540  
 TCCGAGAGAA ACGAACAGAA CGACTTGACT ACCGAAGTGA AAATCATCCA GAATGCGCTG 600  
 GATTTTTCGG GTATTCAAGT GCGAGACTGC ATGATCCAC GCAATGAGAT GATAGCATGT 660  
 70 GAGTTGAAA CGGATATTGA AGTACTCAA ACGACTTTTA TCGATACCGG TTTGTCCAAG 720  
 ATCATTATCT ACAGACAGAA CATAGATGAC GTAGTAGGAT ATATCCATTG GAGCGAAATG 780  
 TTCTGTGGGC AAGACTGGCA AAAACGTATC AATACTACTG TATTGCTACC CGAAAGCATG 840  
 TATGCCAATA AACTGATGCG ACTACTCATG CAGCGCAAGA AAAGCATTGC GATCGTCATC 900  
 GATGAACITG GAGGTACGGC CGGAATGGTC ACATTAGAGG ATTTGGTAGA AGAGATTTTC 960  
 75 GGTGACATTG AAGACGAACA CGACACTCGC AAGATCATAG CCAACACGCT CGGCCCTCAT 1020  
 ACCTATCTGG TCAGTGGTCG TATGGAAATA GATGATGTA ACGAACGTTT TGGGTTGTCC 1080

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TTGCCTGAGT CTGACGACTA CCTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT 1140  
 ATCCCACAGG CCAATGAGGT CGTGGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT 1200  
 TCTTCCACCA AGATCGAACT GGTGAAAATG TCCATCGACG ACCAATCGAA C 1251

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## (2) INFORMATION FOR SEQ ID NO:166

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...879

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

30 ATGAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT 60  
 ATTATGCCAT TGAAGTAGC AGCTCAAGAG ATTATTCCTA ACGAAGAGGT GTTGGAAATCA 120  
 TTGACTTTTC TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG 180  
 CAGGAGATAG TCGCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACACG 240  
 GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA 300  
 GATGTTCTCG CCGGCGAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC 360  
 35 GACAAAGTAT GCGTGGACGT AGAGGTGAAG GACTTCAAAC CGGTTACCAA TCTCACOGGA 420  
 ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGGAAAGAGAA AGCTGAAGAG 480  
 CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT 540  
 ACAGCTGAAA CTCATTATGT GGAGACCGGT GTAGCCATATG GTACATACAT CTACGAAGTG 600  
 40 GAAGTAAAGT ATCCTGACGG TGTATCTCCG AAGGTGGCTG TAACCGTGAC CGTGACCAAC 660  
 AGCTCATTTGA GCAATGTAGA TGGACAGGCT CCTTACACAT TGGCAGTAGA AGGCAAGAAG 720  
 ATTATTGGGG AAGCCCATGG TATGATCAGG CTCTACGACA TCAACGGACG TACCGTGGCC 780  
 GTAGCCCGGA ATCGATTGGA ATACATGGCG CAACCCGGTT TCTATGCAAT GCGCTTCGAT 840  
 GTGGGGAATA AACACCATGT ATCGAAAATA CAAGTAAGA 879

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## (2) INFORMATION FOR SEQ ID NO:167

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 936 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...936

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

70 ATGATTCTCT TAAGCGAGAG TTTTGAATCA GGTATTCAG CTATATGGAA GACCAITGAC 60  
 GCAGATGCGG ATGGCTATAA TTGGATGCAT TTGACCAATT TCACGGGACA GAGTGGTCTC 120  
 TGTGTCTCTT CGGCTTCATA CATAGGCGGC GTCCGAGCTT TGACTCCGGA CAATTATCTG 180  
 ATAAACCCCG AATTAAAACT ACCACAGAC GCGTTGCTGG AAATAATCTA TTGGGTATGT 240  
 ACTCAAGATC TCACTGCTCC ATCGGAGCAC TATGCGGTTT ATTCCTCTTC TACAGGCAAT 300  
 AATGCTGCTG ACTTTGTTAA TCTCTTATAT GAAGAGACTT TGACTGCCAA ACGGATACAA 360  
 75 TCCCCCGAGT TGATCCGCGG AAATCGGACA CAAGGTGTTT GGTATCAAAG AAAGGTGGTA 420

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5 CTCCCTAACG ATACTAAATA TGTGCTTTC CGCCATTTTA ATTCCACGGA TAATTCTGG 480  
 CTCAATTTGG ATGAAGTATC TATCCTGTAT ACCCCTCTTC CCCGAAGAGC TCCGTGTCCG 540  
 CATCCGGGTG GTTACACTTA TTCTGTATTC CGTGATGGAC AAAAGATAGC GAGTGGATTG 600  
 TCGGCATTGG CATATATCGA TACGGATGTA CCGTATGGGA CTCAGAGCTA TTGTGTCCAA 660  
 GTCAATTATC TGCAAGGAGA CTCGTATATA GTCTGCAAAA ATATAGTGGT GGCAAAATTCT 720  
 GCAAACATCT ATGGGGCGGA TAAGCCTTTT GCGTTGACCG TGGTTGGCAA GACCATTGTA 780  
 GCGAGTGCCT TCAAAGGAGA GATCACTCTT TATGACATTC GTGGCCGGCT GATAGCTTCC 840  
 GGCTGCGATA CGCTTAGGTA CAAAGCGGAA AATGGTITTT ACCTCATTAA AATACAGGTA 900  
 10 AACGGAACCTG TCTACTGTA GAAATCCAA ATCCAA 936

## (2) INFORMATION FOR SEQ ID NO:168

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2529 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2529

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

35 ATGAAAAA GTTTCTTT AGCCATAGTA ATGCTCTTG GCATTGCCAT GCAGGGACAT 60  
 TCTGCTCCGG TTACGAAAGA GCGAGCTTTG AGTCTGGCTC GGCTGGCTTT GCGACAGGTA 120  
 TCCTTGCGAA TGGGACAAAC AGCAGTATCT GACAAGATT CCATCGATTA CGTTTATCGG 180  
 CAAGGAGATG CTGAGAGGGG TATCACATCA CAAGAGGAAG GCTCTCCTGC ATATTTTAT 240  
 40 GTAGCTAATC GTGAAATAA TGAGGGCTAT GCTCTGTAG CAGCAGATGA CAGAATACCG 300  
 ACAATTTTAG CCTATTCACC CATTTGGCCGT TTCGACATGG ACAGTATGCC GGACAACTCT 360  
 CGCATGTGGC TACAAATTTA CGATCAGGAA ATAGGCCTGA TACTTTCCGG AAAAGCTCAG 420  
 CTCATGAAG AGATATTACG TACCGAGGGC GTACCGGCTG AAGTACATGC TCTGATGGAT 480  
 AACGGTCATT TTGCCAAGCA TCCCATGCGA TATACCGGCT GTGTTGCTAC TGCTGCAGCA 540  
 GAACCACTGC TTCCTAATGG CAATCATGCC TATACCGGCT GTGTTGCTAC TGCTGCAGCA 600  
 45 CAAATCATGC GCTACCATAG CTGGCCGCTT CAAGGTGAAG GCTCTTTCGA TTATCATGCA 660  
 GGTTCATTAG TTGGCAACTG GTCCGGCACA TTTGGTGAAA TGTACGACTG GATCAATATG 720  
 CCCGAAATC CCGACCTTGA TAATCTGACT CAATCTCAAG TGGATGCCTA CGCCACACTG 780  
 ATGGGTGATG TGAGTGCATC TGTTCGATG AGTTTTATG AAAATGGAAG TGGTACGTAC 840  
 50 AGCGTTTATG TAGTAGGAGC CTTCGGAAC AACTTTCCGT ACAAGCGTTC ACTGCAGCTA 900  
 CATGTACGCG CCTTATATAC CTCACAGGAG TGGCAGGATA TGATCCGCGG GGAACCTGCC 960  
 TCCGGAAGCC CGGTCTATTA TGCAGGGAAT AACCAGAGCA TAGGACATGC TTTCGTTTGC 1020  
 GATGGTTATG CTTCGGATGG TACTTTCCAT TTCVACTGGG GTTGGGGAGG TGTTCCAAC 1080  
 GGCTTCTACA AACTAACACT CCTCTGCGG ACTTCGTTGG GTATCGGAGG TGAGGGAATA 1140  
 55 GCGGTACAG ATGCCCTGCC GATCTTGCCA CTGAAAGACA TAGAAGCCGA GTATAAAAGT 1200  
 GAATCCGGAT TGAACGTAGG GTATTTCGATA TATAATACAG GTGAAGAGCA ATCAATCTT 1260  
 GACCTCGGAT ACAGATTGAA CAAGGCTGAC GGAGAAGTCA TAGAGGTGAA AACTTCATCT 1320  
 ATCAATATCT CTTGGTACCG ATACGGAGAG CATCCCGAGA GTTCTCATT GGCACCTAAT 1380  
 CAGTTGTAC CAGGAATCAA CACCATCACC CTACTTTATC GTCCGACAGG CACCGAACAG 1440  
 60 TGGGAGCGG TACGGCATGC ACAGGGAGGA TATGTCAATA GCATTAAAGT AAATACGACA 1500  
 GACCCGAACA ATGTGCTAGT CACGGTAGAT AATAACGAAG GCAAGCTCAG TATCGTCCCC 1560  
 AACAGCTTTG TCGCAGATCT GAATTCCTAT GAACATAGTA CGATTACAGT ACAGTTCAAT 1620  
 AGCGACAGCC CTGATGAGAT CCGTACACCC GTAGCCTTTG CTCTATCTAC AGGAGCTACT 1680  
 GCGGACGATG TAATATCTTT GGGCTGGGTA ATGGCTGAAG TTCCGGGGCGG TAGCAGCAAC 1740  
 65 TATCCGGTGG TTTGGTCTAA AGACGTTCTC ACTCTCTCGG AAGGCACTA TACATTGTGG 1800  
 TATAGATTTT CCATCAACAA CCAAAAGGAT GAATGGAATA AGATCGGAAG CGTGTCTAGT 1860  
 AAACACCGA CAGAGTATAC GCACCCCTTA TTCGAATGGG GCCATAATCA AACTCTACC 1920  
 TATACGCTGC ATATGGACA CAACAGAGTA TTGCCGACT TTACACTCAA AAATCTCGSA 1980  
 70 TTGCCTTTCA ATGGTGAGT GGTGTGTTT TTCCGCCAAA CACAATCCTC ATCGGGGTCT 2040  
 TTATGGGCGC CTCAGAAAC AGTACATATC AAGCAAGGAG AAATTTCTGT ATATAAACCT 2100  
 GTTGTGCAAG GCCCTATACC TGATGGATCC AAGCAAGGAG AAATTTCTGT ATATAAACCT 2160  
 GGACAACAAC AGTTGTACCT CAAGGGGAAA AGGAACCTACA CGGTGAAGAT CGTCAATGGT 2220  
 ACAGCGGTAG AAGCAATAGA ATCGTCAGAA GAGATCAGAG TATTCCTTAA TCCGGCACCG 2280  
 75 GATTATGTGG AAATATCGGC ACCTTGCATT CCCCAGAAA CATCTATCAT TCTTTTCGAT 2340  
 CTGTACGGCA AGATTGTCAT GAAGAATAGT TTATCAGCGG GGCATGGCAG AATGGATGTC 2400  
 2460

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AGCCGACTTC CTAATGGGGC CTACATCCTT AAGGTGGATG GATATACGAC GAAAATAAAT 2520  
 ATAGTGAC 2529

5 (2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 870 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC	TATTTCTCTC	GCTCAGGAGT	CTTGTAATGG	TCTTCGCTGT	TGCAAGTTGC	60
GATATAATCG	ACAAGGATCA	AACCTCTTGG	CCGGCTCCGA	CCAATGTGAC	ACCCGATAAT	120
CCGGATGACA	ATCCTTCGGA	GATCGACATT	ACGCAGACGC	ACACAGAAAA	ATATGTTTGG	180
GCTGAAGAAT	TTACCGGCCA	AAAATGTCTC	AACTGTCCGA	AAGGTCATCG	CAAACTGGCG	240
GCTCTCAAGG	AGCAATACGG	TAAGAGATTG	ACTGTTGTCG	GTATACATGC	CGGCCCTGGA	300
TCTCTCGTGC	CACCTCTTTT	CCGTACAGAA	GCCGGAGACG	CATATTATAG	CAAGTTCGCC	360
AATAATACCC	CTCTCCCTGC	GCTGATGGTT	TCGCGCAAAA	AGTTGGGCTC	TTCTACGTTT	420
TATGATAAGA	GCTACAAAAC	GTGGGACGTG	CCTATGCGCG	AGCAGATGGA	CCAAAAGGCG	480
AAGATCAATA	TCTTTGCCGT	GGCCGAATAC	ACCGATACCC	AAAAGATCAA	GGTGACTGTA	540
AAGGTAATAA	TACTGGAGGG	GAATACACTC	CCGAAGTCCA	TGGTTCAGGT	GTATCTGTTG	600
GAGGATAAGC	TGATCGCTCC	GCAGGTGGAT	GGCAATACGA	CAGTCGAGAA	TTACGAGCAC	660
AATCACGTGT	TGCGTGGAGC	CGTTAATGGT	ATTGGGGGCG	AAGAATTGTG	GAATCTCAAA	720
GATTATTGTG	ATACTTACGC	CGTTGAACCG	CTCTCGGGTA	TGTCCTTCGT	AGCCGAGAAT	780
TATTCGATTG	TGGCTTTTGT	ATACGATGTG	CAGACGTTGG	AAGTGTATGA	CGTTGTGCAT	840
GTAAGATCA	ATCCGCAATC	CGATGGCAAA				870

45 (2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 669 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT	CAAGTGTAGT	AGCCTCAGTT	TTGGCCGTGG	CTCTCGTGT	CGCCGGTTGC	60
GCACTGAACA	ATATGGCAAA	AGGCGGCCTT	ATCGGCGCCG	GAGTAGGAGG	TGCCATTGGT	120
GCCGGACTAG	GTAACGTAGC	CGGAAATACG	GCTGTCCGGT	CCATCGTCGG	TACTGCAGTC	180
GGTGGAGCAG	CCGGTGCTCT	CATCGGAAG	AAGATGGACA	AGCAGAAAAA	AGAACTGGAG	240
GCCCGAGTAC	CCGATGCTAC	GATTGAGACA	GTAAATGACG	GAGAGGCTAT	TCTGGTTACT	300
TTCGATAGCG	GTATCCTCTT	TGCGACGAAC	TCCAGCACTC	TGAGTCCCAA	CTCAGGCACT	360
GCGCTGACGA	AGTTTGCTGC	AAACATGAAC	AAAAACCCCG	ACAGGGATAT	TCGTATCGTA	420
GGCCATACCG	ACAATACCGG	CTCCGACAAG	ATCAACGATC	CTCTGTCTGA	GAGACGTGCA	480

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GCCAGCGTAT ATTCTTCTCT GAATTCTCAG GGTGTGAGTA TGTCGCGCAT GGCAGCCGAA 540  
 GGGCGTGGGA GCCATGAACC GGTTGCAGAC AATAGCACAG TTGCCGGACG TTCGGCCAAC 600  
 CGCCGTGTGG AGGTTTATAT CTTGCCGAAT GCCAAGATGA TCGAACAAAGC ACAGCAAGGT 660  
 ACGCTGAAG 669

## (2) INFORMATION FOR SEQ ID NO:171

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1011

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

ATGTCGAAAA AATCGATCCT TCTGCTTTCG TGTTGCGCTGT GCTTCATTTC TGCTACGAAG 60  
 GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA 120  
 CGTACAAAGC CCTCGGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCGGCTGGAG 180  
 TTCCGCAACA AGATTCTTC CGAAAAAGAG GTAAGAAAAG CCGAATATGA AAATCGGCTG 240  
 GCGATGGAAG CACTCAATTA CCCTGCCATA GATTATATG GTGAAGATTG TTGGAGCGAG 300  
 TATGTAAACC CTTTCGTGGG TGCAGGAACC GATGTCGAAA TTCCGAAGTC CTATGACATT 360  
 GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTTGGCTAC 420  
 CGTCGGCGTT TCGGACGGAT GCACTATCGT ATTGATCTTT CAGTGAATCG TGGCGATACG 480  
 ATACGAGCAG CTTTGCACGG GAAAGTTCGT GTACGCAGCT ATGAAGCCGG TGGCTATGGC 540  
 TACTACATAG TCTTGCGCCA TCCGAACCGA CTGGAGACTG TGTACGGACA CATGAGTCGC 600  
 CAATTGGTAG ACGAGAATCA GATCGTTTGA GCAGGACAAC CGATCGGATT AGGAGGCAGC 660  
 ACGGGTCGAA GCACCGGTCC TCATCTTCAC TTGAGAGCCC GCTTCATGGG TATTCCCATC 720  
 AATCCGAGTA CCATTATAGA CTTCGATAAC GGAGTCCCGC TCCGAGACAT TTACACATTC 780  
 AAACGAGGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTTCTTCTCG CTATGCAAAA 840  
 AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT 900  
 ACTTTGGAAA CAATAGCCAA AAGGCACGGC ACTTCTGTT AGAAACTCTG TGCTACCAAT 960  
 GGCATTGGCA AGAGTAAAT TTTGACTCCG GGCAAAGCCT TGAGGATCAA A 1011

## (2) INFORMATION FOR SEQ ID NO:172

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATG3CAAAA TCAATTCTA TGCTGAAGGC GTCAGCCTTC CTTCGGATCAG AAGACGGATC 60  
 GTCGGTAAGT GGATAGCCGA AGTATGCAGC GSATATGGGA AAGCGGTGGG AGAAATCTCC 120  
 TATCTTTTCT GTGATGACGA ATATATCTTG AAAGCCCAATC AGGAATTCTT CGATCATGAC 180  
 TACTACACCG ACATCATCAC CTTGATTCC TGCGAAGCGG ATACGGTGAA TGGCGACCTG 240



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5 CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC 300  
 GAACTGCATC GTGTCATTAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC 360  
 AAAAAGGATG AAGCCCAAAT GCGTGCAGCC GAAGAGAAAG CCCTTGTTCAT GCTGCGAGAA 420  
 ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA 453

## (2) INFORMATION FOR SEQ ID NO:173

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

30 ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA 60  
 CAGGAGAATA CTGTACCGGC AACGGGTGAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC 120  
 AATAAAGCAG GCAGCAATTG GTTTGTAAACA CTGCAAGGCG GTGTTGCAGC GCAGTTCCTC 180  
 AATGACAACA ACAACAAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTTCTGTC 240  
 GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAAA TTAACGGAGG TCAAGCCAC 300  
 35 ACTTTCCTCG GAAAAAATGG CGAACAGAA ATCAACACCA ATTTTGGTGC AGCTCACTTC 360  
 GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAATCG TTCTTCCAT 420  
 TTAATTCAT GGGTAGGTGT TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA 480  
 GACAATGTGG AATCACTGAC GCGCAATGTA GGAGTTATGA TGGCTTTCAG ATTAGGAAAG 540  
 CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA 600  
 40 TACAATGCCA AGAAAATCC CGTATTGAA GATCCGCGAG GACGTTATTA CAATGGATTTC 660  
 CAGGGGATGG CTACAGCAGG TCTTAATTTC CGCCTGGGAG CCGTAGGCTT CAATGCCATT 720  
 GAIICCAATGG ACTACGCACT TATCAATGAT CTGAATGGTC AGATTAAACG TTTGCCGAGC 780  
 AAGGTCGAAG AACTCTCAA ACGTCTCTGA TCATGCCCCG AATGTCTCTA AGTAACTCCT 840  
 GTTACTAAGA CAGAAATAT ACTGACGGAA AAAGCTGTAC TGTTCGTTT CGACAGCCAC 900  
 45 GTTGTGGACA AAGATCAAT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAACT 960  
 AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG 1020  
 AATTTGTCTG AGCGTCGGGC TAAAGCCGTT GTTGATGTTG TGACAGGTAA ATATGGTGTG 1080  
 CCTTCCGAAT TAATCTCTGT AGAATGGAAG GCGGACTCTA CGCAACCGTT CAGCAAGAAA 1140  
 50 GCTTGAATC GTGTTGTAAT CGTTCGCTCC AAG 1173

## (2) INFORMATION FOR SEQ ID NO:174

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1155

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

75 ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGGCGG TCTCGCATGC 60

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5 ACATTCAGTG CAACAGCCCA AGAAGCTACT ACACAGAACA AAGCAGGGAT GCACACCGCA 120  
 TTCCAACGTG ATAAGGCCTC CGATCATGG TTCATTGACA TTGCAGGTGG AGCAGGTATG 180  
 GCTCTCTCGG GATGGAATAA TGATGTAGAC TTGTAGATC GTCTAAGTAT CGTTCCTACT 240  
 TTGGGTATCG GTAAATGGCA TGAGCCTTAT TTGGGTACTC GTCTCCAAT CACAGGATTC 300  
 GACATCTATG GATTCCCGCA AGGGAGCAAG GAGCGTAACC ACAATTACTT TGGAAACGCC 360  
 CACCTTGACT TCAATGTTGA TCTGACGAAC TATTTGGTG TATACCGTCC CAATCGTGTC 420  
 TTCCATATCA TCCCATGGGC AGGTATAGGA TTTGGTTATA AATTCCATAG CGAAAACGCC 480  
 AATGGTGAAA AAGTAGGAAG TAAAGATGAT ATGACCGGAA CAGTTAATGT CGGTTTGATG 540  
 CTGAAATTCC GCCTATCAAG AGTCGTAGAC TTCAATATTG AAGGACAAGC TTTTGCCGGA 600  
 10 AAGATGAAC TATTCGGGAC AAAGAGAGGA AAAGCAGACT TCCCTGTAAT GGCTACAGCA 660  
 GGTCTAACGT TCAACCTTGG CAAGACAGAG TGGACAGAAA TTGTTCTTAT GGACTATGCT 720  
 TTGGTCAATG ACCTGAACAA CCAAATCAAC TCACTTCGCG GTCAAGTGGG AGAGTTGAGC 780  
 CGTCGTCTCG TTTCATGCCC TGAATGCCCT GAGCCTACAC AGCCTACAGT TACTCGTGTA 840  
 15 GTCGTTGACA ATGTGGTTTA CTTCGTATC AATAGTGCAA AGATTGATCG TAATCAAGAA 900  
 ATCAATGTTT ACAATACAGC TGAATATGCG AAGACCAACA ACGCACCGAT CAAGGTAGTA 960  
 GATTACGCTG ACGAAAAAAC CGGTACTGCG GCCTATAACA TGAAGCTTTC AGAGCGTCGT 1020  
 GCAAAAGCGG TAGCCAAGAT GCTTGAAAAG TATGGTGTTT CTGGCGATCG CATTACAATT 1080  
 GATGGAAGG GCTCATCAGA GCAATCTAT GAAGAGAAGC CTTGGAATCG TATTGTAGTA 1140  
 20 ATGACTGCAG CGGAA 1155

## (2) INFORMATION FOR SEQ ID NO:175

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 570 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

45 ATGGAATTTT TCATGTTATT CATAGCGGCG GTTTTCGTTA ATAACGTGCT GCTGTGCGCAG 60  
 TTCTGGGTA TATGCCCAT CTTAGGCGTA TCGAAGAAGG TAGACACCTC AATCGGTATG 120  
 GGTGCAGCCG TGACATTGCT ATTGGCACTG GCTACCTTGS TTACCTTCCT GATTCAAGAAG 180  
 TTCGTTTGG ATCGTTTCGG ATTGGGCTTT ATGCACACCA TTGCATTTAT TTTGGTCATT 240  
 50 GCGGCTTGG TGACAGATGGT GGAGATCATA CTCGAAGAAG TATCTCCTCC CCTCTATCAG 300  
 GCACTGGGTG TATTCTTGCC CTGATTACG ACGAACTGCT GTGTGCTCGG TGTGGCTATT 360  
 TTGGTTATCC AGAAGGATTA TACCCTGCTC CAGAGCTTCG TCTATGCAAT ATCCACGGCT 420  
 ATCGGTTTCA CCTTGGCAAT GGTACTTTC GCAGGTATTC GAGAGCAACT CGATATGACC 480  
 AATCTCCCA AAGCTATGAA GGAATACCT TCGGCACTCT TGGCTGCCGG TATATTGGCT 540  
 55 ATGGCTTTCA TGGGCTTCAG CGGTATCGCC 570

## (2) INFORMATION FOR SEQ ID NO:176

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...558

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:176

5	ATGTTATCA TAGCGGCGGT TTTGTTAAT AACGTCGTGC TGTGCGAGTT CCTCGGTATA	60
	TGCCCATCT TAGGCGTATC GAAGAAGTA GACACCTCAA TCGGTATGGG TGCAGCCGTG	120
	ACATTGCTAT TGGCAGTGGC TACCTTGGTT ACCTTCCTGA TTCAGAAATT CGTTTTGGAT	180
	CGTTTCGGAT TGGGCTTTAT GCAGACCAAT GCATTTATTT TGGTCATTGC CGCCTTGGTG	240
10	CAGATGGTGG AGATCATACT CAAGAAAGTA TCTCCTCCC TCTATCAGGC ACTGGGTGTA	300
	TTCTTGCCCT TGATTACGAC GAAGTGTGT GTGCTCGGTG TGGCTATTTT GGTATCCAG	360
	AAGGATTATA CCTGCTCCA GAGCTTCGTC TATGCAATAT CCACGGCTAT CGGTTTCACC	420
	TTGGCAATGG TTAATTTCGC AGGTATTCGA GAGCAACTCG ATATGACCAA TCTCCCAA	480
	GCTATGAAGG GAATACCTTC GGCACCTCTG GCTGCCGGA TATTGGCTAT GGCTTTCATG	540
15	GGCTTCAGCG GTATCGCC	558

(2) INFORMATION FOR SEQ ID NO:177

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2499

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177

40	ATGAACAAC TAAACATTAT CAGCTTCATC AITGCTTTCC TATTCTTAGG AACGAGCGCA	60
	TCGGCTCAGC AATCGGGCGG ATCCGTTACA GGTACCGTAG TGGACAAAAG CTCAAAAGAA	120
	CCTATCGCAT ACGTACAAGT ATTCGTCAAA GGAACCACTC TCGGAACCTC CACGGATGCA	180
	AACGGAAACT ACTCGATCAA GGAATCCCT TCGGGTAATC AAACATACGT AGCCCGACTC	240
45	ATGGGTTACT CCACTTGCGA AGAAAAAGTA CATATAGAAA AGGGTGGTTC CGGCCACGTA	300
	GACCTCTATC TGACCGAAGA GATTCTCTCT CTCGATGGGG TAGTGGTATC TGCCAATAGA	360
	AACGAGACTT TCGGCCGTCA AGCACCCTCG TTGGTAACGG TACTGTGCGC GGAACCTTTC	420
	CTCAAAACCA ACTCTACCAA CCGAGTCAG GGAAGTAAAT TCCAGCCCGG TC'GCGCGTG	480
	GAGGACAACG CTCAGAACTG CGGTTTCAAC CAAGTTGCTA TCAATGGACT CGAAGGAGCC	540
50	TATTCGCAAA TTCTTATCGA CAGCCATCCC ATCTTCAGTT CGCTTGCCGG TGTCTATGGC	600
	TTGGAGCAGA TGCTTGCCAA TATGATCGAA CGTGTAGAAG TAATTCGCGG TGGAGGTTCC	660
	GCTCTGTTCG GCTCTAATGC TGTGGGAGGC GTTATCAACG TAATTACGAA AGAACCCTT	720
	CGCAATTCGG CCGAGATCAG CCATTCTACG ATGACCTTCG ACCACGCGAA AGGGTGGGGG	780
	AGCTTCCAAA ATACGACCCA GTTCAACGGT TCTATGCTGA CGGAAGACCG CAAAGCCGGT	840
55	GTCTAGGTAT TCGGCCAACA CAACTACCGT CCGGACAGG ATATAGACGG CGACAACCTT	900
	ACCGAACTAC CCAATCTGCG CAACCGCTCG CTCGGTTTCC GCTCATACTA TAAGACCGGT	960
	CTCTACAGCA AAGCAACCT CGAATATCAC AGCATGCAGS AGTACCGTGC TGGTGGCGAC	1020
	AGACTGGACA ATCTCTCTTT CGAAGCCGAG ATAGCGGAAT ATCTCCAGCA CTATATCAAT	1080
	GGCGGAAGTT TCAAAATCGA TCAGGGCTTC AGCGGTGGCA AGGATTCTT CAGTCTGTAT	1140
60	GCTTCAGCAC AAGACGTTCA GCGTCGTAGC TACTACGGGG GTGGCGACTA TACCGAAAAT	1200
	CTGCTGAACG GAGCAGTTCA GAGTGGAAAG ACCGAATCGG ACGAATACAA CGATGCTTTC	1260
	ACGGCTCTTA CTCTCTACGG GACTACCAAG GGAATCGATT TGCAAGGAGG AGGTATGTAC	1320
	CGTCATACCT TCGGAGAAAA CTGGGACTTT ACCGGCGGAC TCGAATATAT CTACGGCCAA	1380
	CTCGATGACA GAAGCGGCTA CAGACCGAGC AATATAGATC AGAATACCTC TACTTTTAGT	1440
65	CAGTACGACC AGCTCGAATA TAAGACGGAG AAGTTAAGTG CCCTTATCGG AGCAGGTATC	1500
	GACTATGTTT TCTCAATCA GGATGCCAAA CGCTATATCG ATCCGCTCTT CATTTTCAAT	1560
	CCTAGAGCCA ACGTACGATA CAATCCCAAT AAGAACTCTA GCTTCCGACT CTCATACAGC	1620
	GAAGGATTCC GCGCTCCTCA GTATTTCGAT GAAGATCTGC ACGTAGAGTT GGGCGGTGGT	1680
	ACTCCTATCA GCGGTGTCTT TTCCCAAT CTGAAAGAAAG AACGTTACG AAGCATCAGT	1740
70	GCTTCTTTGG ATTATTACCA CAGAGCCGAC GAATGGCAAT TCAATATCAT GGGAGAAGCC	1800
	TTCTCCACCT TTATCAGCAA TCAGTTCAAA CCATCCGATA AGGTGGAAC CACGAGCGAT	1860
	GGCAAGAAT GGATCATTCG TACCATCTAC AACGACAAGG ATGGAGTATC GAAGGTATAT	1920
	GCTGTGAATC TGGAGGGAAG AATCGCTAC AACAAATCGT TCGACCTCCA GCTCGCGGT	1980
	ACATGGCAGA GAAGCCGCTA CGGAAGCATC TATACCGCTG TGAAGCGGA CAAACACACG	2040
75	GGACAAGCCG AGATCTCTGT GAAAGACTAT GTACGCACTC CGAATCTGTA CGGCTATTTT	2100
	GTTGTACCGG TACGTCCTAC CGAGCACTTC GCCATCAATC TCTCCGTAC ATTCACGGCC	2160

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5 AATGATGGATG TAGTACACGA AGCCTATGAA GGCATATTC CCGCAGACA CATAGCTCCG 2220  
 GACGGATCGT TCGACTTTGA AATGAATGGT CAGCAATTC AAGGTTTGGC CGAAGGTCAT 2280  
 GCCAAGCTCG TCAAGACTCC GGCCTTCGCC GATATAGACC TCAAGCTGAG CCACGACTTC 2340  
 CACCTTGCTT CCACTATGAC CTTGGAATTG AATGCCGGA TACAGAACAT ATTCAACAGC 2400  
 TATCAGAAAG ACACGGACAA GGGACCGGT AGAGCTTCTA CTACGTATA CGGTCTATG 2460  
 CAGCCAGAA GGATTTTCGT CGGTACAAAG ATCAATTC 2499

## (2) INFORMATION FOR SEQ ID NO:178

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2673 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...2673  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGTACAAAA AGATTATTGC CGTAGCAGCT CTCTTCTGCG CCAGCATAGG GATCCTGAAA 60  
 GGACAGTCCT CGGATCTGAC CCCTCAGGAT ACTATATATA GCCCTGAAAT ATCCTATGCC 120  
 AAGCCTATTC ATAAGACCAT AGCATCTATT GAGATCGAGG GAATGAGGTC TTTCGATGAC 180  
 35 TTTGTCTTGC GCAATCTTTC AGGCTTGGCT GTAGGTGATG AAGTCCTGAT TCCTGGAGAT 240  
 GCCATGCTCG CTGCCGTGAA TAGAATTATG CSTCAGGGCT ACTTCTCAAA TGTGCGAATC 300  
 ATCGCGGATA AATATGTCGG CAATAAAGTC TATCTGAAAA TCATTGTGAC TGAACGTGCT 360  
 CGCATCAGTA AGGTACTTT TAGCGGGGTA AAGAAGTCTG AGAGAGAAGA TCTTGAAATG 420  
 AAAATCGGTC TTGCGGAGGG GATTGAGATG ACCAGAAATA ATGAAGACAA GGTCAGGCAA 480  
 40 ATCGTACAGA AGTATTTTAC TGAGAAAGGT TATCGCGATG CCAGCATACG GATAACGCAG 540  
 GAACCGGATA TTTCCAAAGA TGGCTTTGTC AATGTGCTTA TCTCGATGTA GAAGAAAGC 600  
 AAAACCAAGG TGAATGAAAT TATTTTTC CCACAACAGG CCTTAGCAA TCATAAGCTA 660  
 AGAATGGCGA TGAAGAACAC CAATGCCAAA TTCAGTCTTA GAAAGCATAT TCGCTCATCT 720  
 TTCTTGAAC TTTTGTAGTAC TCATAAGTTT GTGGAAGAGA GCTACCGTGA AGATTGGTTC 780  
 45 CGATTGATAG AGAAGTATCA GGAATATGGA TATCGTGATG CTGAAATACT GACCGACAGT 840  
 TCGCTGAGGG CTCCTGACGG CAAAGAGATG GATATTTATC TCAACATCGA AGAGGGGCG 900  
 AAGTATTATA TTAAGGATGT CAACTTTGTG GGCAATTCAC AATATCCATC GGAGTATTG 960  
 GAACGAGTGC TCGGATATAA ATCCGGAGAT GTGTACAATC AGAGACGATT GGCTAAGCGT 1020  
 CTCATGGAAS ATGAAGATGC TGTGGGGAAC CTGTACTATA ACAATGGCTA TATTTTTCG 1080  
 50 TGGGTGATC CCGTGAAAC AAATGTAGTG GGGGATTCTG TTTCCCTTGA TATTCGTATA 1140  
 GCGGAGGGGA AGCAGGCCAA TATCAATAAG GTGATCATCA AAGGAAATAC TGTGCTGTAC 1200  
 GAAGACGTAG TACGCCGAGA GCTTTACACA AAGCCCGGCC AGCTCTTAG TCGCGAGGAT 1260  
 ATCATTAAT CTATTGCTCT CATCAATCAG CTTGGGCATT TCGATGCCGA AAAATCTATT 1320  
 CCCCCTCGGA TTCCCAATCC CGAAACAGGA ACAGTGGATA TAGAGTATGA TTTGGTGGCG 1380  
 55 CGTAGCAGTG ACCAATTGGA GCTTCTGTC GGTGAGATC AGTCGGACT TCTGTTCGGA 1440  
 GGAGCCATTA AGTTCACGAA CTCTCTGTC GGCAACTTGC TCCATCCCTC GATGTATAAG 1500  
 AAAGGGATCA TTCCGCAAGG GGATGGGCAA ACACTATCAC TGAGTGCTCA GACCAATGGA 1560  
 AAGTACTATC AGCAGTATAG TGTACATTT ATGGATCCAT GGTTTGGGGG CAAGCGGCCG 1620  
 GATAATGTTA GCTTCAGTGC ATTCTATTCC AAGACTACGG CGATTGACTC CAAGTTCTAC 1680  
 60 AATAGCAATG CCGGCAACTA CTATAATGCC TACTATAATA GCTACTACAA CAACTATAAT 1740  
 AGTTATTACA ACGGTATGTC GAACATATAC GCGGACCTCT ATACTCAGGC CAGCGATCCG 1800  
 GATCGTTCCG TTCAGATGTT AGGTACTTCG ATCGGTTACG GTAAGCGTTT GACTTGGCCG 1860  
 GACAATGGT TCCAGATTTA TACTTCTCTG AACTACACCT ACTATAGACT CGGAAATTGG 1920  
 AGCTACAAATA CCTTCCAAA TTTCCATCAT GGCTCGGCTA ATGATCTCAA CTGGAGCTG 1980  
 65 CGTCTCTCTG TACTTCCAT CGATAATCCT ATTTATACCA GAAGCGGATC GGATTTCATG 2040  
 GTTCTCTGTT CTGCTACTCT TCCTTATTCT TTGTTGGACA ATCATGACTA TGCCAGCCAG 2100  
 AACCTCAGCG TAAGCGATCG TTACAGATTI ATCGAGTATC ACAAGTGGAA GTTTAGAGGA 2160  
 CGAGTTTITA CTCCATTGCT CAATCCTGCT AOCATATAAT ATACACCGGT GCTCATGAGT 2220  
 70 CGAGTGGGAG GAGCAGTTCT TGGTTCGTAT AATTCCAAIA AGAAATCTCC TTTCCGTACT 2280  
 TTCTATATGG GAGGTGATGG TATGTCCAGC TATTATGGTG GCTACATGAA TGAGACTATA 2340  
 GGTTTGGCTG GTTATAAGAA CGGATCTATT GCGGTAATA ACTACGACTA TGCATATGCT 2400  
 TATATCGGCG TTACGATGGA ACTACGTTTC CCGATTCTGT TTGAAAACCT ATTCAATGCG 2460  
 TGGCTCTTAG CTTTTGGCGA AGCAGGCAAT GCGTGGCGCA GTATCGACAA TTATAATCCC 2520  
 75 TTTAACTCTA AGCGATCGGC CGGTGTAGGA TTGCGTGTAA CGTTACCGAT GGTGCGAATG 2580  
 CTCGGTATCG ATTGGGGATA TGGCTTTGAC CGTCCGGACA ATTCTCTACA GCGAGGAGGA 2640

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AGCAATGTCC ACTTTGTGCT CGGACAGGAG TTC

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## (2) INFORMATION FOR SEQ ID NO:179

- 5 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 522 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- 15 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...522
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG ATATGAAACG GTTTTGGATT TTGATCGGCT TTGCACTGGC GGTAGCTTTC 60  
 TCCGGTTTTT CCCAAAAGTT CGCTTTGGTA GATATGGAAT ATATCCTCAG GAATATTCCT 120  
 GACTATGAGA TGATGAACGA ACAGCTGGAA CAGGTGTCCA AGAAATGGCA AAATGAAATC 180  
 GAAGCTCTCG AAAATGAAGC CCAATCTATC TATAAGAAGT ATCAGAGCGA TCTCGTATTC 240  
 TTGTCTGCTG CACAGAAGAA AACCCAAGAA GAGGCTATCG TAAAGAAAGA GCAGCAAGCA 300  
 TCCGAGCTCA AGCGGAAGTA TTTCCGGCCG GAGGGGGAGC TGTATAAGAA ACGCTCCGAT 360  
 CTGATGAAGC CTATTCAGGA TGAGATTGG AATGCTATCA AAGAGATTGC CAAGCGTAAC 420  
 AACTATCAGA TGGTGCTTGA TAGAGGTACG TCCGGAATTA TCTTTGCCAG TCCGTCTATT 480  
 GACATTAGCG ACCTTGTACT GAGCAAGATG GCCTTTAGCA AG 522

## (2) INFORMATION FOR SEQ ID NO:180

- 40 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 510 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...510

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGAAACGCT TTTGATTIT GATCGGCTTT GCACTGGCGG TAGCTTTCTC CGGTTTTTCC 60  
 CAAAAGTTTCG CTTTGGTAGA TATGGAATAT ATCCTCAGGA ATATTCCTGA CTATGAGATG 120  
 ATGAACGAAC AGCTGGAACA GGTGTCCAAG AAATGGCAAA ATGAAATCGA AGCTCTCGAA 180  
 AATGAAGCCC AATCTATGTA TAAGAAGTAT CAGAGCGATC TCGTATTCTT GTCTGCTGCA 240  
 CAGAAGAAVA CCCAAGAAGA GGCTATCGTA AAGAAGAGCC AGCAAGCATC CGAGCTCAAG 300  
 CGGAAGTATT TCCGCCCCGA GGGGGAGCTG TATAAGAAAC GCTCCGATCT GATGAAGCCT 360  
 ATTCAGGATG AGATTGGAA TGCTATCAAA GAGATTGCCA AGCGTAACAA CTATCAGATG 420  
 GTGCTTGATA GAGGTACGTC CGGAATTATC TTTGCCAGTC CGTCTATTGA CATTAGCGAC 480  
 CTTGTACTGA GCAAGATGGG CTTTAGCAAG 510

## (2) INFORMATION FOR SEQ ID NO:181

- 75 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 489 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...489  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

20 ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCCTT TGAGCCTCTT GGCACAAAAG 60  
GTGGCAGTGG TAAACACTGA GGAGATCATT TCCAAAATGC CGGAACAAGT AGCTGCTACC 120  
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAAGAGTAT GGACGATGAG 180  
TTTGCCAAAA AGACAGAAAG ATTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC 240  
AATCGTCGTC ACCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG 300  
25 ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTTC CTCCTATCCA ACAAAAGGTG 360  
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAAACTGTG CCTACATCAT GGAGGCCGGT 420  
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC 480  
GGAATCAAG 489

30 (2) INFORMATION FOR SEQ ID NO:182  
(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 2481 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
40 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
50 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

55 ATGAAGGAAG CTATTCCTCCG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG 60  
TCATTCAATC TGCTATGCTG CCGTCTATGC TCTCAGGCAG CTATGGGCACA AGGCGTCAGG 120  
GTATCGGGCT ATGTGCTCGA CCGTGGGGAA AAGCCGATCC CGTTCCCGG AGTCAAAGTG 180  
CGTGTACGG GGACAGGCGC AACGACGAAT CTGAAAGGAT ACTACGAGTT TCGGATGAAG 240  
GCCACGACGG ACAGCATCAC GATCGAGTTC AGCTCCATGG GGTACCAAGG GGTAAAGTCG 300  
60 AGCTTTCCGT CTCTGACCAA GGACACTCGG CTGAATGTTT GTTTGGCAGA GGCCGAGATG 360  
GASCTTTGCA GCGTGACGGT ACAGGCCACA AAACGCGAGC TCAACACGAT GGAGCGCGTC 420  
AATACCCGAG ACCTTCGTGT CAATGCAGGG CCTACGGGAG GGGTGGATC GCTCATCAGT 480  
ACCTACGAG GAGTAACGCA GAACAATGAA CTAAGCTCGC AATACCTCGT TCGCGGAGGA 540  
AGCTACGATG AGAATATGGT CTATGTAAAC GGAGTGGAGG TTTATCGCCC GCTGCTGGTT 600  
CGCTCTGCAC AGCAGGAAGG TCTGAGCTTC GTCAAATCCG ATCTGACACA ATCCGTACAG 660  
65 TTCTCCGCG GAGGGTTCAC GGCCGACTAT GGCGACAAGA TGTCCTCGT ACTGGATATT 720  
CGCTACAAGC AACCGCAGGA GAAGGAAGGA GCGGTACTCC TCGGGATGCT ACAATCGAST 780  
GCCTACTATG GCAGCAGTGC CGGAGCCTTC AGCCAAATCA CGGGTGTACG CTACAAGAGT 840  
GCCAAATCGC TCTTGGGCAC TACGGACACG AAAGCCGAAT ACGATCCGAT CTATGCGGAC 900  
GGACAGACAT TCATGACGTA CCGTTTCAGC CCCAAGCTGT CGGTAGTTT CCTCGGCAAT 960  
70 ATTTGCAAAA CTGCTACAA GTTTGTCCCT CAGACCCGTG AGACGAGCTT CGGTACACTG 1020  
AGCGATGCCA AAAAGTTGAA GATCTTTTTC GACGGTCAGG AACAGATOS TTTCTGACC 1080  
TACTCGGGTG CCTTCAGCAT GAACTTCGTG CCGGACGACA AACAGCGGCA TACGGTTACG 1140  
CTTTCGGCT TCAACAGTAA CGAACGGGAG ACCTACGATA TTCAGGGAGA ATACTTTCTG 1200  
AACGATGTGC AGCTGGGGGC GGACGGAAT GCTTCGATGG CTTTCGGGTC AGAGAACTCC 1260  
75 AACGGCTTGG GCATCGGGCG CAATCACGAG CATGCGCGCA ACAGGCTGAG CTACCGCGTG 1320

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5 CTGAACATGG GTTACAGAGG GGAGATGAAG CTGAACGAGA AGCATCGCCT GCAAGCCGGC 1380  
 GTATCGGCAC AGATGGAGAA AATAGCCGAC CATATCAGCG AATGGGAACG GAGGGATTTCG 1440  
 GTAGGATACA ACCTACCTCA CTCGGAGACC GTATTGCTGA TGTACAATAA CCTATATGCC 1500  
 10 GATACGACAGA TGAGGGGAAC GCGCTTGTGG GCATTCTGTAC AGGATCGATT CAACCTCAGC 1560  
 ATGGGAGGAG GTACATTTTC TCTCATTCGG GGTATCAGAG CTTCGTGGTG GAGCTTCAAC 1620  
 AAGGAGTTGC TCGTCAGCCC ACGTATCAGC GTGGGTATT CTCCCGAAAG CAACCCGGCT 1680  
 TTGGTACTGC GTGCAGCCGC CGGACTTTAT TATCAGGCAC CGTTTACAA AGAGCTAAGG 1740  
 CAGAGCATA AGGATGCCGA AGGCAATAAC GTGGTGTCC TCAACGAGAA GATCCGCTCT 1800  
 CAGGGAGCTT TTCACATTCT CGCAGGAGCA GACTATACCT TCGAATGGG GGGGCGAAAA 1860  
 15 TACAAGTTTA CGGCAGAGGC TTAACAAG AGCCTGTTC ACATCAACCC GTATATAATA 1920  
 GAGAACGTGA AGATCCGCTA TCTGGGCGAA AACATCGGTT CGGTTATGC TCGGGGTATC 1980  
 GATCTCAAGC TCTTCGGCGA ACTGGTACCC GGAGTGGATT CGTGGCTGAC GGCTTCCATT 2040  
 ATAAAGCCCC GTCAGAACT GGATGGCTAC GGTCTTTAC CACTGATGAA CGCACCCACT 2100  
 20 TACAATTTCT CCTTCTTCTC TCAGGAGTAC GTGCCGGGCA ATAAACGCAT CACAGCCACC 2160  
 CTGCGGGCTG CACTAAGCGG AGGATTGCCC CAGCTCAATC CGAGCAAAGG GCTTAGCTCG 2220  
 CUGGCTTTTA CCGCACCCGC CTATAAGCGT GTCGATCTGG GGGTAATGTA CAAATGGCTC 2280  
 CACCCGGATG ACTCCTTTGC CGGCCGAAGC AAATGGCTAA TGGGAGTAAA AGGGGCTTAC 2340  
 ATAGGGGCTG ACCTCTTCAA TCTGTTGAC ATGACCAACG TCAATTCTTA CTACTGGGTG 2400  
 25 TCGGATGCTC ACCAACAGCA ATACGCCGTA CCGAATACC TGACACGCCG CCAATTCAAC 2460  
 CTGCGTCTCC TCGTCGAATT C 2481

## (2) INFORMATION FOR SEQ ID NO:183

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2016 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GIUGTVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2016  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

50 ATGTACAGCG GACATCATAA AATCCATTAT CCTTTTCTTA TCCTGTTGGT ATGCCTTGCT 60  
 TTTGCTGCCT GCAAGAGCGT GAAGTTGAAA GATGCGGAGA AGGCACATGA TCGCCAAGAG 120  
 TATACCAAGG CTGCCGATAT GTACAATACA TTATACAGGC GTACCCGAGC AAAGCAGGTG 180  
 GAGATGAAAG CTTATACGGC TTTCCGATCC GGTGAAACT ATCGTGCCGC CGGCAGACAA 240  
 55 GCCAAAGCTT TCGGTGGCTA TCTGAATGCC AGACGCTACG GGTATCCGGA TTCTGTGGTA 300  
 CTGCTCCGTT TGGCAGAGAC TTATCAGCAA GGAGGTAAC ATAAAGGAAGC CGAGGTAATC 360  
 TTCCGTGGAT ATCTGGAAGC TTATCCGAAA AGTTATTTTG CAGCTATCGG TTTGGAGGGG 420  
 TGTCTCTTTG CCGGCCAGCA AAAGGAATAT CCTACACGTT ACCGGATAAG GCGAGCTGCC 480  
 GAGTGGAAAT CGGCACGGGG CGACTTCGGC CCGGCTATG CACCCGATGC TTCGGCTCTC 540  
 60 TATTTACAT CGAGCAGAAG CAAAGACGAC GGTTCGATA ATAGCAGCAT AACGGGACTG 600  
 AAACCCAACG ACATTATAT CATCAAACGA GATGCACAAG GACGATGGGG ACGTCCCGAT 660  
 AGCGTGTCCG GAGGAATCAA CACTCCATGG GATGAAGGCG TGCCAAACGAT CACGCCCGAT 720  
 GGTAAGTCCA TATATTATAC GTTGGCGCAG CAAGGAGCCG ATTACGACCG TACGGTACAG 780  
 ATCTATTCCG CCGCTCGGAG CGGAGAAGGC GGTGGAGCA ACGGTTCCGT CGTGGACATT 840  
 65 ATGCGCGATT CGCTCCGTAT GGCTGCTCAT CCCTCTATGT CGGCATCCGG CGATTACCTG 900  
 TATTTGGTCA GCAATATAGG CGGTAGCTAT GCGGGCAAGG ATATTTATCG TGTCAAGGTG 960  
 TCGGATCGTT CTTATGGTTC ACCGGAGAAT TTGGGGCTTG ATATCAATAC GCGGGGGGAC 1020  
 GAAATGTTTC CCTTCATAGA TGGGGATAGT ACCCTTTTCT TCGCTTCGGA CGGACACGCC 1080  
 GGTCTGGGAG GACTGGATAT TTTCAAAGCC ACGCTGGACT CTACCGGCCA ATGGCATGTA 1140  
 70 GTCAATATGG GACRAACCGT CAATTCCTCT GCCGATGATT TCGGCTTGGC TGTGGAGCCT 1200  
 AAAGGCAAAA ACAAGAAGA AGCTTTGCCG GACAACGGAG TCAAAGGTGT ATTTGTTC 1260  
 AACCGAGGCG ATGCACGCGG ATGGCCGCAC CTCTTCCATT TCGAACTGCC GGCTATCTAC 1320  
 ACCGAGATTC AAGGTTATGT GATGGACAGA GAAGAAAATC CCATAGCCGG AGCCACTGTC 1380  
 AGGATCGTAG GCGAACGCGG CCCCGTAGGA CAGGATTCG TGAATCTCG TGACGATGGC 1440  
 75 TCCTATAAGA TGAGCGTGCA GGGCGATACT CGCTATGTAA TGCTTGGCGG AGCATCGGGT 1500  
 TATTTGAATC AGTACGTAGA ACTCAAGACC GATACCGCCA ASCAGAGTGA GACCTACTAT 1560  
 GTGGACTTTT TCCTTGCATC GCGTGAGAAA GCGAGGGGCT TGCAAAATAT TTTCTATGAT 1620  
 TTCGATAAAG CTACTCTTCG CCCGAAAGC ATGAAGAGCT TGGACGAAC GATTCTATC 1680  
 CTCACGACA ATCCGATAT TCGGATCGAA TTGGGTTCCG ATGCCGACG GAAAGGCCCC 1740  
 GATGCTTACA ACCTCGGACT ATCTGACCGC AGAGCCAAAT CCGTGGTGGA TTACCTCAGC 1800

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AGTCGTGGCA TAGCGGCCGA CAGGCTTACG TGGAAAGGCT ACGGTAAGTC TGTCCCCAAG 1860  
 ACGGTGACAG CCAAAATTGC CGAACGGCAC GATTTCCTGA AGGAAGGCGA TGTGCTCACC 1920  
 GAGGAATTGG TAGCACCTTT GACCGAGGAG CAGCAGTCAG TCTGCGACCA ACTGAACCGT 1980  
 CGTACCGAGT TCCGTGTGAT CGAAGAAGAG TTGCGT 2016

## (2) INFORMATION FOR SEQ ID NO:184

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (11) MOLECULE TYPE: DNA (genomic)
- (111) HYPOTHETICAL: NO
- (11v) ANTI-SENSE: NO
- (1vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (1ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2124
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

30 ATGAAAAAGT TTTTCTTCGC GCTACTATCG ATTGGTATTT CAGCGCAGGC TTTTGCCAAG 60  
 ACGGACAAAG TCCCCGACAGA TTCGCTACGA GTACACAATC TTCAGACCGT CACGGTCTAT 120  
 TCTACACGCA CGGCCGTACC TCTGAAAAAG ATACCGGCCA AGATGGAATC CATCTCATCG 180  
 CGCAACATCA AGCAGTCCGG CTTTAAACAAC ATGACCGACA TCCTCAAGAC GCAAAAGTTGG 240  
 CTCGATGTCA TACAATACCC GGGCTTTAGT TCGAACATCG GTATCCGCGG TTTCAAGCCC 300  
 TCCGGCAAGT ATGTAACCGT ATTGGTAAAC GGCATCCCTG CGGGAACGGA CAATATCTCT 360  
 ACGCTCAACA CGAGCAACAT CGAACAAATC GAGATCCTCA AAGGCCCGTT CTCTTCCATC 420  
 TACGGCACCA ATGCCATGGG CGGTGTGGTG AACATCATCA CCCACAAATC CAAGGACAAG 480  
 ATCCATGGCA ACGTTTCTCT CTTCGGCGGT AGCTACCAGA CCATGGCCGG ATCATTCAAC 540  
 TTGGGTGGCC GCTTCGAGGA TATTTTCTCA TTCGATCTTA GTCTGGGCTT GGACAAGCAG 600  
 40 AACAAAGACT ATAAGACCGG ATCAAACRAAT TFCCTATCCC TGAGCAAACT GGAAGAAGCT 660  
 ATAGTAGATG TAAATGCTAC CAAAAACRAAG AAAATGAAGG GGAGCGACTA TACTGTAGCA 720  
 ACGGGACGTC TGGCTTTCGG TATCGACTTC ACGCCCGAAT GGTGCGTGAA TCTGTATCAA 780  
 AACGTATTCC TCGGAGATGC GATCCCCGTA GGAGGATCTA TATGGGGCGT TTACGGAGAA 840  
 TCCAAAAAAA ATCTGAATCG TTCTTCGACC TCTTTCGAGC TGCTCGGCAA ACATGGGTGC 900  
 45 CACACGCTTC AATTCCTCCC CTACTTCAAC ATAGAGAAAT CGGAGAACTA TAACAATGCC 960  
 GATCCCACCG GTTTCATCAA CTACAAAAGC GACTACTACA CCTATGCTGC CCTACTCCAG 1020  
 GACAAGATTT CCTTTGGAGG ACAAATATC GTACTCGGTG TCGACAGCCG AAACATGACG 1080  
 ATGGAGTCAG AAAGATTGCA GCAGGCAGGA GTGAATACAA AGCCATACAA CCCCAGATAT 1140  
 50 GCCACGAACA ATATCGGTTT GTTCGGACAG GCCAATTCTT ACCTGCTGAA CGATGCTCTA 1200  
 TCGATATCTG CCGGTGCACG TGGCGACTTC ATGTTCTTTG ACCTGAAAGC GAACGAGTAT 1260  
 CTCACAAATG AAGCCAAACA GGAACACTCAT AACGTAATCA ATCCGAATGT CGGAATCAAA 1320  
 TATGAGTTTG TGAAGGCCCT TACAGCTCAT GGTACATTCG GTAGTGCAAT CAGTGCTCCC 1380  
 GATGCTTTCC AAAAAGCAGG CCAATACGTA GGCCCGTTTC GCACGACCAT AGGCAATCCT 1440  
 55 GACCTGAAAC CCGAAAAGTC CATGACCTGG GACTTCGGTA TCGGATACAG CAATGCACGC 1500  
 TGGCGGATCC AAGCCGAGCT AACCTTAACC TATTTCCACA CCGACCACAA AGATCTGATC 1560  
 TTGTCCAGCC CTGACTATGC TAATAATATC ACCACATACA TCAATGCCGA CAAGGCTCGT 1620  
 ATGAGCGGTA TCGAGGCCCT TTTGTCTTAT GACTTCGGCA GCCTCTTTGC CAACAAGTTC 1680  
 TCTCTCCGCG CATTTGCGAA TGCCACGATC ATGCTCAATT CCGAGATGAA GAAAAGCCAG 1740  
 60 ACCGATGCCC CTTGGAGCGA AATGTACTAC GTTCGCAAGC AGAACATCAC CTTCCGTATC 1800  
 GAATATCGTG GCAAGAAGG ACTTGAAGTG ATGCTCAACG GTCGCTTCAT GGCACGCAGG 1860  
 ATCGAGCAAA ACTGGTATGC TTACTACCCC GAAGTTGGCC CCGAACTCCA GCAACTGCTT 1920  
 GCAGCAGNAG AGCCTGAATT GGCTGCTCAG GGACTGCTCC GTCATCCGCA AGCAATGGTG 1980  
 TTCAATGCCT CTGCTTACTA CCNATGAAC AAGTATCTCA CCTTCGGTGT GAACITGAAC 2040  
 AACATCTTGG ATGAGCTTTA TACGGAGAAA GACGGCTACC ACATGCCCGG ACGTAACATC 2100  
 65 ATGGGTAAGG TTATGTCAA CTTC 2124

## (2) INFORMATION FOR SEQ ID NO:185

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular



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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1386

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

ATGAACAGGT	TTTCAAATCA	TGGCCCTGC	ATCCTCGTGG	GSTTTGTACT	CTGGTTTGTA	60
TGGGCGAGTC	GGACTGTGGC	ACAAAACGCC	TCCGAAACGA	CGGTATCGTA	CGATACGGAT	120
ACCGCCGTAC	TCTCCGAAGC	CGATGTGCTT	CGGATCGCTC	TTAGTGAGAA	TGCCACAGTG	180
AAAGTGGCCG	ATATGGATGT	GGCGAAACAG	GAATATGCAC	GTAGGGCAGC	ACGTGCCGAT	240
CTCTTCCCGA	AAGTAGACCT	CAATGGCGTT	TACAGCCATA	CGCTAAAGAA	GCAGGTCTTA	300
TATATAGATA	TGCCCGGTTT	CAGCAGTAGC	GAAGGTATCG	AAATGGGGCG	TACACACAAT	360
ACGCAAGGAG	GGGTGAACGT	CTCCATGCCA	TTGGTGTCCG	CACAGCTTTG	GAAGAGCATT	420
GCCATGACCG	GAGAACAGCT	CGATCTGGCT	CTGGAGAAAG	CTCGCAGCTC	CCGAATCGAT	480
TTGGTGGCCG	AGGTGAAGAA	GGCTTACCTC	AGTGATTGTT	TGGCCGAGGA	CTCTTATGSC	540
GTATTCAAGC	GCAGCTATGA	CAATGCTCTG	GCCAATTATA	AGAACATATC	CGACAAGTTC	600
GATCGTGAGC	TTGTGGCCGA	GTATGATAAG	ATTCGAGCCA	ATGTACAGGT	ACGCAACATC	660
GAGCCTAACC	TCTTGCAAGC	GCAGAACTCC	GTAGCCCTTG	CTCTCTGGCA	GCTCAAGGTC	720
CTGATGACCA	TGGAAGTGGA	AACTCGATC	AGACTCTCCG	GTTCAATTGC	CGACTATAAA	780
GAACAAGTCT	ATACCGGCTA	TTTTGCCGCC	GATACGGCTA	TTTCCAACAA	CTCCTCCCTG	840
CGTCAGCTCG	ATATACAGCG	TCGTCTGGCT	GTCACTGCAG	ACAAGCTGAA	CAAGTACAGC	900
TTCTTGCCTA	CACCTAATCT	GGGAGGGCAG	TACACCTATT	CGCTCAACAG	CAACGACATC	960
AAATTCTGCG	GCGAGGGACA	ACGCTGGACG	CCTTTCTCCA	CCATATCGCT	CAGCCTGTAC	1020
ATTCCTATAT	TCAATGGAGG	CAACGCTCTG	TACAACGTGA	AGCAAAGTGC	TTTATCGATC	1080
CGTCAGATCG	ATCTGCAACG	ACGCCACATA	GAGCAATCCA	TCCGAATGGG	AATCAAGAAC	1140
CAAAATGACC	GTCTGCGTAC	CTGTATGCAG	AGATTGTGGG	CCTCGGAAGA	GGCTGTCCGA	1200
AGTGCAAGAA	AGGGCTATCA	GATAGCAGAG	AAACGCTATC	AGACAGGCGA	AGGCACTCTC	1260
GTGAGCTCA	ACGATGCCGA	TGTGGCTCTT	TTGCAGGCTC	GACTCAATTA	TAATCAGGCC	1320
ATATTGCACT	TTATGACCGC	AAAGGCCGAA	TTGACAAGA	TGAACGGCAT	GGGGATTCCC	1380
GAACAA						1386

(2) INFORMATION FOR SEQ ID NO:186

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

ATGTGGGGGG	ACAGCCATGG	AGTGGCGCGG	AACCAAGTGC	GCCGAACGCT	GGTGAAGGTA	60
GCCTTAAAGTG	AATCCCTTCC	TCCGGGTGCA	AAACAGATTG	GTATCGGATT	CTCTCTCCG	120
AAAGAAACGG	AGGAAAAAGT	CACCGCCCTA	TATCTCCTTG	TGAGTGATTG	TTTAGCGGTG	180
CGCGACTTCC	CGGACTACAA	AGGGCGAGTC	TCTTACGATA	GCCTCCCGAT	CTCAAAGGAA	240
GATCGTACCA	CAGCCCTTTC	TGCGGATTGG	GTAGCCGGAC	GCCGCTTCTT	TTATTTGGCT	300
GCGGATATAG	GGCCTGTTGC	TTCTTTTTC	CGATCCGATA	CGCTGACTGC	CCGTGTGGAA	360
GAGGTGGCTG	TCGATGGCCG	CCCTTTGCCG	TTGAAACAGC	TGTCGCCATG	CTCCCGTCGT	420
CTGTATAGGG	GGTATAGGCG	CCTCTTTGTA	CCCGGTGATG	GCGGATCGCG	GAACTATCGT	480
ATCCCGGCCA	TTTTGAAAC	GGCTAATGGA	ACACTCATAG	CGATGGCCGA	CAGACGAAAA	540
TATAATCAGA	CGGATCTGCC	GGAGGATATA	GATATAGTCA	TGCGGCGCAG	TACGGACGGA	600
GGGAATCGT	GGAGCGATCC	CAGGATTATC	GTACAGGGAG	AGGGGCGCAA	TCATGGCTTT	660

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5 GGCGATGTAG CCTTGGTGCA AACCCAAGCA GAAAAGCTCC TGATGATCTT TGTGGGTGGA 720  
 GTAGGCCTGT GGCAGTCTAC CCCCAGTCGT CCTCAGCGCA CTTATATATC GGAAAGTCGG 780  
 GACGAAGGAC TGACTTGGTC GCCTCCTCGG GATATAACCC ATTTTCATCTT CGGCAAGGAT 840  
 TGTGCGGATC CGGGACGAG TCGCTGGTTG GCCTCCTTTT GTGCTTCGGG ACAAGGGCTT 900  
 GTGCTGCCAT CCGGTCGTAT CAGGTTGTG GCTGCCATCC GCGAATCAGG GCAGGAGTAC 960  
 GTCTTGAACA ACTATGTCTT CTATAGCGAC GATGAGGGCG ATACATGGCA GCTTCCGAC 1020  
 TGTGCATACC GCCGTGGCGA TGAGGCAAAG CTTTCATTGA TGCCCGATGG CAGGGTACTG 1080  
 ATGAGCATAC GCAATCAGGG ACGGAGGAG AGCCGACAGC GTTTCCTCGC TCTCTCTCC 1140  
 10 GACGATGGCC TTAATTGGGA GAGAGCCAAG CAGTTCGAGG GCATCCATGA CCCCGLTGT 1200  
 AATGAGGCTA TGCTTCAAGT GAAAAGGAAC GGAAGGGATC AAGTGTCTGA CTCCTGCCT 1260  
 CTCGCCCGG ATGGGCGTCG CGATGGAGCT GTCTATCTCT TCGATCATGT CTCGGCCGC 1320  
 TGGTCCGCTC CCGTTGTGT CAATTGAGGA TCGAGTCCCT ACTCGGATAT GACTCTGCTG 1380  
 GCGGATGGA CGATCGGTTA TTTCGTGAA GAGGGCGATG AGATCTCATT GGTTCATT 1440  
 15 CGGTTCGTCC TTGACGATCT CTTCGATGTC CGGCAA 1476

## (2) INFORMATION FOR SEQ ID NO:187

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 735 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...735

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

40 ATGAAAAAAG AAAAAGTTTG GATTGCGATC GTCGCCGGTT TGGCTTTCGT ATTGGGCCTT 60  
 TATGCTCTTG GCCGAGTGT CGCTCAGCTA CGCCGCTCTC AGCCTTCGGT GACTGTGACC 120  
 GGTATGGCCG AGCGTAATTT CAAATCCGAT CTGATCGTTT GGACTGCTTC GTACCAGCTC 180  
 CAGATGATGG ATCTCGAATC GGCCTACAAG GCTTTGAAGG AAAACAGAT ATTGGTAGCA 240  
 45 GACTATTGGA AAAACAAGCA GTCGCCGAT TCGTCTTATA TCTTCTCAAG CGTAGCCATC 300  
 TCTAAAGAAT ACAACTACTA TTACGATCCT CGGCAGGAAC AAAACGTCAG GACCTTTGCC 360  
 GGGTATCTGC TCAGCCAGAC AGTTACGGTG ACCTCAGAG ACATCGAACA TGTGGAGAAA 420  
 ATATCTCGCG ATATAACGGA GCTGATCAAT CAGGGGGTAG AGATTACCTC CGACCGTCCG 480  
 GCCTATTACT ACACCAAGCT CAATGATCTG AAGGTGGAGA TGCTGCGCAA TGCCCTCCGA 540  
 50 GACGCTTCA ATGCTGCTTC GGTCAATGCG GAGGGGAGCG GTTCTCCGT GGGTAAGATG 600  
 CTATCTTCTT CGATGGCGT GTTCCAGATA GTGGGGCTCA ACTCGAACGA AGATTATAGC 660  
 TGGGGAGGTT CGTTCAATAC GTCTTCCAAG ATGAAGACGG CAAGCATAAC GGTTAAGGCT 720  
 TCTTTCGCTT TGAAG 735

## (2) INFORMATION FOR SEQ ID NO:188

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 75 (B) LOCATION 1...828

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

5 ATGAAAAA CAATTGCAAT TATCGCCTCA GCCCTCTTGG CTTTAGGAGC CGTCGGCTGT 60  
 AAGAAAAATG CTGACACTAC CGCTGTCACT GAAAAGGATA GCATAGCCTT GTCCATGGGT 120  
 ATTTTGTACG GACAGGATTT TGCCAAATCAG TTCGAAATGT CCGGCTTGCA AGGCCAGCCG 180  
 ATTGATTCGG TAGCTTTCTT GGACGGTTTC AAATATGGTA TCGATACGAC GCGCTTCTCG 240  
 TACAATCTGG GAGCCATCTA TGCTTCCAAT ATAGCTCGTC AGCTGGCTCA TGATTCCATC 300  
 GATATCGACA AGTTCTATGC AGCCATGCGT GCGGCTCTTC TTAAGACAC CGTATCTATC 360  
 10 GCCATGAAGC CTGCAGATGC ACAGGCTTTC ATGCAACGAA TCCAAGCCAA AAAGCAGCGA 420  
 GAAAAAATA TGAAGCAGTT TGGCCAGAAC ATCGAAAAGG GTAATGAATA CATCGATACC 480  
 TTTAAAAAAG AAGATGGTGT AACTGTTACG ACAACTGGTC TGSCATACAA GACTCTTCAG 540  
 GAAGGTACGG GAGCTACTCC CTCTTGGGCC GATACTGTAC GTGTCAAGTA TGTGGGTACT 600  
 CTGGTCAATG GTAAGAGATT CGACAAAAAC GAAGAAGGAA TCGAATTTCG CGTTACCGGT 660  
 GTGATTAAAG GCTGGACGGA GATGCTCCAA CTCATGAAGG TCGGTCAGAA AGTTCGCGTG 720  
 15 GTAATCCAC AGGAGCTGGC TTATGGGGAG ACCGGCAACT ATACCATCGA ACCGTTCTCT 780  
 ACCCTGACGT TCGAGATGGA ACTTATCGGG ATCAAGCCCG GGA AAAAG 828

## (2) INFORMATION FOR SEQ ID NO:189

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2325 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 30 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2325

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGAAAGTAT TACGGCAAGT ATTCCTCCCC ATCCTTTTGG TCCTACTGAC AGGTGCCTGC 60  
 TCCACCACAA AGAATCTGCC GGAAGGGCGAA CAGCTGTATA TCGGAATGGG CAAGACACAG 120  
 ATACTCCGGC AGGACAAGAG CCACGCCGGC CAACAGGCTC TGACCGAAGT GGAGAGTACA 180  
 45 CTGAAAGTTA CACCCAATGG AGCTATTTTC GGCAGTGCAA GTGCCTCCTT ACCCAAGATA 240  
 CCATTCCGGC TATGGCTATA CAACAGCTTC GTGGGGGATT CCCTGTCTAT TCGAAATGG 300  
 ATATTGACA AGTTTGACGC CAAGCCGGTT TTCATCAGTC AGGTCAAATC CGTAGCCGG 360  
 GCTAAGGTGG CGACGAACAT OCTCCGGA CAACGGGTACT TCGATGCTAA AGTAAAAAGC 420  
 AGTGTACCA CTCTGAAAAA GGAATCGCTC AAAGCCAAA TCTCTATAC GGTGGATATG 480  
 50 GCCTCTCCTT ATCATTACGA CAGCATCATY CCCTTACCGA TCAGCACTTT CCCCAGACGC 540  
 ATTCTGGCTT ACAGGCAGAC TCCGTCTTTG ATCAGGAAAG GAGACCAATT CAATTTGGCA 600  
 AAGCTGCACG AAGAGCGTCA GACCATCAGT GCCCTGCTGA GAGACAATGG TTACTACTAC 660  
 TTCGCCCCAC AGGATATTAT CTACGAAGCC GATACCTCC TCGTAAGAGG TGCGTATGC 720  
 CTGCGAGCCA AGCTCTCGGA AGATACTCCA CCCCAGCCA TCGCCCGGTG GAGGATAGGG 780  
 55 AAACGGACAG CAGTCTGTCT CGGAATGAAC GGAGAAAGCC CGACAGACTC GCTCGAAGTG 840  
 GAGGATATGA AAGTCCTTTA CTATCGTAAA ATGCCGGTTC GCCCAAGAT TTTGGCCAAA 900  
 CGCTTTCCCT TCTTCTCCGG CAATCTGTAT CGGCAGAAAG ACGATGAGAC GACACGCCAA 960  
 TCCTTGGCTC GTTTGGGAGC CTTCTCCGTT ATCGATCTCA ATTTTTTGCA ACGCGATTCC 1020  
 ATTTCCGGCC TTTTGGATGT GCGACTGCTA ACCACCTCG ACAAACTTG GATGTCATCA 1080  
 60 TTAGAGACCT TGTTACGAG CAAAAGCAAT GACTTCATCG GTCCCGGACT GAATTTTGCT 1140  
 CTTGCTCGGC GCAATGTATT CGGCGGAGGA GAAATCTTT CITGGAATAT CGGTGGATCG 1200  
 TATGAGTGGG AGACCGGCAA TCGTCCCGAA AATAGCAGCA ATCGGCTGAT CGATATAAAT 1260  
 TCGTACAACA TGAATACGGC CGTGAACCTC TCGTTTCCCT CGATTGTATT TCCCGTCTG 1320  
 CTGGATAAAT ACTATTACTA CCCCACGACT ACGACTTTTC AGGCTTCTGC CACCGCGCTG 1380  
 65 AACAGGCGAC ACTACTTTAG CATGTACTCT TTGGGCTTTT CGACCACTA CGAATTCAG 1440  
 CCGTCCAAGG AACACCGGCA TGCTATTTTC CGCTCAAGC TCAACTACAA CCTCTGGGG 1500  
 CATCAGACAG AAACCTTCCA GGCCATTACG GCGAACATC CGCCCTGCT GCTCAGCCTT 1560  
 CAGAGTCAGT TCCTTGCTCA AATGGGGTAT ATCTATACGT TCAACAAATC CGTTTCAGAG 1620  
 70 AAAGTCCCTC ATCATCTTTG GATGCAATTC GGAATATCCG AGGCAGGCAA TCTCCTGAAT 1680  
 CTGATCTATC TGGCAGCCGG CAAGAAGTAC AGCGACACCA AGAATTTCTG CGGCGTCCCC 1740  
 TTCTCTCAGT TCATCAAAGC CACGGGAGAA CTGCGCTATT CCTATACCAT AGACCGCAAT 1800  
 CAGTCACTGG CAACCGTTT CGGACAGGC GTGATATATA GCTATGGCAA TATCGAGTG 1860  
 GCACCCTATA GCGAGCAGTT CTATGTAGGC GGTGCCAATA GTATCAGAGC TTTCACCGTC 1920  
 75 CGTAGCATCG GCCCGGACG GTTCAATCCG GATTCCGACA ATCAGTATTC CTATTGGGAT 1980  
 CAGGTGGGCG AATTCAAACT CGAAGCCAAC GTGAAATATA GAGGCAAGCT TTTGGGGAT 2040

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CTCCACGCAG CCGTTTTCCT CGATGCGGGC AACGTTTGGC TCTTGAGGGA GGATTCTTCC 2100  
 CGTCCGGGCG GTGCTCTGTC CGAAGTGGGA TCGGTGAGCA ATTTCTGAA TAGCATCGCT 2160  
 CTCGGCACCG GTGTCGGGCT TCGCTACGAT CTGGCATTTC TCGTGGTTCG TGTCGATGTC 2220  
 GGCTTCGGTC TCCACCTTCC TTACAATACG GGTAAGAAAG GTTACTACAA TATCCACGC 2280  
 5 TTTAAGGATG CCATCGGTTT CCATTGGCT GTCGGCTATC CCTTC 2325

## (2) INFORMATION FOR SEQ ID NO:190

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2322
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCCTCGC ATTCCGTTTC GTATCTAATC GGCATTGCCG GCTGCTTGCT CCTCATGCTT 60  
 GCTTCCTCCT GCTCGGTAC CCGTTATGTG CCGGACGGTA GCAGACTATT AGACAGGGTA 120  
 ACATATCGCA GCGAAACGGG CAGTATCGCT CTGCCGGAAG ATATTGCGGA CTATACCCCTC 180  
 35 CAGCAACCCA ATTACAGACT GTTCGGGATG ACTCGCTGGC TACTGCGCGT CTATAGCAGC 240  
 TCGAATCCGA ACAGCAACAG CTGGTGGAAAC CGTTCGCTCC GGAATATGGG CGAACCCTCCT 300  
 GTCTCATCG ATTCTGTCCT CACGATCGT ACTGCCAACC GTCTGGCAA GGCATGGGCC 360  
 GGCATGGCT TTCTCGATGC TACTGCTCGT GCCGTGGTAG ACACCGGCTT GTACAAGAAA 420  
 GCTCGCATT CTATCTGAT TCAGCCCGGA AGCCGTTATT ATATACGCA TATGGCTTTG 480  
 40 GATGTGAAGA ATCCACTCCT TCCTCCCGTT GCGCTTGGCA ATTCGCTTCC TTCGGCATAC 540  
 AAGTTCGGGA TCAGCGAGGG TTCTCCCTTG TCGCCCATCG TACTCGATGA AGAGAGAAAG 600  
 GCGATAGCTC GTCATATGCG CAACAACGGC TTCTGGAAGT TCTCCGCCGA GGATGTTTAT 660  
 TATGAAGCAG ATACTACCGT TTCAGGAGGA TCGGGTACGA AATCTGCCGA TCTGAAATTA 720  
 GTGGTCAATG GCATCGGGCG TTATCCATAT CGGATCGGCA GGGTATTCTT TCATGCCGAT 780  
 45 TATGATCCTC TCGAATCGGA CTTCAGAGTT CAGGAGCTGC CAGGTATCGA TTCGATTTCG 840  
 CTGGCGGATT ACAGCTGTTA CTATGGGAGT AGGGGACGTT ATATCCGGGC ATCGGCTCTC 900  
 ACCCGGTCGG TGTCCGTTAC ACCGGGAGCT TTTTCTGCG AGGATGATGT GGAACGCTCT 960  
 TATATCAAGC TGAATGCGCT CCTATCGTT CCGAACGTGA ATATCCGATT TGTGGAGCAC 1020  
 AATGGTAAGG ATGAGATTGC TCTGGCGGAT AGCTCTCGCC TTGTGGACTG CTATATTCTT 1080  
 50 ACCGTTCCGG CCAAGAGCAA ATCGTTGAA GCGCAAGTCC TCGGCACCAA TTCGCTGGA 1140  
 GACTTCGGGG CCGCTTTGTC TCTCGGTTTC ACCGATCGCA ATTTGTTTCG TGGGGCGGAG 1200  
 ATGTTCAATA TCAAACTCAA GGGTGGCTTAC GAAGCCATTG GCAAGGGTTC GCACAGCTTC 1260  
 ATGGAATATG GGGTGGAAAG CTCGCTCCGT TTCCCTCGTC TCCTCTTCCC ATTCATTCTT 1320  
 GACGAAACGC GCGGGCGGCT ACGGGCATCC ACGGAATGGA AGATCGGGTA TAATTACCAG 1380  
 55 ACAGTCCCG AGTTTGATCG GGTGATTCTC TCCGCTCAAC TCAATTATTC ATGGCAGACC 1440  
 TACCTGCACA ATCGTCTGCG TCATACGATC CGCCTGCTGG ATGTGATTA TCTCCATCTC 1500  
 CCGTACATCG ATCCCGACTT CGCCCAATCC CTTCCGCTTA CGACTGCACT GTATAACTAC 1560  
 ACGGAGCAGT TTATCTCGG CTCGGCATAT ATACTGAAT ATACCAACGC TTCGTCCATG 1620  
 GAGCGTACCG TATCCAATCC TTTACGGCA CGGTTCACTA TCCAGACAGC CGGCAACCTG 1680  
 60 CTGCAAGCCA TTCTTATCT GACCGATTCT CCGAAAGACG AACACGGGTT GTATAAATG 1740  
 TTCGGTCTGC ACTATGCTCA GTTCGTCAAG CTCGATCTCG ATCTGGCTAA AACCGTTCTT 1800  
 CTCGAAAAGG ACAATACTTT GGCAGTGCAT CTGGGTTTCG GACTGGCTTT CCCTATGGC 1860  
 AATGCTCGCC ATATACCTT TGAGTTACGT TACTTTGCG GAGGATCGAA CAGCGTTCGC 1920  
 GGCTGGAGTG TCCGTACCT CGGCCGGGG AGTATGAAGA TGACTCCGA CAAGACCTTC 1980  
 65 TTCGATCAGA TGGGTGATAT TCGTCTGGAT CTGAATGTCG AATACAGGAC AAAGCTGTTT 2040  
 TGGAAGTTTC GGCAGCAGC TTTTGTGAT GCGGCAATG TCTGGACGAT AAAGGATAT 2100  
 GAGAATCAGG AGGACGGTCT CTTTGTGAT GATCGCTTCT ACAAGGAAAT AGCTTTGGCC 2160  
 YACGGTCTGG GGCTTCGTCT CGACTTCGAT TATTTCTTGT TGCGGCTGGA TGCGGAGCTG 2220  
 AAAGCTACG ATCCTCAGCA GACAGGGCGT TACAAATGGG CTATCACAG CCCAAACCTT 2280  
 70 TCTTCAATT TCGCTTGGCA CATTGCAGTA GGCTATCGCT TC 2322

## (2) INFORMATION FOR SEQ ID NO:191

- 75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2601 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc feature  
(B) LOCATION 1...2601  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191  
20 ATGAGAAAAA GAATTCTACA ACTTTTCCTG ACCGCATTGC TGCTGGCATT AGGCTCCTCT 60  
CTCGCCATAG CGCAAAACAGT GGTGACCGGT AAGGTGATCG ATTCAGAAAC GTCCGAACCG 120  
CTCATCGGTG TATCGGTAAG CACCGGTGAG GGAGCATCCC TCCGCGGTGT AACCAACCGAT 180  
ATGGATGGTG GGTTCGGATT CGAAGTACCG GCCAAATCTG TCTTGACTTT CCGTTGCGTA 240  
GGTTATGCTA CCGTAACTCG CTCTATAGGC AGAGTTTCTC AAGAAGACCT CGGTACGATT 300  
25 TCCGTCGATC CCGAGGCCAT CGGCTTGGAT GAGATTGAGG TAATAGCTC TGTGGTGCCC 360  
AAGACCGTA TGACGCCGCT ACCGTTTTC AATATCCGTG TGCTGATAT TCAGGCAGCA 420  
TCGTTGAATG TCGAATTTC CGAACTGGTT AATCCACTC CCTCTACCTA TACGACAAA 480  
GGAAGCGGAG GTTTCGGTGA TGGTCGTACC AATGTGCGTG GATTGACAC TTACAACCTC 540  
GGTGTACTCA TCAACGGAGT TCCTGTCAAT GGTATGGAAG ACGGGAAGT ATATTGGAGC 600  
30 AATTGGAGTG GTCTGATGAA TCAAGCCAGT ACCATTGAGA TTCAGCGCGG ACTCGGAGCC 660  
TCCAAGCTCG GTATCAGCTC GGTAGGTGGT ACGATGAACA TTATCAGCAA GACTACGGAC 720  
GCCAACACCG GAGGTTGCGG TTATGTCGGT ATGGGTAATG ATGGATTGCA CAAAGAATCG 780  
TTCTCCATTT CTACGGGTAT GAACGACGGT TGGGCTATCA CCATTGCAGG CTCCTCATAG 840  
ACGGGCTCGG GTTATGTGAA GGGGCTGAAG GGACGTGCAI TCTCTTACTT CTCACACGTT 900  
35 TCGAAGAAGT TCAATGAACG TCATACCCCT TCTCTTACCG GATTGCGTGC ACCACAATGG 960  
CACAAACCAAC GTTCTTCCAA ATATTCTGTA GCCGACTATG ACAAATACCG CATCCGTGAC 1020  
AATCAATCCT TCGGCTATCT GCGAGCGGAA CTGACTCCTA CGGCTTATGC TTACAATACG 1080  
TACCRAAGC CCCAGTTCTC GCTGAACCA TCTGGAAGA TGGATGAAA TACCTCTCTT 1140  
TATACGCGAN CCTACGCATC TTTGGCTACC GGTGGAGGTC GTCCGCTTA TGGAAAGAAC 1200  
40 AGTAAGTGGG TATTGATCAA CTACACACC GGACAACCT ATGAACAAAC AAAGGTGACT 1260  
CCCGATGGAC TTATGACTA CGATGCGTA CTGGCTGCCA ATGCTGCGGC GAGCAATGGC 1320  
TCGGAAGCAA TTTTGGCCCT TGGCTCCAA TCTCACAAGT GGTTCGGTCT ACTCTCTTCA 1380  
TTCAAGAGA AACTTAATAG TTCGTGACT TTGACAGCG GATACGATG GCGTTACTAC 1440  
CGTGGCGACC ACTATGACAA GATCACCAGT CTGCTCGGCG GTAGCTACTA CATAGAGGAT 1500  
45 CCCAAGACAA AGCTCGCATA CCATGCGGAA GGTGAGCAAC TGAAAGTGGG TGACATTGTA 1560  
AATCGGACT ACACAGGCGA ATCATGTGG CACGGCTCT TCGCACAGAT GGAGCATTG 1620  
TCCGAATGGA TCGATGCATT CGTATCAGGA TCTATCAACT ACGAATATA CCGCAATCAC 1680  
AACTATGGCG GTAGCAAGTC CACCGGCTAC CTGCCCGGCG TATCGCGTG GAAAGCTTC 1740  
CTTCCGTGGA GTGGCAAGGC AGGTCTGAGC TACAAGTTGG CACAGGGACA CAATGTATT 1800  
50 GCCAATGGCG GTTCTTCCAC ACGTGCAACA CTCTTTGGCA ATATCTATGC TGGGGGGGCT 1860  
ATCATTCCCA ATGACAAAGC CAATATGGAA AAGGTGCTTA CAGGAGAGGT CGGCTATGGA 1920  
TTCACGAATC ACAAACCTT CGAGTTCAAT ATCAACGGAT ACTATACGAA GTGGATGGAT 1980  
CGCGTGACCT CGAAGAGAT CGGAAACGAG TATGTTTATC TCAATGGCGT TGATGCTGTT 2040  
CACTGTGGGG TAGAGGCTGA GGTGAGCTAT CGTCTATTG GTCAGATGGA CCTTCGCGGT 2100  
55 ATGTTCTCTC TCGGTGACTG GACTTGGCAA AACAATGTAA GTTACACTTC TTACGACGAA 2160  
GCCGGCAATG AGACAGGCGA GGATATAACC TATATCAAGG GTCTTACGT CGGAGATGCA 2220  
GCACAGATGA CGGCTGCTGT ATCGGCAGAC ATAGAGCTGT TCAAGGGTTT CCATGTCATA 2280  
GGTAAGTACA ACTTCCTTGG CAAGAATAT GCAGGATTCA ACCCGCAAC CGGTAATGCA 2340  
CAGCAGTACG AAGCGGATGG CAAAGAAATC GTGGAATCAT GGAAGTTGCC CGATGTAGGT 2400  
60 CTGTTGATC TGTCTGCATC CTACAATTC AAGCTTGGTT CACTGAGCAC CACATTCTAT 2460  
TTCAACATGG ACAACGTAGC CGACAAGCGA TATGTAGCG ATGCCGACCA CAATATCATC 2520  
GGTAAGAAAC ACGATGAGGC TTGGGCTCTC GTATGGTACG GTTTCGCGCG CACTTGGTCT 2580  
ACCGGTATTC GTGTAACCTT C 2601

(2) INFORMATION FOR SEQ ID NO:192

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

15	ATGAAGTTT CAATCGGCT TTCTCTGTC ATCATCTTC TCCTCTGTC ATTTATCCTG	60
	CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC	120
	CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAATA CCAAGAAAGA CAAGCAAGAC	180
	AAACAAAGC ATCTCAACCT CCTGAACAG CAGGTTGCTC AACGCAAGCA GATCGTACAA	240
	CTCTGGACA ATGAGGTCAA AGAGTTGCAA TCCGACATTG ATTCATGAC GGGTGTATGT	300
20	CATCAGTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCCAAGC TCTACAGTCT	360
	ATGCAAAAGC GGAAACGCTC GTTGGATCGC ATCCTTTTCA TTTCATCGGC CAAGAGCTTT	420
	GACGAAGGCA TGCGACGGAT GCGTTTCTTG GAACAATACG CTTCTGCATA CAAGCTGGCA	480
	TCTGTCCGGC TGCGCGATAC ACGTAGCAAG TTGGAGACTG AACGTGCGAC TGTAAGAGAC	540
	GCCAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA	600
	GGACAGCAAG CCGAGCAACG TCGGCAGGTG CAGGCTTTGG GAGCCAAACA AAAAGACTTG	660
25	GAAGCGCAGC TCGGAAGCA GAAAAAGCAA GCGGAAGCTC TGAACAGAAA GATCGAGAAA	720
	CAGATTGCCA AGGAATAGA ACCTGCCGAA CGTCGTGCTC GAGAAGAAGC TGAACGGTTG	780
	GCACGCCAAG CCAAGGCCAA GGGTAAGCCG GTTCTTGCAG AACCGGAACG GAAGCGGAGC	840
	ACCAAGGGCG GCTATGCTAT GGATGCCCTC GAGCGTGCTC TCTCGGGCAG CTTTGACACG	900
	AACAAAGGTC GCCTGCCCGG CCCCGTTCCG GGCAGATACC GAATCGTAAG CGACTTTGGC	960
30	GTGCATCAGC ACAGTGAGCT GAAAAAGTA CAGTTAATA ATGGAGGTAT CGACATCGCT	1020
	GTAGCAACAG GATCCGATGC TACCAGCGTA TTCGATGGTG TAGTGTCCAG TGTATTCTGT	1080
	ATACCGGTTT ATAATTCCGC CGTAATGGTT CGTCACGGTA ACTATATCAC GGTTTATCGC	1140
	AATCTGAGCA AAGTGATATG AAATTCCGGC ACTCGTGTTA AAACGGGTCA GGCTCTTGGT	1200
35	CGTGCTTATA CGGATCCTTC CAACAACCAG ACCATTATTC ACTTCGAAAT CTGGAAGAA	1260
	CGCAGCAAAC AAAACCCAAG ACTATGGTTA CGA	1293

(12) INFORMATION FOR SEQ ID NO:193

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60	ATGAAAAAGT ATTTGTTATA TGCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCCTGTTCA	60
	AAGAACAATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGGTAGAT	120
	GATTTACCA AAGCGGGTGA GGCAGTACGC TATGAAGGA ATCAAGGAAG TGTGCGCGAA	180
	AGGCTCATTA CCAATCTTTA CCTCTTGTTC TTGATCAGT CAGGGGCGAA TCCGCGGAAA	240
65	TACTATATTA CCGGTAACAC TTTACCCGGA GGGACCTGGC TTCTGACGTA TATGAAGGTG	300
	AAGTTGGATA TGACACAATC CGAGGCCGGA GAGCGCAAG TATATGTGCT AGCCAATGTT	360
	GATAATCGCG TTAACACGGC TCTTGATGCT GTCGCTAACG AAAGCGATTG GCAGACTGTA	420
	AAGAGGACGA CTGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCTC GATGTCCGGA	480
	AACAGACAC ACGACTTCTT GGCCAATCGT CTTTGGACA ATGTGCCCTT TGTGCGTGCC	540
70	ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTGT GCCGATAATT	600
	GTCATCGGTA GTTTGAGTGA GTTCAAGTTC AGATACGTAA ACTTCGACAA GGAGACCTAC	660
	GTAGTGAAGC CAACGACCAA GCCGGACAAT CTCATTAGTT CTGCTAATGG TGTTTGGCCT	720
	CAGATTACAG ATTGGAATGT ATGGGGTGCT TCCTTAAATA CTTCTCTGTC TCCGGATGCG	780
	GGCAGAGGTT ATACATTGGA TGCAAATGGC AAGGTAACGG CACTACGGAT TGTACCTAT	840
75	CTGAATGAGC GCGATAGCAA ACGGGCTACG GTAGAGGTG CATTGCCCTG TGTGGATGAT	900

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GGCACCCCTTC CTCCTCCGGA ATTCGGTCCG GAGCTTTATC GTTTGCCTTT GCCGGACVAG  
ATCCTGCGCA ATCATTGGTA CAAGTATGAA GTCGAGATT

960  
999

5 (2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 945 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...945

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA	CGATACTTTC	ACGATATGTA	TCCTCGAACT	TTTGGAGTCG	GGGAGCTACC	60
TTTTTTTCA	CGATTTTCCC	GGCCTTCATC	CTCGCCGCTA	CTGCTTTGGC	GGCTTGTTGA	120
GGGGGTACTG	CTTCAGGCTC	CGATCGTACG	CTGGCTGTGA	CCATCGAGCC	ACAGAAATAC	180
TTCATCGAGT	CCATTGCGGA	TAAGTCGGTG	CAGGTGGTGG	CATTGGTACC	GGCCGGCAGC	240
AATCCGGAGG	AATACGACCC	TTGCGCTACC	GTGATGAAGC	GTITGTCCGA	AGCAGATGCC	300
TACTTCTATA	TAGGAGGACT	GGGGTTCGAG	CAAAGAAATC	TCGCTGCCAT	TCGGGACAAAT	360
AACCCCTAAG	TCCTCTTTT	CGAAATGGGC	AAAGCCTTGG	CGGATGCCCG	AAGTGCAGAT	420
CTCCACGGCT	CCTGCACAGA	TCATTCTCAI	ACAGACCTGC	ATGCCCATGA	TCCGCACTAT	480
TGGAGCAGTG	TGGTAGGGGC	AAAGGCACTC	AGTCGTGCTG	CATACGACGC	GCTTGTGGAG	540
CTTTATCCGA	ACGAGAAAGA	CAATGGGAC	AAAGGGCACG	ACCGTCTCAA	CGGACGTATC	600
GACAGCGTGA	AGAGACTCGT	CGATACCATG	TTTGCCAATG	GCAAAGCAGA	CAAAGCCTTC	660
GTCAATATAT	ACCCATCGCT	CAGCTTTTTC	GCCCAAGAGT	TCGGCCTGCG	GCAGATCGTC	720
ATAGAGGAAG	ATGGGAAAGA	GCCTACGGCT	GCCCACTTTC	GTGCTGTGAT	CGATCAGGCA	780
CGTGCCGATG	GTGTCAGAAAT	CGTATTATC	CAACCCGAAT	TTGAAACGCG	TCAGGCGGAG	840
GACATCCGAC	GCGAGATCGG	TGCTCGTCCG	GTAAGGATCA	ATCCTCTGCG	CAGCTCGTGG	900
GAGGAGGAAA	TTTTACATAT	TGCTCGCGCT	TTGGTCTATG	AACGG		945

45 (2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2544 base pairs  
50 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

65 (A) NAME/KEY: misc feature  
(B) LOCATION 1...2544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA	AAAAAATCTT	TTTTATCTTG	CTGGCGCTCA	TTGCGTTCAG	TGGGCTGAAC	60
GCAGCGACAG	ACACTGAGTT	CAAGTACCGG	ACCGATGCCA	ATATCATCGG	TCACGTCAAA	120
GACAGCAAGA	CGGGTGAACA	CCTTGTCGGT	ATCACTATTG	CTATCAAAGG	CACTACCTTT	180
GGTACATCTA	CAGATGCAAC	CGGGCACTAC	TATCTTCGTA	ACTTGCCTCC	GGGTGAGATC	240
ACTTTGATTA	TGCGTGGCAT	GGGCTATAAG	AGCCAGGAGC	GCCTAGTCCG	CGTAGAAAAA	300
GACAGACTA	TCGAGGTGAA	TTTCGAAGCA	GAAGAGGATG	CCATCAATCT	GGACGAAGTC	360
GTGATTTCGG	CCAACCGCGA	ACTGACGCTT	CGCCGTCTTG	CTCCTACTCT	GGTAAATGTA	420

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5	TTGAACGAAA AAGTCTTCTC GCAAGTCAAT GCTTCTAACC TGGCTCAAGG CTTGTCAATC 480
	CAGCCGGGAC TTCGTGTAGA GAACAACTGT CAGAACTGTG GTTTCATCA AGTTCGTATC 540
	AATGGACTGG ATGGTGGTTA TGCACAGATC CTCATCGACA GCCGTCCCAT CATGAGTGCC 600
	CTTGCCGGTG TTTACGGTCT GGAGCAGATC CCTGCCAATA TGATCGAACG TGTGGAGGTA 660
	GTACGTGGTG GAGGATCGGC CTTGTACGGT TCTTCTGCTA TTGCCGGAGT GGTGAATATC 720
	ATCACCAAGG AACCTTCTCA CAATTCTTTC ACATTCAATG AATCTCTGAG CTTTACCGGT 780
	TTCAGCAAGC TGGATAACAA CACGAACCTC AATGCCTCCA TCGTCAGCGA TGACAACCGT 840
	GCCGGTGCCA TGGTATTCCG GCAGGCTCGT TACCGCAACC ATTGGGATGC TAACAATGAC 900
	GGTTATTCCG AATTGGGTAA AATAGATGCC CGCTCGCTGG GAGCGCAATC TTATTGTGCG 960
10	TTGAGCGACT ACAGCAAATT GACGGGAGAG TTTCACACGA TCAGTGAATT CCGCCGTGGT 1020
	GGCGATCGTA TCGATTTGCC TCCTCACGTA GTGGGTGTAG CTGAACAAAC TGACCATAGC 1080
	GTATTAGCG GAAACTTGAA ATACGATCTC TTCTCTTCCA ACTATAACA CCACTTCCAG 1140
	GCTTATACTT CCGGACAGAT CGTAAATCGC AAGAGCTATT ACGGAGGTAT CGGAGAGATT 1200
	GACGTCAATG CCCACCCCGG TGGTACGGAA GGCTACCCTA TCCCTCAAGA TCAATACGGC 1260
15	AATAATTATG GCGTGACCAA AGGCAAGACA TATATGGGCG GTATCCAGTA CAGCTACGAC 1320
	TTGGACAAAT TCCTCCTCAT GCCTTCGCAA CTTTGTGTCG GAGCCGAATA TACCGGTGAT 1380
	GAACCTCAATG ACGTGATGCC CATCCTTTCA TGGCAGACCG GCGAGGATGC CAATGGGAAT 1440
	ACCATTCGCC TCTATCCCGA ATTGGATCAG AATATCAACA ACTACAGCCT ATTCGGTCAG 1500
	AACGAATGGA AAAATGACAG ATGGAGCATC CTTGTTGACG CTCGCTTGGA CAAGCATAGC 1560
20	GAACTCAAGG ATATGATTCT GAGTCTCTGT ACCACACTGC GTTTCACCGT GAATCCGGAC 1620
	ATCAACCTGC GCGCTACATA TGCAAAAGGG TTCCGCGCAC CGCAGGTATT CGATGAAGAC 1680
	TTGCACGTAG GGGTTGTAGG CCGTGAGGCA CAGAAAGTAT TCRAACGATCC GAACCTCAAG 1740
	CCTGAAATTT CTCTGTGATT CAGTTTGTAGT GCCGATATGT ATCATCGTTT CGGTAACGTC 1800
25	CAGACCAACT TCCTTGTGGA AGGCTTCTAT ACTCGTTTGC TGGATGTATT CACCAACGAG 1860
	GAGGAGCCTG ATCAGCAGCA TGGCATCAA CGCTACACGC GTATCAACGG TAGCGGAGCC 1920
	AAAGTATTCT GTCTCAATCT GGAAGGTAAG GTCGCATACA AGTCCTTCCA GCTCCAGGCC 1980
	GSTCTTACCC TGGCCAGCAA CAATACGAC GAAGCACAGG AGTGGGTCT GAATACGGTG 2040
	AAAGACACCA ACGGAGCTTT TGTACCGAG GCCAATGCAA ATGGACAAAC GGAATACAAG 2100
30	AACGAATCCA TGACGGATAC GCAGATCACC CGTACCCCCA GCGTATACGG TTATTTTACT 2160
	TTGGCCTACA ATCTGTCTCA CTCATGGAAC ATAGCCCTTA CGGGAGCATA TACCGGTGAG 2220
	ATGTATGTAC CCCACGCTAT CGAATATGGT GTGAAGTCTG CCGAACTGGA TATTATGAG 2280
	AACAATCCTG AGATTACCGA CGAAACCGGA AAGGCTCCCC GTATTGATGA GCTGAAGAAG 2340
	ACACCTGCAT TCTTCGATTT GGGCTTGAAA GTGGGTATG ACTTCCACGT ATTCCAGGCT 2400
35	ACTGAGGTTT AACTCTATGT AGGTATGAAC AATATCTTCA ACTCTTCCA GAAGGACTTC 2460
	GATCGTGGAG CTGCACGTGA CAGCGGATAT ATCTATGGTC CTACGCAGCC GCGTACAGGC 2520
	TACATGGGCT TGGTAGTGAA GTTC 2544
40	(2) INFORMATION FOR SEQ ID NO:196
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 606 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
50	(iii) HYPOTHETICAL: NO
	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
55	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...606
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196
	ATGACAGTAA AGCGCGCAGT GCGAATAGCA CTTCTCACGC TGATAGGCAT TCTTTTTC 60
	TCACCTTCTC TTGTTCCGGC GCAAAGTCTT TTCAGCACCG AACATGTCTT GCAACTATAC 120
65	AACAAGATAC TCTATGGAGA GTCGCGCGCG GATACCGTCG CAGAGAAAAC GGCAGGTGAG 180
	TCGGCATTTT CTTTATAGA CAAACTCATC AATCTCGGCC GCACTTTCCT CGGCAAAACA 240
	TATCGCTATC CCGGTCTTC CCCATGGCGG ATGGAAGTGT CCGGCTATGT GTCTTACCTC 300
	TACTCCAAAT TCGACATCAA ACTCCACGT GGTGCGGCAG CACAGAGCCA ATATACGAAT 360
	CCTATCGAGC GCGAGGATGT TCGTCCGGGC GACCTCCTTT TTTTCAAAGG CGCAATGCA 420
70	GCGAGCAACC GTATCGGGCA TGTAGCTTTG GTCGTATCTG TCGATGAAGA TGATATTACC 480
	ATGATGCACA GCGCAATTC GCGAGCGATC GTGATCGAAA AACTCAATCG CAGTGACATC 540
	TTCTCCCGTC GCTTGGTGAG CTATGGCAGG GTACCCGGAG CCAAGAGAGT GATCCACGA 600
	AAAAGT 606
75	(2) INFORMATION FOR SEQ ID NO:197



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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAAACGGA	CAATCCTCCT	GACGGCACTG	ACCGTCCTAT	CTTCGGCTCTC	CTTGCTTCGT	60
GCACAAAATG	AATCGGAAGC	ATCAACCAAT	CCGATGTCAG	GCCTCTCCCT	GGAAGACTGT	120
ATCCGGATAG	CCAAGGAGCG	CAACCTGAAT	CTGCGCAGAC	AGGAGATCGA	ACAAGAAAAC	180
CGAATCATTA	GTCTCGATGC	AGCAGGACAC	AGTTTCCTGC	CCTCGGTCAA	TGCAGGCATC	240
GGACACAAT	ATAGCTTGGG	ACGTTGAAA	GACAAAACGG	GAGTAACUGT	AGATCGCTCC	300
TCGATGATA	CCAATCTCAG	CATCGGAGCT	TCGGTGGAA	TATTCAGCGG	CACACGTGCT	360
CTGCACGACC	TCAAGCAGCA	AAAGTACAAC	GTGGAGGATG	GTATAGCCCG	ACTTCAAAAA	420
GCGCGTGAAG	ACCTCAGCCT	GCAAAATCGCG	GCTCTCTATA	TCAATTGTCT	CTTCCGTCAG	480
GAAATGACTC	GTACGGCAGA	AACACAGTTG	GCACTGATTC	GCGAGCAACG	CAATCGCACG	540
GCCGAAATGG	TTCCGCTAGG	TAAATGGGCA	GAGGGTAAGC	TCCTCGACAT	AAATGCCGAG	600
ATGGCCAAGG	ACGAACAAC	TCTCGTACAA	TATCGTTCCG	AGGAGGAGCT	GGCTCGTCTG	660
GACTTGGGGC	AAGCCCTCGA	ACTGGAGCAC	CCCGAAAGCA	TTGCAGTCAA	GGCTCCCGAC	720
ACAGACGTTT	TCGTAGCAGA	AAGGTTGGGA	TCTCTCCTTG	CTCCCGAAGA	GATCTATCGC	780
ACGGCTCTCG	GCTTGAAACC	GGCACTGCAT	TCGAGCGAGC	TGCAAAATAGC	TTCCGCACGC	840
GAAAGTCTGG	CCTCGGCTCG	TGCGGCATAC	TTCCCGACGC	TCAGCCTCTC	TGCCGGATAC	900
AGCAACGGTT	ACTTCGCGA	CCTCGGCAAG	GAGTATGCCG	CCATCAACCC	CTCCTTCTCC	960
GAACAGTGA	AGAACAACGG	CAGCTACAGT	ATCGGACTCT	CTTTGAATAT	CCCATCTTTC	1020
TCTGCCATGC	AAACGCAAGA	TGCGGTTCCG	AGCAGTCCGC	TGCAAAATAGC	CTCAAGCGAG	1080
CTTCGACTCG	TCGAAGAGAA	AAAAGCCCTC	TATTAAGAGA	TCAGGCAAGC	ATACAGCAAT	1140
GCCGTGGCAG	CCGATAAGGC	CATCGCAGCA	GCCGAAAACA	GCAAGGCCGC	TACGCTCAAG	1200
GCAIACGAAT	ACGCTCGCGA	CAGCTTCGAG	GCAGGGCGCT	TGTCTGCCTA	CGAATATGCC	1260
GAGGCAAAAA	CAAAATACGC	CCTCAGCCAA	GTGGAAGAAC	TTGCTGCCAA	GTATGACTTC	1320
ATATACAAAG	CCAAAGTTT	GGATTCTTAT	CAGGGCAAG	ACTTC		1365

(2) INFORMATION FOR SEQ ID NO:198

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC	AACATTATCT	CATCTGTACG	GCTGCCGTAG	CGGCTTTGGC	TGCGAATCCC	60
CTTACGGGCC	AATCGAATAT	GACCTCGAA	GAGTGACATG	ACTATGCACG	CCGGCACAGT	120
TCGGCCGTGG	CGCTGTCCGC	TGCGGAAC	GAGCAGTCCA	AGGCCGATTA	CCTTCAGGCC	180
GTCGGCAATT	TTCTGCCCCG	TGTATCGGCC	GGAACCGGTG	CTTCGTGGAA	TTTCGGACGC	240
GGATTGGATG	CCGAGACGAA	TACCTACACC	GACATCAACA	GCTTCAACAA	TTCTACACG	300

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	ATACATGCCA	CGATGACCTT	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGGATGGGG	360
	CATGCACGGC	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420
	GGCACCACGG	AGGCGTACTA	CGAOCCTCGT	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
	CAGAAGTACG	AGGAGAGCAG	CCGCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
5	ATGAAGATGC	GTCCCGATGT	CCTCGAGATG	CAGTCGCGAA	TGGCCGGTGA	CCGTTTGGCC	600
	CTGACTCAAG	CGGACAATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
	TTCCCATCG	ATGACGAAT	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
	ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTGCCCGGTG	CTGCCCATCA	TCATCCCGTC	780
	CTCCTCGGTG	CCAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTCGCGAGC	CGCGCGAGGT	840
10	GCATTCCTGC	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACGCTTTTTC	900
	AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAAATACGTC	960
	ACTCTGAATC	TGAGTATCCC	CATCTTTTTC	GGATTCAGCC	TTGTGAGCCA	TCTGCGTCAG	1020
	GCGCGTGGCG	AACGCAGGGC	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
	AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCTTA	CCGCCAGGCG	1140
15	AAGGAGCATA	CCGACGCCAT	GCAAAACCGCT	TACGAAGCCG	TCTTGACGCG	TTATGAGGAG	1200
	CGGCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCGGTGT	1260
	CAGCGACTGA	GAGCGCCAT	GACCTACCGG	CTCAAATGCA	AACTCATAGC	CTATTACGGC	1320
	TGCCTTTTCG	AC					1332
20	(2) INFORMATION FOR SEQ ID NO:199						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2820 base pairs						
25	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
30	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
35	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
40	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2820						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199						
45	ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCCTTCGT	GTTCATGGCA	60
	ACTGCACTGA	CGGCTTCTGC	ACAGATTTTC	TTCCGAGGGG	AACCCCTTGA	TTTCTCTTCA	120
	AGATCCGTCG	GAACGCATTTC	ATTTCGACGAT	GCAATGACTA	TCCGCTTAC	TCCGGATTTC	180
	AATCCGGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGGCCCGTC	240
	CGGATAGGAC	AAGTAATACC	GCTGGATGTG	GACTTTGCAT	CCAAGGCTTC	GCACATCTCT	300
50	TCCATCGGAG	ACGTAGATGT	ATATCCGCTG	CAATTCAAGT	TGGAAGGAGC	CAAAGCCATT	360
	ACGCTTTATT	ACGATGCATT	CAATATTCCT	GAGGGCGGAC	GCCTCTATAT	CTATACCCCC	420
	GACCATGAAA	TTGTCTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
	GCCACAGAGC	CGGTACCGGG	GAGTGAGCTT	ATTATGGATT	ATGAAGTGTC	TGCGGAGGGG	540
	ACTTTGCCCTG	ACATCAAGAT	CTCCGCTGCG	GCTTATATAT	TCGACAAAGT	CGGCGGACGC	600
55	CCCGTACCGG	ATAACCAATTA	CGGGATCCGT	GAGGACGATT	CCGATTCCGA	TTGCGAGATC	660
	AACATCAATT	GTCTGTAAGG	TGCAGACTGG	CAGGCAGAGA	AGAAGCGGTG	GGTGCAAAATG	720
	ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATAAGAAA	780
	GGAGACTTAA	CTCCGCTGAT	CATTCTGCCC	GGACACTGTG	CTTCCATAAC	AACCAATTTC	840
	GGTGTAACGC	AATCCGAGTT	GGATAAGTGG	ATCTTCACTT	TCCACTATGA	MAAAGAGGA	900
60	TGCAGCAATG	GTACATTGGC	CATCTTCGTG	GGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
	GCTTTCTCTC	CGATCAAGG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
	CCTCTGCGCT	ATCGTGTCTA	TTACAATGGA	TGGGACAGTA	CGCCCGATAT	TCCCTCGAGC	1080
	GGTCCCGGTA	TTATCATCC	GGCCGGAGAT	GCCATGAAGA	TTCCATCTCT	AAAGAAGACT	1140
	CCGCTCTGTA	ATACATGGAT	CTCCTCCAGT	GGTCCGGAG	GGACTGACGA	TCACTTCTAT	1200
65	TTCAAAATCG	ATCAAGGTGG	TACGGAAGGA	GGATCCTCCG	GTCTTCTCT	CTTCAATCAG	1260
	AATAAGCAGC	TGGTCGGCAC	ACTGACCGGA	GGTGCCCGCA	ATTGTGGCGG	GACGGAGTTC	1320
	TACGGCAGAC	TGAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCGCATG	1380
	GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
	GACGGTTATA	AGCCTTTGCC	CTCTGTGCC	GGGCTATTGT	TGCACTCTAT	AGGCGATCAG	1500
70	GTGCAATTGA	ATTGGACGGC	TGTTCTCTGC	GATCAATATC	CATCATCTTA	TCAGGTGCGA	1560
	TACCACATAT	TCCGAAATGG	AAAGGAATA	GCTACGACAA	AGGAGTTGTC	CTATTCCGGAT	1620
	GCCATCGAGC	AAAGTATTAT	CGGTAGCGGT	ATCATTTCGAT	ACGAAGTAA	CGCACGCTTC	1680
	ATTATCCCTT	CGCCGTTGGA	TGGAGTGGAA	TCTTATAAGG	ATACGGACAA	GACTTCTGCC	1740
	GACCTTGCCA	TAGGAGACAT	TCAGACCAAG	CTGAAGCCGG	ACGTAACACC	TCTCCCGGGA	1800
75	GGAGGAGTAT	CATTAGCTG	GAAAGTTCCT	TTCTTAAGCC	AGTTGGTTTC	CCGATTCGGA	1860
	GAAAGCCCCA	ATCCTGTGTT	CAAPACCTTT	GAAGTGCCCT	ATGTTCTTCG	CGCAGCCGCA	1920

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5 CAAACCCCA ATCTCCCGT TGGCGTAGTC ATTGCAGACA AGTTTATGGC CGGTACATAT 1980  
 CCCCAGAAAGG CTGCTATCGC TGCCGTTTAT GTAATGCCAT CCGCTCCGGA CTCTACTTTC 2040  
 CACCTCTTCC TCAAGAGCAA CACAAACAGA AGATTGCAGA ASGTGACAA CCCCCTCCGAT 2100  
 TGGCAGGCCG GAACATGGTT GAGGATCAAT TTGGATAAGC CGTTCCCGGT GAATAATGAC 2160  
 CATATGCTTT TTGCCGGTAT CAGAATGCCT AATAAGTACA AGCTCAATCG TGCTATCCGT 2220  
 TATGTAAGAA ATCCGGATAA CCTTTTCTCC ATTACCGGTA AGAAGATTTC ATATAACAA 2280  
 GGAGTCTCTT TCGAAGGCTA CGGAATACCC TCGCTCTTGG GCTATATGGC TATCAAAATAT 2340  
 CTGGTGGTAA ATACCGATGC TCCGAAGATC GATATGTGCG TTGTACAGGA GCCTTATGCT 2400  
 10 AAGGGAACGA ATGTGGCTCC ATTCGCCGAA TTGGTCGGCA TATATGTCTA TAAGAACGGA 2460  
 ACATTTATCG GCACACAGGA TCCATCCGTC ACAACTTATT CGGTTTCAGA CGGAACAGAG 2520  
 AGCGATGAAT ACGAAATAAA ACTGGTATAT AAGGGATCGG GCATTTCGAA TGGCGTTGCT 2580  
 CAGATTGAGA ATAACAATGC TGTCGTTGCA TATCCGCTCG TTGTAACAGA TCGTTTCAGC 2640  
 ATTAAGAACG CTCATATGGT TCACGCTGCC GCCCTCTACT CATTTGGATGG CAAGCAGGTT 2700  
 CGTTCTTGGA ACAACCTCCG CAATGGCGTG ACATTGAGTG TTCAAGGACT TACGGCCGGT 2760  
 15 ACTTATATGC TCGTTATGCA GACGGCAAA C GGCCTGTGA GCCAAAAGAT CGTGAAGCAG 2820

## (2) INFORMATION FOR SEQ ID NO:200

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2010  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAATATC TTATCAGACT CTCTTATCA TTGATGTTAC TCTCTCTCG GACGGGCTGT 60  
 ACACACGAGG AGCTCTCTAT TTGCGATGGC GAGAATACGC TTGTTTACG CGTAGAGACC 120  
 GGTAAAGCCC CAAATGCTCG TGCCACAGAA CCGGTCAGG GCATATACAA TGAGAATAAA 180  
 GTAGGCTCCA TTTCTGTGCT CTCTATTTA GAGGGACAAC TTCGTTGGCA GGTGAAGTCT 240  
 45 ACAGACTATC AAATCCATGA AGGGGCTAT ATCATTCCGG TCAAAGAGCA AATGCGACCA 300  
 CTATTCAATG GCAACAACAA CTTCAGCATC TATGTAGTGG CCAATCTCGA TTTCAATGCT 360  
 CCGGCACAGC AAGCTGCGCT TTCTCAATTT GTGGTAGAGA AATCTATTGA AGTCTCTTCT 420  
 ACGACAGCCC CTGCCGATTT CGTAATGCTT GTCATGGCA ATAAGCAGAT CAATATGGCT 480  
 ACGACAGAGG SGAAACTGTT GGGGGATTAT AAATCAAAC GAGTGGCAGC AAAGATTCCG 540  
 50 ATGATAAAAC CCACCATCAA TGTGCRAGGA TATGAAGTGG TCGGAAATAT ACAGGCAAG 600  
 TTTGCAATTT CGGTAACGAA GGGGTTCTTT ACCACAGAAG CTCGAAGAGAT CCGAGCTGCT 660  
 GCATCCTATA AGACATCGGA ATATCTTGAT ATTGCAGAGT CGGCACCTGC CAATTCTATC 720  
 CATTCTATT CTACTATAA CAAATGGACA CTCTCCACAC CGGAGAAGCG ACCGGAATTC 780  
 55 TTATCATGCG TCAAATTCAA AAAGACAGGA CAGCCGACAC ACACAGCCAA ACCGTACTAC 840  
 TACAGAGTGC CCTCGAATC TCAGGACAAT CAGGTCAAGA GCAATGTCTT CTATAATCTG 900  
 AATGTGAAAA TCGAATCTTT GGGTTCTTTA CAAGAGCCGG AAGCTGTTTC TGTAAACGGC 960  
 ACACTCGCAA TAGAAGATG GATTCTCCAT CAGGATGCAT TCAATCTGCC TGCCACCAAT 1020  
 TACTTGATAG TGGACAGCA CGAAATCTTC ATGAATAACG TGAACACATA CTCGGTGAAA 1080  
 60 TATCAAACTT CGCAGAAACC AATCAGCATT AGCATACAGT CAGTTACCTT TAGCTAOGTC 1140  
 TCTTCTGATG GCACTCAGCA CAATGATCTT GTAGCAAGTA GTAGCGACCA GTATCCTACG 1200  
 ATTACAAGCG ATAATACAAG CATCATAATC ACTTCCAAGA TACCGTTAA TAACGTACCA 1260  
 AAGAAGATCG TTTTGTAGGT AACTAATGGG GTAGCCGTTT TGAAGAGAC TGTACAGTA 1320  
 CTCCAATATC CTGCACAATT TATTGTCAAT ACACTTGGCA CAGCATCGGC ATGGAGACCA 1380  
 GACGGATCTT TGGCTCCGGG GCTTAACAAT AAAGCGATTT ACCATGTCGT AGTACTGGTT 1440  
 65 CCACCCGAGA ATTTATTTGA AGATGGGACA CAGACAATCA TCGGTTATCC CCCCCTGAA 1500  
 ACAATTTCTT TTCATAAGAA AGAGAACAAT ACCTATCCGA TAGTATGGTC TGACACAAAT 1560  
 ACGACAAAC AGGACCTTGA GACATCAAGA ATGATTTTAC CTTCCTTTGA GTTAGCCTCC 1620  
 CAACCTGGGG CTACTCTCCC GATGCCCTAT CTCGAGTATT GGCCAGGGAC ATCATATCTC 1680  
 70 CTGTACTATT CGGGAACTA TAATAATAAG AGATACGCTT TGTTAATTG CGCTTTTAC 1740  
 TGGGAGAAAA GAAAAGTTAA TAACGAAGAA ATTAATTCG ATGACTGGCG TTTGCCGACA 1800  
 GAAGCTGAGA TCAAATTGAT AGATAAGCTG CAACATAATG AGCAGAGTGC TGTCCAAGCT 1860  
 ATCATGACAG GGAATTATTA TTGGGATAGT TACTCTGCAA ATGGGTCTTA TAAATGCAA 1920  
 GGAGGAGGGG GCAAGGAAA TTCTCCAAA GCCTATGTTT GTTGGCTGCG GGATGTGAA 1980  
 75 AAGCCGATTC GTGACAACAA GTCAGGTAAG 2010

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## (2) INFORMATION FOR SEQ ID NO:201

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3846
- (x) SEQUENCE DESCRIPTION: SEQ ID NO:201

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25  ATGCGAAAAA TTTTGAGCTT TTTGATGATG TGCCTCTGCG ATTTAGGTCT ACAATCTCAG      60
    ACTTGGCATTG GAGATCCGGA CTCAGTGGCA GCCCTACCTT CTATCGGTAT TCAAGAGTCA      120
    AGTTGTACCC GAATCACGTT CGAGGTTGTT TTCCCGGGAT TTTATAGTGT GGAAAAACGA      180
    GAAGGCAACC AAGTCTTTCA GCACATTTC ATGCCGGGTT GTGGCTCCTT TGGGAATCTG      240
    GCGGAAGCTG AATTGCCTGT TTTGAAAAAG ATGATAGCCG TTCGGGAATT TTCAACAGCT      300
    AACGTTGCTG TAAAAATCAA AGAGACGGAG ACATTCGACA ATTATAATAT CTATCCTAAT      360
    CCTACCTATG TCGTAGAGGA GTTGCCCTGAG GGGGGGACTT ATCTGGTAGA GGCTTTCCGG      420
    ATAAACAATG ACTATTATAG CCAAAATGTA AGCCTCCCTT CTACTCACTA TGTCTATTCT      480
    CAAGACGGGT ATTTTCGCTC ACAAAGATTT ATCGAAGTTA CCCTGTATCC TTTTCGATAC      540
    AACCTCTGCC GACAAGAAAT TCTATTTGCA AAAAAAATCG AGGTTACAAT AACTTTCGAT      600
    AATCCTCAGC CACCTTTACA AAAAAACACC GGCATATTTA ACAAAGTAGC CTCCTCTGCA      660
    TTTATTAATT ATGAAGCTGA TGGCAAATCG GCGATAGAAA ATGATATGGT GTTCAGTCTG      720
    GGTACAACAA CGTACATAAG CGGAAATGTT GCCAGCAACC TCCTCAGAAA CTGTGACTAC      780
    TTGGTTATTT ACGATGATAT GTTCAACGTA AATCAACAAC CACACGACGA AATCAAAACGG      840
    CTGTGCGAAC ATAGAGCCIT CTACAACGGC TTTGATGTAG CTGCTGTAAG TATAAAGGAC      900
    GTATTGAATA GCTTCCCATC AAATGCCACC TCATACATCA ACGAAACTAA ACTGAAAAAT      960
    TTCAITCGCT CAGTTTACAA CCAAGCAAT GCGAAGAGGA CTTTAGATGG CAAACTGGGA      1020
    TACGTGCTAC TGATCGGAAA ACCATTGAGC AAATATTGG CTGACACTGA TAATACAAAA      1080
    GTCCCAACCT CTTTATTCA TAATGTCTCC TTAATCCAA GTCACTCAAC TTTTGGTTCC      1140
    ATATGCGCCT CCGACTATT TTTAGTTGT GTTTCGCCCC TTGATACTGT CGGCGATTG      1200
    TTTATCGGTC GATTAGCGT CACCAATGCT CATGAATTGC ACAATCTGAT TGAAAAGACT      1260
    ATCAACAAAG AAATCTCATA TAATCCTATT GCACACAAAA ATATTCTTTA CGCAGAAGGG      1320
    AAAGGCTGCC ATGCTCCAAT CTACGTTTA TTCTTAAAG AAATCGCCTC TGGTTACACA      1380
    GTCAACTCTA TCTTAAATC TAATCAGGTC TCTGCAATAG ACTCGATATT TGACTGCTTG      1440
    AATAATGGTT CCCATCATT TTATTTTAAC ACTCATGGAA TGCCGACTGT TTGGGGGATA      1500
    GGGCAGGGAC TCGACGTCAA TACTCTAACA GCCCGATTGA ACAATACATC TTCGCAGGGA      1560
    TTATGTACGA GTCTATCATG TAGTTCCGCT GTAGCAGATT CAACTATTAG ATCGCTTGGA      1620
    GAAGTCCTGA CCACATACGC ACCTAACAAAG GGATTCTCGG CTTTCTTAGG AGGAAGCAGA      1680
    GCCACCCAAAT ATGCCGTTTA TTTAGAAGGC CCCTGTCTCT CGTCAGAATT TTATGAATAT      1740
    TTACCTTATT CTTTATATCA CAATCTCTCG ACTGTTGTG GCGAAATGTT GCTATCATCC      1800
    ATTATCAATA CTAATTCTGT TGATACGTAT TCGAAATTCA ACTTCAATTT GCTTGGCGAC      1860
    CCTGCACTAA ACATTATGGC TCATGGCATG GAGGTTAGTA ATTGTATTAC ACTACCAAAC      1920
    AACACCATTA TAAGCAGTCC GATAACAATA AAAAATGGTG GCTGCCTAAA AATACCGGAA      1980
    AAAGGAGTTT TGCATTTTAC TAATAATGGC TCCATACAAG TCATGTCCCG AGGAACTCTG      2040
    GAAATAGGCA ATCAGGCTAA AATATCCGGA GAGACCGGTG CTAACCCAC CTTTATTACC      2100
    GTTTACGSCG ATGGTCTTGC GATTACAAG CAGGTAGAGA TAGACAATAT AGACCGACTT      2160
    AACTGTGTTT CTACGCATTC GGTCAATGCC AAATTTCAAT TTGACAGTGT GAAATTC AAC      2220
    CGAATGACA TTATTTCAAA GAATTGTGAC CTAAGCGTTG AAAACAGTAT GTTTAGCAAT      2280
    TCGGGGATAA CGGTATTCAA GCCTATGGCT ACAAGCTCCA TCACCGGATT ATCTACAAAA      2340
    GCAAAGATTA CCGACAATAC TTTTTTGGC ACAGGAACT TCGCTACCA TATCACAAAC      2400
    ACGCCAGGCT TAACAGCAAC CTCCAATGCT GCCATCAAGT TAGACAATAT TCCTGAGTAT      2460
    TACATTTCCG GTAATAAAAT AGTCAATTGC GATGAGGCTC TTGTACTAAA TAATAGTGGC      2520
    AACAGAACGA ACAGACTCCA CAATATCACA CGGAATGTGA TAAAAAATCG TAGGATTGGG      2580
    ASCACGCTTT ATAATTCCTA TGGTATTTAC AACCGAAATA AGATCAGTAA CAATCATATA      2640
    GGAGTACGTC TCCTCAACAA CAGTTGTTTT TATTTCGATA ATGCTCCTGT AATCAATGAA      2700
    GAAGATAAGC AGACGTTTAT TTCTAATAGG ACTTGGCAGC TCTATTATC AAACGGTACA      2760
    TTCCCTCTCA ACTTCCATTA CAACAGCTTC CAGGGGGGAG ATACAGATAC ATGGATTTAC      2820
    AACGACACGT ATACGAATCG CTATATTGAC GTTTCAAATA ATCACTGGGG CAACAATGAT      2880
    TTGTTTGATC CGAATCAGGT TTTCAATACG CCAGACTTGT TCATTTGGAT ACCTTTTGTG      2940
    GATGGATTGC CAAATGGGAG ATCGGGCAAT AGCTCTGCTG AAGCAGTAGA ATTCCAAACA      3000
    3060
  
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SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

137/490

5	GCATTGGACT	GTATTGGCAA	TAGCGATTAT	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	3120
	GTTGAAACCT	ACCGGGAATC	CGACTTTGCA	ATAGCTGCCT	TGAAGGAATT	GTTTCAGGATA	3180
	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	TTGAAAGAAT	ATTTTCAGATC	CAATCCAACC	3240
	ATCATCTCTT	CCCAGAACTT	GTTCCCGACA	GCTGATTTCC	TGTCGCGCG	ATGCGATATT	3300
	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	TGGTACGAAA	ATCGCTTGAA	TAGTGAATC	3360
	TCCTATCAGG	ACAGTGTITT	TGCAGTCATT	GACCTTGGTG	ACATTATATG	GAATATGCAG	3420
	TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	TTGAACATAC	TTTCCTGTGA	ACAAAGGAAA	3480
	TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	TATTTGTTGT	CAACTCTTCC	CGAATCAACA	3540
	GGTACTCTCC	TGCTCCATT	AGAATGCAAC	AAATCAAGCC	TTGATAAATC	CAAGATAATC	3600
10	TCTATTTGCG	CCATTCGGGC	GAAAGCTGTT	GTAACAATAA	TCTACTATAC	CGATAACCTT	3660
	TCCTGTTCTG	TAATAAAAAAT	ATATGGAATA	AATGGAGCCT	CGGCTGATAT	AACCGGGTTG	3720
	CCCAACATC	TATCCGAAGG	TTATTACAGC	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	3780
	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	CAGAAAAATTA	TAGATACGGA	AAAATTACGA	3840
15	ATCAAA						3846

## (2) INFORMATION FOR SEQ ID NO:202

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...3822

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

40	ATGATGTGCT	CTCTGCATTT	AGGTCTACAA	TCTCAGACTT	GGCATGGAGA	TCCGGACTCA	60
	GTGGCAGCCC	TACCTTCTAT	CGGTATTCAA	GAGTCAAGTT	GTACCCGAAT	CACGTTCCGAG	120
	GTTGTTTTCC	CCGGATTTTA	TAGTGTGGAA	AAACGAGAAG	GCAACCAAGT	CTTTCAGCGC	180
	ATTTCCATGC	CGGGTTGTGG	CTCGTTTGGG	AATCTGGGCG	AAGCTGAATT	GCCTGTTTGT	240
	AAAAAGATGA	TAGCCGTTC	GGAAATTTCA	ACAGCTAACG	TTGCTGTAAA	AATCAAAGAG	300
45	ACGGAGACAT	TCGACAATTA	TAATATCTAT	CCTAATCCTA	CCTATGTCGT	AGAGGAGTTG	360
	CCTGAGGGGG	GGACTTATCT	GGTAGAGGCT	TTCGCGATAA	ACATGACTA	TTATAGCCAA	420
	AATGTAGCC	TCCCTTCTAC	TCATATGTC	TATTTCTAAG	ACGGGTATTT	TCGCTCACAA	480
	AGATTATCG	AAGTTACCCT	GTATCCTTTT	CGATACAACC	CTGTCGACA	AGAAATCTA	540
	TTTGCAAAAA	AAATCGAGGT	TACATAACT	TTTGATAATC	CTCAGCCACC	TTTACAAAAA	600
50	AACACCGGCA	TATTTAACAA	AGTAGCCTCC	TCTGCATTTA	TTAATTATGA	AGCTGATGGC	660
	AAATCGGGGA	TAGAAAATGA	TATGGTGTTC	AGTCGTGGTA	CAACAACGTA	CATTAAGCGGA	720
	AATGTTGCCA	GCAACCTCCC	TCAGAACTGT	GACTACTTGG	TTATTTACGA	TGATATGTTT	780
	AACGTAAATC	AACAACCACA	CGACGAAATC	AAACGGCTGT	GCGAACATAG	AGCCTTCTAC	840
	AACGGCTTTG	ATGTAGCTGC	TGTAAGTATA	AAGGACGTAT	TGAATAGCTT	CCCATCAAAAT	900
55	GCCACCTCAT	ACATCAACGA	AACTAACTG	AAAAATTTCA	TTGCTCAGT	TTACAACCAA	960
	AGCAATCGGA	AGAGGACTTT	AGATGGCAAA	CTGGGATACG	TGCTACTGAT	CGGAAAACCA	1020
	TTGACCAAAAT	ATTTGGCTGA	CATGATAAT	ACAAAAGTCC	CAACCTCTTT	TATTCATAAT	1080
	GTCTCCTTAA	TTCCAAGTCA	TCCAACCTTT	GGTTCCATAT	GCGCCTCGA	CTATTTTTTT	1140
	AGTTGTGTTT	CGCCCTTTGA	TACTGTGCGC	GATTGTGTTA	TGCGTGCATT	TAGCGTCAAC	1200
60	AATGCTCATG	AATTGCACAA	TCTGATTGAA	AAGACTATCA	ACAAAGAAAT	CTCATATAAT	1260
	CCTATTGCAC	ACAAAATAT	TCCTTACGCA	GAAAGGAAAG	GCTGCGATGC	TCCAATCTTA	1320
	CGTTTATTCT	TAAAAGAAAT	CGCCTCTGGT	TACACAGTCA	ACTCTATCTT	AAAATCTAAT	1380
	CAGGTCTCTG	CAATAGACTC	GATATTTGAC	TGCTTGAATA	ATGGTTCCCA	TCATTTTAT	1440
	TTTAACAATC	ATGGAATGCC	GACTGTTTGG	GGGATAGGGC	AGGGACTCGA	CGTCAATACT	1500
65	CTAACAGCCC	GATTGAACAA	TACATCTTCG	CAGGGATTAT	GTACGAGTCT	ATCATGTAGT	1560
	TGCGCTGTAG	CAGATTCAAC	TATTAGATCG	CTTGAGAAAG	TCCTGACCAC	ATACGCACCT	1620
	AACAAGGGAT	TCTGCGCTTT	CTTAGGAGGA	AGCAGAGCCA	CCCAATATGC	CGTTTATTTA	1680
	GAAGGCCCTT	GTCTCCGCTG	AGAAATTTAT	GAATATTIAC	CTTATTCTTT	ATATCACAAT	1740
	CTCTGACTG	TGTTTGGCGA	AATGTTGCTA	TCAATCCATT	TCAATACTAA	TTCTGTTGAT	1800
70	ACGTATTGCA	AAITCAACTT	CAATTTGCTT	GGCGACCCTG	CACATAACAT	TATGGCTCAT	1860
	GGCATGGAAG	TTAGTAATTG	TATTACACTA	CCAAACAACA	CCATTATAAG	CAGTCCGATA	1920
	ACAATAAAAA	ATGGTGGCTG	CCTAAAAATA	CCGGAAVAAAG	GAGTTTTGCA	TTTTACTAAT	1980
	AATGGCTCCA	TACAAGTCAT	GTCCGGAGGA	ACTCTGGAAA	TAGGCAATCA	GGCTAAAAAT	2040
	TCCGGAGAGA	CCGGTGCTAA	CCCCACCTTT	ATTACCGTTT	ACGGCGATGG	TCTTGCGATT	2100
75	AACAAGCAGG	TAGAGATAGA	CAATATAGAC	CGACTTAAC	TGTTTTCTAC	GCATTCCGTC	2160

WO 99/29870

PCT/AU98/01023

138/490

5	ATGCCCAAAT	TTCATTTTGA	CAGTGTGAAA	TTCAACASTG	CCCCGCTGTA	TACAACGAAC	2220
	TGTATTTGTG	AGATAAGCAA	TTGCGAATTT	ACCAATCGAA	GTGACATTAT	TTCAAAGAAT	2280
	TGTGACCTAA	GCGTTGAAAA	CAGTATGTTT	AGCAGTTCGG	GSATAACGGT	ATTCAAGCCT	2340
	ATGGCTACAA	GCTCCATCAC	CGGATTATCT	ACAAAAGCAA	AGATTACCGA	CAATACTTTT	2400
	TTTGGGACAG	GAACCTTCGC	CTACCATATC	ACAAACACGC	CAGGCTTAAC	AGCAACCTCC	2460
	AATGCTGCCA	TCAAGTTAGA	CAATATTCCT	GAGTATTACA	TTTCCGGTAA	TAAAATAGTC	2520
	ATTGCGATG	AGGCTCTTGT	ACTAAATAAT	AGTGGCAACA	GAACGAACAG	ACTCCACAAT	2580
	ATCACACGGA	ATGTGATAAA	AAACTGTAGG	ATTGGGAGCA	CGCTTTATAA	TTCCTATGGT	2640
10	ATTACCAACC	GAATAAGAT	CAGTAACAAT	CATATAGGAG	TACGTCTCCT	CAACAACAGT	2700
	TGTTTTTATT	TGCATAATGC	TCTGTAAATC	AATGAAGAAG	ATAAGCAGAC	GTTTATTTCT	2760
	AATAGGACTT	GGCAGCTCTA	TTCATCAAAC	GGTACATTCC	CTCTCAACTT	CCATTACAAC	2820
	AGCTTGACGG	GGGGAGATAC	AGATACATGG	ATTTACAACG	ACACGTATAC	GAATCGOTAT	2880
	ATTGACGTTT	CAATAATCA	CTGGGGCAAC	AATGATTTGT	TTGATCOGAA	TCAGGTTTTC	2940
15	AATACGCCAG	ACTTGTTCAT	TTGGATACCT	TTTTGGGATG	GATTGCCAAA	TGGGAGATCG	3000
	GGCAATAGCT	CTGCTGAAGC	AGTAGAATTC	CAACACAGCAT	TGGACTGTAT	TGGCAATATC	3060
	GATTATCTTT	CGGCAAAAGT	GGCTCTCAAG	ATGATGGTTG	AAACCTACCC	GGAATCCGAC	3120
	TTTGCAATAG	CTGCTTTGAA	GGAATTGTTC	AGGATAGAGA	AAATGTCAGG	CAACGATTAC	3180
	GAAGGCTTGA	AAGATTATTT	CAGATCCAAI	CCAACCATCA	TCTCTTCCCA	GAACCTGTTC	3240
20	COGACAGCTG	ATTTCTCTGC	TGCCGCGATG	GATATTGTGT	GTGAAACTA	TCAGTCTGCC	3300
	ATCGATTGGT	ACGAAAATCG	CTTGAATAGT	GAAATCTCCT	ATCAGGACAG	TGTTTTTGCA	3360
	GTCAATTGACC	TTGGTGACAT	TTATTGGAAT	ATGCACTTAG	ACTCACTCAG	AGGGACTGGT	3420
	ATAGATTTGA	ACATACTTTC	CTGTGAACAA	AGGAAATCGC	TCGAAAGCCA	TCRAAATGTA	3480
	AAAAATTATT	TGTTGTCAAC	TCTTCCCGAA	TCAACAGGTA	CTCTCTGCC	TCCATTAGAA	3540
	TGCAACAAAT	CAAGCCTTGA	TAAATCCAAG	ATAATCTCTA	TTTCGCCCAA	TCCGGCGAAA	3600
25	GCTGTTGTAA	CAATAATCTA	CTATACOGAT	AACCTTTCCT	GTTCTGTAAT	AAAAATATAT	3660
	GGAATAAATG	GAGCCTCGGC	TGATATAACC	GGGTTGCCCA	AACATCTATC	CGAAGGTTAT	3720
	TACAGCATAC	AGTTCAATAC	ATCCAACTTT	GATCCCGGTT	TCTACCTGGT	AACGCTAAAT	3780
	GTTGATCAGA	AAATTATAGA	TACGGAAAAA	TTACGAATCA	AA		3822
30	(2) INFORMATION FOR SEQ ID NO:203						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2775 base pairs						
35	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
40	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
45	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
50	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2775						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203						
55	ATGGCTATCA	TGATGAAAAG	TATTGTTTTT	AGAGCATTTC	TAACGATTTT	GCTCTCGTGG	60
	GCAGCGATCA	CGAATCCGAC	TGCTCAAGAG	ATCTCAGGCA	TGAATGCATC	CTGTCTGGCT	120
	GCTCAGGCTC	AACCGGATAC	TATCTTATAT	GAAAGTTTTG	AGAATGGACC	TGTTCCCAAT	180
	GGCTGGCTTG	AGATAGATGC	TGATGCTGAT	GGTGCCACTT	GGGGAAGCCC	ATCAGGCTCT	240
	TTCTCTGTAC	CTTACGGACA	CAATGGCCTT	TGCACCTACT	CCCATATACG	TTCCGGTATC	300
	TCAACAGCGG	GCAACTATCT	GATTACACCC	AATATAGAAG	GAGCCAAACG	GGTCAAGTAC	360
60	TGGGTATGCA	ATCAGTATAG	TACCAATCCG	GAACATTACG	CAGTAATGGT	ATCGACAACG	420
	GGGACTGCCA	TTGAAGACTT	TGTTTTGTG	TTTGATGATT	CCATAACAGG	GAAACCGACT	480
	CCTCTTGTAT	GGCGTAGACG	AATCGTGGAC	TTACCGGAAG	GGACCAAATA	TATTGCATGG	540
	CGACATTACA	AACTCACCGA	CTCACACACA	GAATTCCTGA	AATTGGATGA	TGTCACTGTG	600
	TATAGTTCGA	TCGAAGGGCC	CGAACCTGCT	ACCGACTTCA	CAGTAATCAA	TATTGGTCAG	660
65	AATGTGGGAC	GATTGACTTG	GAACATCCG	GAGSATTATC	AACCGGAAGG	AAAGGGGAAT	720
	GAAGAGTTGC	AGCTTAGCGG	CTACAAACATC	TATGCCAAGC	GTACACTACT	GGCACAATA	780
	AAAGATGTCT	CCATACTCGA	GTATGTGGAC	AGCACTTACT	CTTTGCGAGA	CAATCCCTTG	840
	CAAGTGGAGT	ACTGCGTTAC	AGCCGTTTAC	GATGAAAGCA	TAGAATCTTC	GACCGTATGT	900
	GGCACGCTGC	ATTACGCCAC	GGATGCCATC	CTTTATGAAA	ATTITGAGAA	TGGACCTGTT	960
70	CCCAATGSET	GGCTTGTGAT	AGAAGCTGAT	GGAGATGSAI	TTAGCTGGGG	ACACTATTTG	1020
	AATGCATACG	ACGCTTTTCC	CGGCCATAAT	GGAGGCCAAT	GCTCCTTGTG	GGCTTCTTAT	1080
	GTTCCGGGTA	TAGGCCCGGT	GACTCCCGAC	AACTATCTGA	TTACCCCAAA	GGTTGAAGGA	1140
	GCCAAACGCT	TCAAGTACTG	GGAAGCAAGC	CAGGATGCCA	ATTGGGCAGC	GGAACATTAC	1200
75	GGGGTGATGG	CTTCGACNAC	GGGGACTGCT	GTCGGAGATT	TGTCATATT	GTTGGAAGAA	1260
	ACCATGACAG	CGAAGCCGAC	CGGCCCATGG	TATGAAAGAA	CCATCAACTT	ACCTGAAGGG	1320

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

139/490

	ACTAAATACA	TCGCATGGCG	GCATTACAAC	TGTACCGATA	TATATTTCTT	GAAGTTGGAC	1380
	GATATCACTG	TATTCGGGAC	TCCTGCATCA	GAGCCCGAAC	CTGTTACCGA	TTTCGTTGTC	1440
	TCGCTTATTG	AAAACAAACAA	GGGACGATTA	AAGTGGAAAT	ATCCTAACGG	CTACGAACUC	1500
5	GATAAGACTG	ATGATAAAGA	CCCAATTGCAG	CTTGCCGGCT	ACAATATCTA	TGCAACCGGC	1560
	TCGCTCCTTG	TTACATACA	AGACCCGACT	GTTTGGAGT	ATATCGATGA	GACTTATTCT	1620
	TCACGAGACG	ATCAGGTGGA	AGTGGAAATAT	TGTGCTACTG	CCGTTTATAA	CGACAAATATC	1680
	GAGTCCCAAT	CGGTTTGGGA	TAAGCTGATT	TATGATTCTC	AATCGGACAT	TATCTTATAT	1740
	GAAGGCTTTG	AGGCCGGAAG	TATTCCTGAA	GGCTGGTTGT	TGATTGATGC	TGATGGCGAC	1800
10	AATGTTAATT	GGGACTATTA	TCCTTGGACT	ATGATGGAC	ATGACAGTGA	GAAGTGATT	1860
	GCATCCCTT	CGTACTTACC	GATGATTGGC	GTTTAACTC	CGGATAACTA	TTTGGTTACA	1920
	CCCAGACTCG	AAGGAGCCAA	GCTTGTCAAG	TATTGGGTAA	GTGCGCAAGA	TGCTGTTTAT	1980
	TCGGCTGAGC	ATTATGCTGT	GATGGTTTCT	ACTACGGGAA	CTGCTGTTGA	AGATTTTGTC	2040
	CTCTTGTTTG	AAGAGACAAT	GACCGCTAAG	GCTAACGGTG	CATGGTATGA	GCGAACTATT	2100
15	ACATTGCTTG	CAGGAACAAA	ATATATTGCC	TGGCGGCATT	ATGATTGCAC	CGATATGTTT	2160
	TTCTTGCTCT	TGGATGACAT	TACGGTTTAT	CGTTCTACTG	AGACTGTTCC	CGAGCCTGTT	2220
	ACTGATTTG	TGTCTCGCT	TATTGAGAAT	AACAAGGGTC	GCCTGAAATG	GAATTATCCT	2280
	AACGGCTAGC	AACCGATAA	GACTGATGAT	AAAAAACCAT	TGCAGCTTAC	CGGCTACAAC	2340
	ATCTATGCAA	ATGGCTCGCT	CCTTGTTCAC	ATACAAGACC	CGACTGTTT	GGAGTATATC	2400
20	GATGAGACTT	ATTCTTCACG	AGACGGTCAG	GTGGAATGG	AATATTGTGT	CACTGCCGTT	2460
	TATAACGACA	ATATCGAGTC	CCAATCGGTT	TGCGATAAGC	TGAACATAC	TATCACATCC	2520
	TTGGATAATA	TTCAATCTGA	TACAAGCTTG	AAAATATATC	CTAATCCGGC	ATCGTATGTS	2580
	GTAAGGATAG	AGGGATTGAG	TCGGAGCAAG	TCGACAATCG	AGTTGTATAA	TGCGCTGGGA	2640
	ATTTGCATAT	TAAGGGAAGA	GACTCATTCA	GAGAAAAACGG	AAATCGATGT	TTACGCTCTC	2700
25	AATGACGGAG	TCTACTTGAT	TAAAGTAGTC	GGTGGAAATA	AAACAACAAC	CGAAAAGGTA	2760
	GAGATAAAGA	GGCCG					2775

## (2) INFORMATION FOR SEQ ID NO:204

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2766

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

	ATGATGAAAA	GTATTGTTTT	TAGAGCATT	CTAACGATT	TGCTCTCGTG	GGCAGCGATC	60
	ACGAATCCGA	CTGCTCAAGA	GATCTCAGGC	ATGAATGCAT	CCTGTCTGGC	TGCTCCGGCT	120
	CAACCGGATA	CTATCTTATA	TGAAAGTTTT	GAGAATGGAC	CTGTTCCCAA	TGGCTGGCTT	180
	GAGATAGATG	CTGATGCTGA	TGGTGCCACT	TGGGGAAGCC	CATCAGGGTC	TTTCTCTGTA	240
55	CCTTACGGAC	ACAATGGCCT	TTGCACCTAC	TCCCATATAC	GTTCCGGTAT	CTCAACAGCG	300
	GGCAACTATC	TGATTACACC	CAATATAGAA	GGAGCCAAC	GGGTCAAGTA	CTGGGTATGC	360
	AATCAGTATA	GTACCAATCC	GGACATTAC	GCAGTAATGG	TATCGACAAC	GGGGAAGTGC	420
	ATTGAAGACT	TTGTTTTGTT	GTTTGATGAT	TCCATAACAG	GGAAACCGAC	TCCTCTTGTA	480
	TGGCGTAGAC	GAATCGTGGA	CTTACCGGAA	GGGACCAAT	ATATTGCATG	GCGACATTAC	540
60	AAAGTCAACG	ACTCACACAC	AGAATTCCTG	AAATTGATG	ATGTCACGTG	GTATAGGTG	600
	ATCGAAGGGC	CCGAACCTGC	TACCGACTTC	ACAGTAATCA	ATATTGGTCA	GAATGTGGGA	660
	CGATTGACTT	GGAACTATCC	GGAGGATTAT	CAACCGGAAG	GAAAGGGGAA	TGAAGAGTTG	720
	CACCTTAGCG	GCTACAACAT	CTATGCGAAC	GGTACACTAC	TGGCACAAAT	AAAAGATGTC	780
65	TCCATAGTGG	AGTATGTGGA	CAGCACTTAC	TCTTTGCGAG	ACAATCCCTT	GCAAGTGGAG	840
	TACTGCGTTA	CAGCGTTT	CGATGAAGC	ATAGAATCTT	CGACCGTATG	TGGCAGCTG	900
	CATTACGCCA	CGGATGOCAT	CCTTATGAA	AATTTTGAGA	ATGGACCTGT	TCCCAATGGT	960
	TGGCTTGTGA	TAGACCGTGA	TGGAGATGGA	TTTAGCTGGG	GACACTATTT	GAATGCATAC	1020
	GACGCTTTTC	CCGGCCATAA	TGGAGGCCAT	TGCTCCTTST	CGGCTTCTTA	TGTTCCGGGT	1080
70	ATAGGCGCGG	TGACTCCCGA	CAACTATCTG	ATTACCCCA	AGGTTGAAGG	AGCCAAACGT	1140
	GTCAAGTACT	GGGTAAGCAC	GCAGGATGCC	AATTGGGCAG	CGGAACATTA	CGCGGTGATG	1200
	GCTTCGACAA	CGGGGACTGC	TGTGGGACAT	TTGCTCATAT	TGTTGGAAGA	AACCATGACA	1260
	GCGAAGCCGA	CCGGCGCATG	GTATGAAAGA	ACCATCAACT	TACCTGAAGG	GACTAAATAC	1320
	ATGCGATGGC	GGCATTACAA	CTGTACCGAT	ATATATTTCT	TGAAGTTGGA	CGATATCACT	1380
75	GTATTCGGGA	CTCCTGCATC	AGAGCCCGAA	CCTGTTACCG	ATTTGTTGT	CTCGCTTATT	1440
	GAAAAACAAC	AGGGACGATT	AAAGTGAAT	TATCCTAACG	GCTACGAACC	CGATAAGACT	1500

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5 GATGATAAAG ACCCATTTGCA GCTTGCCGGC TACAATATCT ATGCAAACGG CTCGCTCCTT 1560  
 GTTCACATAC AAGACCCGAC TGTTTTGGAG TATATOGATG AGACTTATTC TTCACGAGAC 1620  
 GATCAGGTGG AAGTGGGAATA TTGTGTCACT GCCGTTTATA ACACAAATAT CGAGTCCCAA 1680  
 TCGGTTTGGC ATAAGCTGAT TTATGATTCT CAATCGGACA TTATCTTATA TGAAGGCTTT 1740  
 GAGGCCGGAA GTATTCTGA AGGCTGGTTG TTGATTGATG CTGATGGCGA CAATGTTAAT 1800  
 TGGGACTATT ATCCTTGGAC TATGTATGGA CATGACAGTG AGAAGTGTAT TGCATCCCTT 1860  
 TCGTACTTAC CGATGATTGG CGTTTAACT CCGGATAACT ATTTGGTTAC ACCCAGACTC 1920  
 GAAGGAGCCA AGCTTGTCAA GTATTGGGTA AGTGCSCAAG ATGCTGTTA TTCGCTGAG 1980  
 CATTATGCTG TGTATGGTTT TACTACGGGA ACTGCTGTTG AAGATTTTGT CCTCTTGTTC 2040  
 10 GAAGAGACAA TGACCGCTAA GGCTAACGGT GCATGGTATG AGCGAACTAT TACATTGCCT 2100  
 GCAGGAACAA AATATATTGC CTGGCGGCAT TATGATTGCA CCGATATGTT TTTCTTGCTC 2160  
 TTGGATGACA TTACGGTTTA TCGTCTACT GAGACTGTTT CCGAGCCTGT TACTGATTTC 2220  
 GTTGTCTCGC TTATTGAGAA TAACAAGGGT CGCCTGAAAT GGAATTATCC TAACGGCTAC 2280  
 15 GAACCCGATA AGACTGATGA TAAAAAACCA TTGCAGCTTA CCGGCTACAA CATCTATGCA 2340  
 AATGGCTCGC TCCTTGTTC AATACAAGAC CCGACTGTTT TGGAGTATAT CGATGAGACT 2400  
 TATTCTTAC GAGACGGTCA GGTGGAAATG GAATATTGTG TCACTGCCGT TTATAACGAC 2460  
 AATATCTGAGT CCAATCGGT TTGCGATAAG CTGAACATA CTATCACATC CTGGATAAT 2520  
 ATTCAATCTG ATACAAGCTT GAAATATAT CCTAATCCGG CATCGTATGT GGTAAAGGATA 2580  
 GAGGGATTGA GTCGGAGCAA GTGACAAATC GAGTTGTATA ATGCGCTGGG AATTGCATA 2640  
 20 TTAAGGGAAG AGACTCATTC AGAGAAACG GAAATCGATG TTTCACGCTC CAATGACGGA 2700  
 GTCTACTTGA TTAAGTAGT CCGTGGAAAT AAAAAACAA CCGAAAGGT AGAGATAAAG 2760  
 AGGCCG

## (2) INFORMATION FOR SEQ ID NO:205

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2763

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

ATGAAAAGTA TTGTTTTAG AGCATTCTA ACGATTTCG TCTCGTGGGC AGCGATCACG 60  
 AATCCGACTG CTCAGAGAT CTCAGGCATG AATGCATCCT GTCTGGCTGC TCCGGCTCAA 120  
 50 CCGGATACTA TCTTATATGA AAGTTTGGAG AATGGACCTG TTCCCAATGG CTGGCTTGAG 180  
 ATAGATGCTG ATGCTGATGG TGCCACTTGG GGAAGCCCAT CAGGCTCTTT CTCTGTACCT 240  
 TACGGACACA ATGGCCCTTG CACCTACTCC CATATACGTT CCGGTATCTC AACAGCGGGC 300  
 AACTATCTGA TTACACCCAA TATAGAAGGA GCCAAACGGG TCAAGTACTG GGTATGCAAT 360  
 CAGTATAGTA CCAATCCGGA ACATTACGCA GTAATGGTAT CGACAACGGG GACTGCCATT 420  
 55 GAAGACTTTG TTTTGTGTT TGTATGTTCC ATAACAGGGA AACCAGCTCC TCTGTATGG 480  
 CGTAGACGAA TCGTGGACTT ACCGGAAGGG ACCAAATATA TTGCATGGCG ACATTACAAA 540  
 GTCAUCCACT CACACACAGA ATTCTTGAAT TTGGATGATG TCACTGTGTA TAGGTGATC 600  
 GAAGGGCCCG AACCTGCTAC CGACTTCACA GTAATCAATA TTGGTCAGAA TGTGGGACGA 660  
 TTGACTTTGA ACTATCCGGA GGATTATCAA CCGGAAGGAA AGGGGAATGA AGAGTTGCAG 720  
 60 CTAGCGGCT ACAACATCTA TGCGAACGGT AACTACTGCG CACAAATAAA AGATGTCTCC 780  
 ATACTGGAGT ATGTGGACAG CACTTACTCT TTGCGAGACA ATCCCTTGCA AGTGGAGTAC 840  
 TGCGTTACAG CCGTTTACGA TGAAGCATA GAATCTTGA CCGTATGTGG CACGCTGCAT 900  
 TACGCCACGG ATGCCATCCT TTATGAAAT TTTGAGAATG GACCTGTTCC CAATGGTTGG 960  
 CTTGTGATAG ACGCTGATGG AGATGGATT AGCTGGGGAC ACTATTGAA TGCATACGAC 1020  
 65 GCTTTTCCCG GCCATAATGG AGGCCATTGC TCCTTGTGCG CTCTTATGT TCCGGGTATA 1080  
 GGCCCGGTGA CTCCGACAA CTATCTGATT ACCCCCAAGG TTGAAGGAGC CAAACGTGTC 1140  
 AAGTACTGGG TAAGCACGCA GGATGCCAAT TGGGCAGCGG AACATTACGC GGTGATGGCT 1200  
 TCGACAACGG GGACTGCTGT CCGAGATTTC GTCATATTGT TCGAAGAAAC CATGACAGCG 1260  
 AAGCCGACCG GCGCATGGTA TGAAGAACC ATCAACTTAC CTGAAGGGAC TAAATACATC 1320  
 70 GCATGCCCGC ATTACAACG TACCGATATA TATTCTTGA AGTTGGACGA TATCACTGTA 1380  
 TTCGGGACTC CTGCATCAGA GCCCGAACCT GTTACCGATT TCGTTGTCTC GCTTATTGAA 1440  
 AACACAAGGG GACGATTAAA GTGGAATTAT CCTAACGGCT ACGAACCCGA TAAGACTGAT 1500  
 GATAAAGACC CATTGCAGCT TGCCGGCTAC AATATCTATG CAACCGGCTC GCTCCTTGT 1560  
 75 CACATACAG ACCCGACTGT TTTGAGTAT ATCGATGAGA CTTATTCTTC ACGAGACGAT 1620  
 CAGGTGGAAG TGAATATTG TGTCACTGCC GTTTATAACG ACAATATCGA GTCCCAATCG 1680



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5 GTTTGGGATA AGCTGATTTA TGATTCTCAA TCGGACATTA TCTTATATGA AGGCTTTGAG 1740  
 GCCGGAAGTA TTCCTGAAGG CTGGTTGTG ATTGATGCTG ATGGCGACAA TGTTAAATTGG 1800  
 GACTATTATC CTGGGACTAT GTATGGACAT GACAGTGAGA AGTGTATTGC ATCCCTTCG 1860  
 TACTTACCBA TGATTGGCGT TTAACTCCG GATAACTATT TGGTTACACC CAGACTCGAA 1920  
 GGAGCCAAAGC TTCTCAAGTA TTGGGTAAAGT GCGCAAGATG CTGTTTATTC GGCTGAGCAT 1980  
 TATGCTGTGA TGGTTCTAC TACGGAACT GCTGTTGAAG ATTTTGTCTT CTGTTCGAA 2040  
 GAGACAATGA CCGCTAAGGC TAACGGTGCA TGGTATGAGC GAACCTATTAC ATTGCTTGCA 2100  
 GGAACAAAAT ATATTGCCCTG GCGGCATTAT GATTGCACCG ATATGTTTTT CTGTCTCTTG 2160  
 10 GATGACATTA CGGTTTATCG TTCTACTGAG ACTGTTCCCG AGCCTGTTAC TGATTTCGTT 2220  
 GTCTCGCTTA TTGAGATATA CAAGGTCGCG CTGAAATGGA ATTATCCTAA CCGCTACGAA 2280  
 CCCGATAAGA CTGATGATAA AAAACCATTC CAGCTTACCG GCTACAACAT CTATGCAAT 2340  
 GGCTCGCTCC TTGTTACAT ACAAGACCG ACTGTTTTGG AGTATATCGA TGAGACTTAT 2400  
 TCTTCAGGAG ACGGTCAGGT GGAATGGAA TATTGTGTCA CTGCCGTTA TAACGACAAT 2460  
 ATCGAGTCCC AATCGGTTTG CGATAAGCTG AACTATACTA TCACATCCTT GGATAATATT 2520  
 15 CAATCTGATA CAAGCTTGAA AATATATCCT AATCCGGCAT CGTATGTGTT AAGGATAGAG 2580  
 GGATTGAGTC GGAGCAAGTC GACAATCGAG TTGTATAATG CGCTGGGAAT TTGCATATTA 2640  
 AGGGAAGAGA CTCATTGAGA GAAAACGGAA ATCGATGTTT CACGCTCAA TGACGGAGTC 2700  
 TACTTGATTA AAGTAGTCGG TGGAAATAAA ACAACAACCG AAAAGGTAGA GATAAAGAGG 2760  
 20 CCG

## (2) INFORMATION FOR SEQ ID NO:206

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 40 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1779  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

45 ATGAACAGCA TCATGAATA TCAATTATAT ACGGCCGTCA TAATGGCTCT CTCTGTATCA 60  
 TCGGTTTGGG GTCAAACCCC ACGAATATACA GAAACCAAAC GCCCGACAC GCTGCGCAGG 120  
 CAGCTTACTA TCGTTAATGA CCAGACTGTG GAGATGGAGC ATGCCGATCC GCTTCGGGCT 180  
 GCATACAAGG CCATCGAACC TCGATTAAAA CCTTCCGTC CGGAATATAA CAAGCGTACA 240  
 50 TTCGGAATTG TCCTGAAAGT TTCTCTTCA GGCAGGAACA ATCTTCCGAA TATCCTGCCG 300  
 ACGGAAGGTC ATATGAAGCA CCGGGGGTAC CTGAATATCG GTATCGGCCA TACGCTAAAC 360  
 CAGCGAATGG ATGCCGGCTA TCGTCTGATA GATGCAGAGC AGGAGAGACT GAATCTTTTC 420  
 CTCTCTATC GTGGGATGAA ATCGGCTTTC AATACCGGTG ACTTCGACGG CGACAGAAAG 480  
 GATAGACGAA TGATGGCAGS AGTGGACTAC GAGCAGCGCA GGCCTTCCTT TGTGCTTGCT 540  
 55 ACGGCTTGT ATATTGCAA CCATTATTC AATAACTACG GACGGGGAGC TACCACCAAT 600  
 GTGGGCGACA TCCCTCAGCT ATCGACACCT GTTACTCCTC AGATGGACAA CGGGACCCAC 660  
 AACGTCCTG TATACTTGGG TGCAAAAAAT GATGTGATCG ATGCCAGGAT CGACTATCGT 720  
 TTCITCCGTT CTATTCCCTA TCTGGGTACC GATCCGATGA AGGCTCTCAC AGAACATACG 780  
 CCTGAATGA ACGTGACGAT GAGTAATGAG TTGTCCGATG ATATTAGCT CGGTGTCGAA 840  
 60 GTTCGTACGG GAGGATTGTT TTTTGCCAAA AACAGCGAAA TGATTCAAAC GGGCGTTCTG 900  
 TCCGAAACCG ACGCAACCT GTATTATGTG GAGGGCGGCG CCACAATCGG ATTTGTCCGA 960  
 GACTCGGACA ATATGCAATG GAACATACAG GCCGGAGTAG GGATTTCCTC CCATTTCGGA 1020  
 GCCAAAGGGA GGTGTTTTT CTGGCCATAA CTGGATGCTT CGCTTAGTAT CTTCCCTTCA 1080  
 TGGCGTGTGT ATGCGAAAGC CTTCGGCGGT GTGATTCGAA ATGGTCTCGC CGATGTTATG 1140  
 CRAGAGGAGA TGCCCTACCT GATGCCCAAT ACGATTGTAC TCCTTCGCG CAATGCTTTG 1200  
 65 ACUGCCCAAT TAGGGGTGAA GGGGAATATA GCCGATGTG TACGTATGGA GGTTTATGGC 1260  
 GACTTCTCCA AGCTGACAGG TGTGCTTTC TATACTCCGA CTCTACCTT ATATAATCCA 1320  
 TCCGACTTGT ATCAGTATAA TGTGAGTTTC TTGCCGATAT ATGCCGACGG CAGCGCTGG 1380  
 CGCGCAGGTG GTAAGCTGGA ATACTCTTAT CGCGATATGC TCCGCTTCT GGTAGACGCA 1440  
 TCCTATGGCA AGTGAATTT GGATGGAGGA CTGTGCGCCT CCATGCAGCC CGATCTTATA 1500  
 70 TTGAAGGCAG AAGTAGGTGT TCATCCCAT GCGCCATTGG ATGTCAGACT CCGGTATACA 1560  
 CAGCTGAACG GACGGTATCG GTATTCTTTC GGCTCGGCTG GCTCGGAAGC CTTGGGATC 1620  
 GGTAATGTAC ATCTTCTTAG TGCGGATGTT TCATACAAGC TGAAAAAGAA CTTGAGCCTT 1680  
 TATCTCAAAA TCGATAATAT GCTGGCGGAA ACGACAGAGC TTATCGGTTA TTATCCTATG 1740  
 75 CAGCCGTTCC ATTGTTTCCG CGGTTTTAGC TGGACTTTC 1779

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## (2) INFORMATION FOR SEQ ID NO:207

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1767
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

25 ATGAATATC AATTATATAC GGGCGTCATA ATGGCTCTCT CTGTATCATC CGTTTGGCGGT 60  
 CAAACCCAC GAAATACAGA AACCAACGC CCGACACGC TGGCAGGGA GCTTACTATC 120  
 GTTAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCCGGCTGC ATACAGGCC 180  
 ATCGAACCTC GATTAAACC TTTCCTCCG GAATATAACA AGCGTACATT CGGATTGTG 240  
 CCTGAAGTTT CCTCTTCAGC CAGGAACAAT CTCCGAATA TCCTGCGGAC GGAAGSTCAT 300  
 30 ATGAAGCACC GGGGGTACCT GAATATCCGT ATCGGCCATA CGCTAAACCA GCGAATGGAT 360  
 GCCGGCTATC GTCTGATAGA TGCAGAGCAG GAGAGACTGA ATCTTTTCT CTCTATCGT 420  
 GGGATGAAAT CGGCTTTCAA TACCGGTGAC TTCGACGGCG ACAGAAAGGA TAGACGAATG 480  
 ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTTG TGCTTGCTAC CGGCTTGAT 540  
 TATTGGAACC ATTATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC 600  
 35 CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACVACG GGACCCACAA CGTCCGTGTA 660  
 TACTTGGGTG CAAAAAATGA TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGGTTCT 720  
 ATTCCTATC TGGGTACCGA TCCGATGAAG GCTCTCACAG AACATACGCC TGAAGTGAAC 780  
 GTGACGATGA GTAATGAGT GTCCGATGAT ATTAAGCTCG GTGTCGAAGT TCGTACGGGA 840  
 40 GGATTGTTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTTCTGTC CGAAACCGAC 900  
 CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGSAT TTGTCGGAGA CTCGAGCAAT 960  
 ATGCAATGGA ACATACAGGC CGGAGTAGGG ATTTCTTCCC ATTTCCGAGC CAAAGGGAGG 1020  
 TTGTTTTTCT GGCCTAAACT GGATGCTTCG CTAGTATCT TCCCTTCATG GCGTGTGTAT 1080  
 GCGAAAGCCT TGGCGGTGT GATTGGAAT GGTCTCGCCG ATGTTATGCA AGAGGAGATG 1140  
 45 CCTACCTGA TGCCCAATAC GATTGTACTC CCTTCGCGCA ATGCTTTGAC CGCCCAATTA 1200  
 GGGGTGAAGG GGAATATAGC CGATGTGGTA CGTATGGAGG TTTATGGCGA CTCTCCAAG 1260  
 CTGACAGGTG TGCCTTTCTA TACTCUGACT CTACCTTAT ATAATCCATC CGACTTGTAT 1320  
 CAGTATATG TGAGTTTCTT GCCGATATAT GCGGAGGCA GCGGCTGGCG CGCAGGTGGT 1380  
 AAGCTGGAAT ACTCTATCG CGATATGCTC CGCTTTCTGG TAGACGCATC CTATGGCAAG 1440  
 50 TGGATTTGG ATGGAGGACT TGTCCCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA 1500  
 GTAGGTGTTT ATCCCATTCG CCCATTGGAT GTCAGACTCC GGTATACACA GCTGAACGGA 1560  
 CGGTATCGGT ATCTTTTCGG CTCGGCTGGC TCGGAAGCCT TGGGTATCGG TAATGTACAT 1620  
 CTCTTAGTG CGGATGTTT ATACAAGCTG AAAAAAAGT TGAGCCTTTA TCTCAAAATC 1680  
 GATAATATGC TGGCGGAAAC GACAGAGCTT ATCGGTTATT ATCCTATGCA GCCGTTCCAT 1740  
 55 TGTTTCGCCG GTTTTAGCTG GACTTTC 1767

## (2) INFORMATION FOR SEQ ID NO:208

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1038 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

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5  ATGATGGAAT AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTCGCAAG      60
   CATTTCGGTA TCATTTTGGG ATTTCTTTCT CTGTGTTTTC CGGCAGGTGC TCAACAAGAG      120
   AAGCAGGTGT TTCATTTTCT GAACCTTCCG GCTACTGCAC AGGCTTTGGC TGCCGGAGGC      180
   AAAGCTATCA CCATCGTAGA CGACAATCCC GGACTGGCTT TTGAGAATCC GGCTCTGCTC      240
10  GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCTATTAT ATTATATGAG TGGTTCGCAT      300
   ATGGGCAATG CCGTGTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGGCATG      360
   CGTTTCCTGA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT      420
   TTTAGTGCTT CGGATATAGC TGTACAAGGA TTTTACAGCC ATGAACATGAG CAACCACTTC      480
   CGCGGTGGAG TCAGCCTAAA AGCATTGTAT TCTTCTATCG AGACGATAG TTCTTTGGC      540
15  CTGTGTGGAG ATGTCCGTAT CAGTTATTAC GACGATGACA AAGGATATTC CGCTTCGCT      600
   CTGTTCAAGA ACGTAGGGGC GCAACTGAAA GGCTATAATG AAGAACGGGA ACCGCTCGAT      660
   TGGGATTTCC AGCTCGGCTT TTCCGCGAGT TTTATCAATG CTCGTTTCG CTTCACATC      720
   ACCTTGTGTA ATCTGAATCC GCACTATTTC AAGCGTCTTG TACCACGCGA TCTGTCCAAG      780
   ATGCAAAAGT TCCTCCGACA CTCTCGATA GGAGCAGAAT TTAATCTTC CGAGAGGTTT      840
20  TGGGTCCGGC TGGGATATAC GCCACAGATT GCACAGGATT TCGAGGTGGA AGGCGGCAAC      900
   AAATGGGAGG GTCTTTCGGC CGGCGTCGGT TTCACTTCAG GTGTAGTACG TGTAGGCGTA      960
   TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCATGT GTTCGGTAGG TATCCGTTTG     1020
   GACGATAAGA GCATCTTC                                     1038

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(2) INFORMATION FOR SEQ ID NO:209

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   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1035 base pairs
       (B) TYPE: nucleic acid
30  (C) STRANDEDNESS: double
       (D) TOPOLOGY: circular

   (ii) MOLECULE TYPE: DNA (genomic)

35  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

40  (vi) ORIGINAL SOURCE:
       (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

   (ix) FEATURE:
       (A) NAME/KEY: misc_feature
45  (B) LOCATION 1...1035

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

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   ATGGAATAAT GTATCTTTCG TCACTATCCA CATAACCTTG TGTTTCATGAT TCGCAAGCAT      60
   TTCGGTATCA TTTTGGGATT TCTTCTCTT GTGTTTTCGG CAGGTGCTCA ACAAGAGAAG      120
   CAGGTGTTTC ATTTCTGAA CCTTCGGCT ACTCCACAGG CTTTGGCTGC CGGAGGCRAA      180
   GCTATACCA TCGTAGACGA CAATCCCGGA CTGGCTTTTG AGAATCCGGC TCTGCTCGGA      240
   TATGAATCCG GTGGCCGGCG CTTCCTTTCC TATTATATAT ATATAGTGG TTGCGATATG      300
   GGCAATGCCT GTTATGCCTC GTCCGTCCGA GAGCGTGGCA TGTGGGTTGT TGGCATGCGT      360
55  TTCTGAATC ACGGGTCTAT GCAAGGATAC GATCAGAATG CGATTGCCAC CGGCTCTTTT      420
   AGTGCCTCGG ATATAGCTGT ACAAGGATT TACAGCCATG AACTGAGCAA CCACTTCCGC      480
   GGTGGAGTCA GCCTAAAGC ATTGTATTCT TCTATCGAGA CGTATAGTTC CTTTGGCCTT      540
   GGTGTGGATG TCGGTATCAG TTATTACGAC GATGACAAAG GATATTCGCG TTCCGCTCTG      600
   TTCAAGAACG TAGGGGCGCA ACTGAAAGGC TATAATGAAG AACGGGAACC GCTCGATTG3      660
   GATTTCCAGC TCGGCTTTTC CGCAGTITT ATCAATGCTC CGTTTCGCTT GCACATCACG      720
60  TTGTTCAATC TGAATCGCA CTATTTCAAG CGTCTGTAC CACGCGATCT GTCCAAGATG      780
   CAAAAGTCC TCCGACACTT CTCGATAGGA GCAGAAATTA CTCCTCCGA GAGTTTGG      840
   TCGGGCTCGG GATAATACGCC ACAGATTGCA CAGGATTTCG AGGTGGAAGG CGGCAACAAA      900
   TGGGGAGGTC TTTCCGCCGG CGTCGGTTTC ACTTCAGGTG TAGTACGTGT AGGCGTATCT      960
   GCTGCCACCT ATCATCCTGC AGCTCTTTCG TTCATGTGTT CGGTAGGTAT CCGTTTGGAC     1020
65  GATAAGAGCA TCTTC                                     1035

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(2) INFORMATION FOR SEQ ID NO:210

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70  (1) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 990 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
75  (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

15

ATGATTTCGCA	AGCATTTCGG	TATCATTTTG	GGATTTCITT	CTCTTGTTT	TTCGGCAGGT	60
GCTCAACAAG	AGAAGCAGGT	GTTTCATTTT	CTGAACCTTC	CGGCTACTGC	ACAGGCTTTG	120
GCTGCCGGAG	GCAAAGCTAT	CACCATCGTA	GACGACATC	CCGGACTGGC	TTTTGAGAAT	180
CCGGCTCTGC	TCCGATATGA	ATCCGGTGGC	CSGCGCTTTC	TTTCCTATT	ATATTATATG	240
AGTGGTTGCG	ATATGGGCAA	TGCCTGTTAT	GCCTCGTCCG	TCCGAGAGCG	TGCCATGTGG	300
GGTGTGGGCA	TGCGTTTCCT	GAACTACGGG	TCTATGCAAG	GATACGATCA	GAATGCGATT	360
GCCACCGGCT	CTTTTACTGC	TTCCGATATA	GCTGTACAAG	GATTTTACAG	CCATGAACCTG	420
AGCAACCACT	TCCGCGGTGG	AGTCAGCCCTA	AAAGCATGT	ATTCTTCTAT	CGAGACGTAT	480
AGTTCTTTTG	GCCTTGTTGT	GGATGTGGGT	ATCAGTTATT	ACGACGATGA	CAAAAGATAT	540
TCCGCTTCGG	CTCTGTTCAA	GAACTAGGG	GCGCACTGA	AAGGCTATAA	TGAAGAACGG	600
GAACCGCTCG	ATTGGGATTT	CCAGCTCGGC	TTTTCCCGCA	GTTTTATCAA	TGCTCCSTTT	660
CGCTTGCACT	TCACGTTGTT	CAATCTGAAT	CCGCACTATT	TCAAGCGTCT	TGTACCAAGC	720
GATCTGTCCA	AGATGCAAAA	GTTCTTCCGA	CACCTTCTGA	TAGGAGCAGA	ATTTACTCCT	780
TCCGAGAGGT	TTTGGGTCCG	GCTGGGATAT	ACGCCACAGA	TTGCACAGGA	TTTCGAGGTG	840
GAAGGCGGCA	ACAAATGGGG	AGGTCTTTTG	GCCGGCGTCG	GTTTCACTTC	AGGTGTAGTA	900
CGTGTAGGCG	TATCTGCTGC	CACCTATCAT	CCTGCAGCTC	TTTCGTTTAT	GTGTTCGGTA	960
GGTATCCGTT	TGGACGATAA	GAGCATCTTC				990

35 (2) INFORMATION FOR SEQ ID NO:211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...972

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

ATGTGCCTCG	AACCCATAAT	TGCTCCGATT	TCATCCGAGT	TGCTCGAGCA	GGAGCTGACT	60
GCCGATGTTT	TTCTGCGGAT	GACAAACAAA	GCCGGCAATG	AGATCTATGT	TTTTACGGCC	120
GAAGAAGCTC	CGCATTGCAAT	GAAAGAAGTA	GGCCGACTGC	GAGAAGAAGC	CTTTCGGCAT	180
TATGGCCGAG	GTACTGGCA	GGCGATCGAT	ATAGACGAGT	TCGACACCAT	GCCCGGGAGC	240
TACAAACAGC	TGATCGTATG	GGATCCGCAA	AACAAGGCTA	TACTCGGAGG	CTACCGCTTT	300
ATCTATGGGC	GGGACGTTGC	TTTCGATACC	GATGGCAAGC	CTTTGCTGGC	AACGGCAGAG	360
ATGTTTGGCT	TCAGTGATGC	TTTTTTGAC	GATTATCTCC	CTTACACAGT	CGAATTGGGA	420
CGTTTGTTCG	TGTCGCTCCA	GTACCAATCG	ACACGGATGG	GCACAAAGGC	CATTTTGTG	480
CTGGACAATC	TTTGGGACGG	TATCGGAGCA	CTCACTGTAG	TCAATCCAGA	GGCACTCTAT	540
TTCTATGGCA	AGGTGACCAT	GTACAAAGAC	TATGATCGGC	GAGCTCGCAA	TCTGATCTTG	600
TATTTTCTTC	GCAAGCACTT	CTCCGATCCG	GAAGGCTTGG	TCAAGGCTAT	TCATCCCTTA	660
CCGATAGAGA	TCAGTGCGGA	GGACGAAGCC	TTGTTCTCCT	CATCCGACTT	TGACACCAAT	720
TACAAGACTC	TCAATATAGA	AGTGGCGAAG	CTGGGTATCA	ATATCCCTCC	TCTCGTGAAT	780
GCATATATAG	CTTTGTCTCC	GGAGATGCGT	GTTTTCGGCA	CTGAGTGA	TGAGTCTTTT	840
GGAGAGGTGG	AGGAAACCGG	CATATTCTAT	GCTGTGGGTA	AGATCTTGGA	AGAGAAAAAA	900
CAACGGCACA	TAGAGAGCTT	CATCCTCAGC	CGGAACGAAA	AAAAAGGTCT	CGACAGTAGC	960
AATGGCCGAT	CA					972

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## (2) INFORMATION FOR SEQ ID NO:212

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1641 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

25	ATGAAACCA TTGTAAGATA CAGCCGCTT CGGTCGCTC TCTTCTTTG CCTTTGGGA	60
	GCTGTGCACT TGTCTGTGGA GCGCGAGATG CTCGAATCTC CTTTCGAGCT GTCGGATCAG	120
	ATCGTCCTGT CTCCCACCGA AAGGCAATAC AGGGAGATTG GTGTGCAAC GAAAGAAAAA	180
	AGGGGGGCGG ATCTTTTCCC GTTGAGCGAT AACCTGCGCG ATTCGGCCTA TGTTGCTTTC	240
	GGCTCGGCCT ATGGCGATAT TCGGGGCGAC TATCTTCCST ACAACGGCAA TAACTACTCC	300
30	TGCTCTCGC TCGAATCGGG TGGTCGCATC AGTGTCCGTA ACTATGGCAC ATTGCAGGGC	360
	AGTGCTTCTT ACTCAGTGG CATGCACAAA CGCATCGGCT GGAATGCTCT GCGCAACGCC	420
	GAAGCCTACT ATCCCTATT GGTGTCCGAT TCGACCGGCG GAGACTATCA TTTGGAAGAC	480
	TATCGGCTTG CCGGCTACTA TTCTTTTCGC GCGGGCGGCT TGCCCTCGG TATAGGCTTC	540
35	TCATACAGGG GCGAAGTTGC TTATCGGCTG ACOGATCCCG GTACGACCAA TACGACCGGT	600
	GCATTGGAGC TTTCTTGTGC TACCTCTTTG ACGCTGCCTC GAGAGAACAG GCTATCGCTT	660
	TCCGCTGCGT ATCTCTATCA TAGACAACAC CTCACACAGT ACAACTGGCG TCCCGGGCAG	720
	CAGGACAAAT TCTTCGTGAG CTACGGTTTC GGTCAAGTGG ATGTCAAGCA CAGCCCTATC	780
	TGGTTGCGTA TCTCCAGAAAT GAATACGTC AACGGATGGA AGCTTAGCTC CCGTCTGGAT	840
40	ACCGTAGGG GCGATGCCAT CGGTCTCGAC TACAGCGGCT ACTTCCTCGA TACCGAAGAG	900
	AGGTGCTCCA TCAATCTCTT TGCTTTGCTT TACAATCGCC TGCGACTCTA TGGTAGCTGG	960
	CATCTGTGCG ACTTCGATT TTTCTTTTCA GCGGACTATG CTCTGCGCCA AGGGATAGAG	1020
	CGGATATACG AAGACTACAA GCCGGATGAT AATTATCATA TCTACGACCT CCGTATCTTG	1080
	GCCATTGCGC GCTGGTATAT GCTCAATGAG TTTTCTGCCC AAGCCCAAGC CTCTACCGT	1140
45	ATTGCGACGG ATAGAGGTTG TGCCCTGAGA GTGAGTGCCG GTAGTGATT TACGGCTAT	1200
	GATGAGAGCT ATCGCAAGCA TGGACATCAT ACCATGAGCG GAATGCTACG TCCTTTTGCC	1260
	GGTATAGCCT ATGACCATGC CGGATCCAAA TTGGATTITG GACTTTGCTT TCGGCTGCT	1320
	TATCGAATGG TGCTGAGCGA TTCGTATAAG ATTCGTACCA TCCAGAAAGA GCAGCTCGAC	1380
	TATCAGCTGG CCTATTGGCC CTATGCCTAT CGTAATAGAG AAGGCGTGGG GGTGCGTTCC	1440
50	TCTCTGTACG TCTCGATTCC GATGCAGAAT ACCCACCGCC TGATGACAGA GCTGCGGTTG	1500
	TATGGCGACC TGATGAAAG AAAGGACGGT ATAGCCTATG GCAAAACGCC CGGTGTCATC	1560
	TCACATATCC TGTCCGATCC GCAAGCCGAA CGAACGTCGG GCCATACCAT CGGGGCTATC	1620
	TGCAATATCT CCTACCTCTT C	1641

## (2) INFORMATION FOR SEQ ID NO:213

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2250 base pairs  
 60 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

65 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 75 (B) LOCATION 1...2250

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:213

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5  ATGAAAAAAC TTCACATGAT TGCCGCTTGA GCCGCTCTGC CTTTCTGCCT GACGGCACAA      60
   GCACCCGTCT CCAACAGCGA GATAGATAGT CTTAGCAATG TGCAGCTCCA GACCGTACAG      120
   GTCTAGTCTA CTCGCGCCAC GCGGAAAACC CCTGTCGCTT ACACCAACGT TCGCAAGGCC      180
   GAACCTTTCCA AGTCCAAATTA TGGTCGTGAC ATCCCTATC TGCTGATGCT GACTCCCTCC      240
   GTGGTAGCCA CCAGCGATGC CGGTACGGGT ATCGGATATT CCGGCTTTCG CGTGGCTGGC      300
   ACCGATGCCA ATCGCATCAA CATAACTACC AATGGAGTAC CCCTCAACGA CTCCGAATCT      360
   CAGTCCGTCT TTTGGGTGAA TATGCCCGAC TTCGCTCTT CCATCGAAGA CCTTCAGGTG      420
10  CAGCGAGGTG TGGGTACTTC CACCAATGGT GCCGAGCTT TTGGGGCAAG TGTCATATG      480
   CSTACGGATA ATTTGGGACT GGCTCCTTAT GGCCTGTGCG ATTTGAGCGG AGGTTCTGTC      540
   GGCACATTCC GCGGATCGGT CAAACTCGGT AGCGGACGCA TCGGTGCGCA TTGGGCAGTG      600
   GATGCCCGCC TGTCCTAAAT CGGTTTCGAC GGCTACGTGG ATAGAGGAAG CGTGGATCTG      660
   AAATCCTATT TCGCACAGST GGGCTATTTT GGTAGCAACA CGGCTCTCAG GTTCATCACT      720
15  TTCGGAGGAA AAGAAGTTAC GGGTATCGCA TGGAACGGTC TTTCGAAGGA GGATGAAGCC      780
   AAATATGGCC GTCGATACAA CAGTGCCGCT CTTATGTAAG TGGACGCGCA AGGAGTACCG      840
   CACTACTACC ACAATACCGA CAATTACGAG CAGCGTCACT ACCATGCCAT CATGACGCAC      900
   AGCTTCTCTC CTTCCGTTAT CTTCAACCTC ACGGCACACT ACACGGCCGG ATATGGCTAT      960
20  ACGGACGAAT ATCGTACCGG ACGTAACTA AAGGAATATG CACTGCAGCC CTATGTGGAA      1020
   AACAGTGTGA CCGTGAAGAA AACGGATCTC ATCCCTCAGA AGTATCTGGA CAATGACTTC      1080
   GGAGGACTCA TCGGTTTCGCT TAACTGGCAC ACCGCTGCAT GGCATTGCA GTTCGGGGCC      1140
   TCGGGCAATA TCTATAAAGG AGACCACTTC GGCGGTATCA CTTACATCAA AAAGTACAAT      1200
   CAGCCCTTAG CTCCCGACTT CGAATATTAT CGGAACAGGG CAGACAAAAG AGAAGSTGCA      1260
   GCCTTTGCCA AAGCCAACTG GCAGATCACT CCGGAACCTG ACATGTATGC CGACCTCCAG      1320
25  TATCGTACCA TCGGCTACAC GATAAACGGC ATCAGCGAGC AATATGATGA GGTACAGGGA      1380
   AGATGACAGC ACATCGATT TGGACAAGAC TTCCGCTTCC TCAATCCGAA GGCCGGTCTT      1440
   ACCTATAGTT TCGACGATG TCATCTGCTC TATGCTTCTG TTGCGGTAGC ACACCGCGAG      1500
   CCTAACAGAA CCAATTACAC CGAAGCGGGA ATAGGACAGT ATCTACGCC TGAGCGACTG      1560
   ATCGACTATG AGCTGGGCTA CCGCTATGCT TCGCCCTCTT TGTGGCCGG AGTAGGTCTC      1620
30  TATTATATGC AATACAAGGA CCAACTCGTG CTGGATGGCC GTTTGAGCGA TGTGGGACAG      1680
   ATGCTCACAA GCAACGTCCC CGACAGCTAC CGTATGGGAC TGGAGCTGAC TCTCGGTTGG      1740
   CAGATCCCTC CTCGTTTGCT GCGTTGGGAT GCTTCTTTCA CTATGAGTGC CAACAAAATC      1800
   GACCGCTACG TACAATATAC ATCCGTATAT GATGCGGACT ACAACTGGCT CGAACTCAAG      1860
   GAGGAGACCC TCGAAAGCAC GGATATAGCC TACTCGCCCA ATGTCATTGC CGGCAGCATG      1920
35  CTTACCCCTC CTATGCGCGG TTTCGAAATG GCTTGGACGA GCGGCTTCGT CAGCAAGCAA      1980
   TATCTGGACA ATACACAGCG CAGCGATCGC ATGCTTTCTT CCTATTGGGT GAACGACCTC      2040
   CGCCTCGGCT ATGTGCTGCC GGTTCACCTT GTTAAGAGAG TGGCACTGGG CGTACAGCTC      2100
   CCAATCTCT TCAACCTCAT GTATGCGTCC AATGCCTACA TCTACGATGC CGGTTACGTA      2160
40  CAGGCATCCG GAGAACTAAG TGCAATGCC GATCTGCGTT ATTATCTCA GGCCGGATT      2220
   AATGCATGGG GTAGTCTGAC AATCGATTTC

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(2) INFORMATION FOR SEQ ID NO:214

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45  (1) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1482 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
50  (D) TOPOLOGY: circular

     (11) MOLECULE TYPE: DNA (genomic)

     (111) HYPOTHETICAL: NO

55  (1v) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: PORPHYROMONAS GINGIVALIS

60  (ix) FEATURE:
     (A) NAME/KEY: misc_feature
     (B) LOCATION 1...1482

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:214

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65  ATGAAAGAA GGTTCTATC GCTGTTACTG CTGTACATAC TCTCTCCAT CAGCCTTCT      60
   GCTCAGCGGT TTCCGATGGT GCAGGGAATC GAGTTGGATA CCGATTGCT TTTCTCTCTG      120
   CCAAGCGTC CTTGCCGCGC CATCGGTAAA ACGATAGGCG TCAATCTGCC CGTATGGGAC      180
   TTCGATCATT TCATCATGAA CGAGGACTTT GCAGACATCA GTTGGCAGAC TATCAAGAGC      240
   AATTTCCAA CAGGCTTTGG CTGGGACAA GACAAGTTTG TCACCAACCT CTTCCGACAT      300
   CCTTATCAG GATCGCTCTA TTTCAATGCA GCGAGGTGCA ACGCTTTGAG CTTCAGGCAC      360
   TCTGCTCCGT TTGCTTCTT TGGCAGTCTC ATGTGGGAGC TGCTTATGGA AAACGAGCCA      420
   CCGAGTATCA ACGACCTCTG TGCCACCACC ATAGGCGGTA TAGCTTTGGG GGAGATGGGG      480
   CACAGGCTGT CCGACCTGCT CATCGACAAT CGTACCACAG GGTGGGAACG TATGGGCGC      540
75  GAGGTGGCTA TCGCTCTGAT CAATCCGATG CGCTTTCTCA ACCGCTGAC ACCAGGAGAG      600

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5 GTGACTTCTG TCGGGAGTCG CAGCGGACAG ATATTTCACT CTGTCCCCAT AAACATAGTC 660  
 GTCGATGCGG GCTTTGCTT TTTGGCAGAC AAGCGGCATG CCGGAACCGG TGCCACGGCT 720  
 CTGACCCCTGA ATCTGAGATT CGACTACGGC GATCCATTCC GAAGCGAGAC TTTCTCTCCA 780  
 TACGATTCTT TCCAATTCAA AGCCGGATTG AGTTTCTCCG AATCGCAACC TCTGCTGAGC 840  
 CAGATCAATC TGATCGGAAT CCTAAGCGGA TGCCAACTGC TCGCACACGA ACGAACGGTT 900  
 TTSGTGGGAG GTCTCTTTCA GCACTTCGAC TACTACAATT CGGAAAAACG AATAAGCAAA 960  
 AATTCGGAGG AGGTACTCGT CACCCCATAC CGTATCTCGC AAGTGGCAGC TCTGGGAGGC 1020  
 GGTCTTATCT TCCAGCACCA CGGAAAATTT CGACGACGTC CTCTGGAGCT ATATGCCGAG 1080  
 10 ACCTACCTGA ATGTCGTCCC GATGGGAGCC AGTCTGTCGG ATCACTACAA CGTGGACAAT 1140  
 CGGGACTATA ACCTCGGCAG CGGATTGAGC GGCAAGCTAT ACCTTGGTGC TACGTACAAT 1200  
 GATCTGTGGA GCTGGCTCTT GGGAGTCGAA AGCTATCGGC TCTACACATG GATCGGGTAT 1260  
 GAAGAGCCGC ACCAGAAAAA TACCGATGTC AGCTCTTTTA TGGTGCAGGG GGACGAAAGC 1320  
 AAGGCGCGCC TACTGGTGAC GAGTTCGGAG TTCGCATTTC ATCCTGGCCC CTGGCATGTA 1380  
 15 GCCATCGTCG CTCGCCGTTT CATCCGCAAA ACAGCCTATC AATTCTACCC TAACGTATCA 1440  
 TTCGATACCG GCGACATACA GCTGCGTGTC GGATTTCAC T 1482

## (2) INFORMATION FOR SEQ ID NO:215

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 882 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...882  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

40 ATGAACGAC TGATTGTTTT TCTGGCAATG GGTGGCTTGC TGTTCACCCT TGCGAACGCA 60  
 CAAGAAGCAA AACTGTCATC TGACACTCCC AAAAAGGACT GGACTATAAA AGGTGTGACC 120  
 GGACTAAATG OCTCTCAGAC TTCTCTGACC AACTGGGCTG CCGGTGGAGA AAACACGGTG 180  
 45 GCAGGTAACC TCTATTGAA CATAGATGCC AACTACCTGA AAGATAAATG GAGTTGGGAC 240  
 AACGGTTTGC GTACAGACTT CGGTCTGACC TACACAACAG CCAACAAATG GAACAAAAGT 300  
 GTAGACAAGA TCGAATCTTT CACGAAGGOC GGCTATGAGA TCGGCRAACA TTGGTACGGA 360  
 AGTGCGCTTT TCACTTTCTT CTACAGTAT GCCAAAGGAT ATGAGAAGCC CTCGGATCAC 420  
 TTGACAGGAG TCAAGCATAT CTCTAATTTT TCGCTCTCTG CATATCTCAC TCTCGGTATT 480  
 50 GGTGGCGACT ATAAAGCCAA TGAGAAGTTC TCTCTTACC TCTCTCTAC AACGGGCAAG 540  
 CTGACTGTAG TAGCAGACGA CTACCTCTCA AGTTTGGGAG CCTTCGGGGT GAAAGTTGGT 600  
 GAAAAGACAA TGTTGGAATC TGGTGCTTTG GTAGTGGGTT CGGCCAATAT AAATCTGATG 660  
 GAGAATGTCA ATTTGATAAC CAAGGCTTCA TTCTTCTCGG CTATACGCA CGACTTTGGC 720  
 AACATTGACA TCAATTGGGA GGCTATGCTG GCCATGAAGA TCAACAAGTT CCTCAGGGCT 780  
 55 ACGATAGCCA CCAATCTTAT CTACGACGAT GATGTGAAGA TCAACGATGG CCCGAAAATC 840  
 CAGTTCAAAG AAGTTGTGGG CGTGGGTGTT CGGTACACTT TC 882

## (2) INFORMATION FOR SEQ ID NO:216

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 612 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...612

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:216

5  
10  
15  
ATGAAGAAAA TGATTTTGGC AGCTACTATG CTGCTCGCAA CAATCGGTTT TGCAAATGCT 60  
CAGAGTCGTC CTGCTCTTAG ACTGGATGCT AACTTTGTG GTAGTAACTT AATGCAAAAA 120  
GTCGCAAAACA CGAGCGTGAA CAATAAGATG ATCGTAGGCT TACGTGTTGG TGCTGCTGCT 180  
GAGTTCGGCTC TTAGCAATGA TGGATTCTAT CTCGCCXXUUY GATTGGCCTA TACGATGAGA 240  
GGTGCTAAGA TGAATCACT AAGTGAAACG ACAACTCGCT TGCATTATCT GCAAATACCG 300  
GTGAATGCCG GTATGAGATT TAGCTTTGCT GACAACATGG CTATTTTATT GGAAGCAGGT 360  
CCCTATTTTC CATATGGTGT CGCCGGAACG ATTAAGACTA AAGTTGCAGG CGTTACGGCT 420  
TCTGTAGATG CCTTTGGTGA TAACGGATAT AACCGTTTCG ACTTGGGCTT GGGCTTGTCT 480  
GCTGCCCTGA GCTACGACCG TTATTACGTA CAAATTGGAT ATGAGCATGG ATTGCTTAAT 540  
ATGTTGAAGG ATGCTCCGGA TAAGACTTCT TTGCGTAATC ATGACTTCTT TGTGGGTCTC 600  
GGTGTTCGCT TC 612

(2) INFORMATION FOR SEQ ID NO:217

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 729 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...729

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:217

40  
45  
50  
55  
ATGAAAAGGA TTTTACTGT AGCCCTTGTG CTACTTGCTT CGGTCACTAT GGCCATCGGA 60  
CAAAGCCGCC CGGCACTTCG CGTAGATGCC AACTTCGTAG GCAGCAATCA GAGCATGAAA 120  
AGAGACGGAT ATGTGTGGGA CACCAAAATG AATGTGGGCC TGCGGGTCGG TGCCGCTGCC 180  
GAATTCATGA TCGGATCAAG AGGATTCTAC TTGGCTCCGG GTCTGAACTA TACGATGAAG 240  
GGCTCCAAAA CCGAATGGGA TATACCCGAA ATGGTTCCCTG GTACCTATAT TACGATGGTT 300  
TCCACTCGCT TGCATATCT GCAACTGCCG ATCAATGCCG GCATGCGGTT CGACCTGATG 360  
AATGACATGG CGGTTTCGAT CGAAGCGGGT CCTTTCCTTG CATACGGTAT ATATGGTACA 420  
TATCGGAGGA AGTTGGAAGG ATGGAAGCGG AACAACTACA GCACAGAGTT TTTTGGCCCA 480  
ACGCTTGGTG GCCCAACAAA TATCCGCTGG GACATCGGGG CAAACATAAT AGCCGCATTC 540  
CACTATAAGC GTTATTATAT ACAGATAGGC TATGAACATG GATTGTGGA TATTGTGTCA 600  
GGTGGAGGTT CTGATATTCC CCGACTGAAC GACAATAGGC AATCCTCTTC GACGACCGCT 660  
CTAAGAGAAA AGGGAAATAA CGAATACGCT TATAATCGTG ACTTCTTCGT GGGCATAGGT 720  
TACCGCTTT 729

(2) INFORMATION FOR SEQ ID NO:218

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 621 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature



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(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

5	ATGAAAAGAA	TGCTGCTGCT	TCTCGTTGTA	TTATTATATG	GAATTGCAGG	CCGATTGGCT	60
	GUACAAGACG	TTATCAGACC	ATGGTCATTG	CAGGTCGGAG	CGGGATACTC	CGATACGGAG	120
	AACATCCCGG	GAGGATTAC	CTATGGTTTC	TATTTGGGAA	AGCGTATGGG	GAGCTTTCTG	180
	GAAGTGGGGG	TGTCCATGTA	CAACTCCACA	CGTCAACAG	CCAACAATGC	AGACTCCTTT	240
	GCATCGAAGC	AAGGAGACGG	ATCTTTTCAG	GTAAATATGT	CTTCTCCGAA	TGAGAAGTGG	300
10	TCATTCTTCG	ATGCAGGCAG	TGCCAACTGC	TATATGATCG	TCGTCCGGAGT	CAATCCTCTC	360
	CATCTGTTTT	GGCAGAATAG	CCGGCACAAT	TTGTTTCTGG	CAGTACAAGC	CGGCCTGTCC	420
	AATAAGCACA	ATATTCATT	CATCTATGGA	GACAAGGGAG	CCAAAGTCAG	TATCTACACC	480
	AATTCGAATA	CCTACATCGG	TTACGGAGCA	CGTGTAGCCT	ACGAATATCA	AATTCATAAA	540
15	AACGTGGGGG	CGGGTGCCGC	TGTAATGTAC	GACCACGGCA	ATAAGATGCT	TACGGCCATG	600
	GCCACGCTCT	CCACTCATT	T				621

(2) INFORMATION FOR SEQ ID NO:219

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2853 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYRONOMAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

40	ATGAGAGTAT	CCGATCTCTG	TTCCAGACTT	TCATGGTTAT	TACCCGTAAT	CCTTGTGCGA	60
	TTGCTCTGTG	CTACTTTGGT	CGCTGCGGAA	CGTCCTATGG	CCGGAGCAGT	CGGATTGCAC	120
	CACCGTCGGC	ATGCTGCGCT	GTCTGATTCT	ACAGCGAAAG	ACACGGTGCC	TCTCGCAAAA	180
	CCTATTCCCTG	ACAGTGCTTT	TGAGATTCC	CTTCTGCGG	ATTCACCGG	ATCGATGCGG	240
45	CAAGATAGCG	TGTATGACGA	TGAATTCGAA	TTGGAAGATA	TAGTGGAGTA	CGAAGCTGCC	300
	GATTCCATCG	TTTTGCTCGG	ACAGAATCGT	GCCTATCTTT	TGGGCAAGAG	CTATGTGASC	360
	TATCAAAAAG	GTGCTTGGA	GGCAAACCTC	ATGTATCTCA	ATACCGACAG	CAGTACGGTT	420
	TATACTCGCT	ATGTCTCGA	TACGGCGGGT	TATCCGATGG	CCTTTCCTGT	TTTCAAGGAT	480
	GGAGAGCACT	CGTTTCAAGC	CAAGAACTTT	ACCTACAAC	TCCGACCGGA	GAAGGGGATT	540
50	ATCAGCGGAG	TGATCACGCA	GCAGGGCGAA	GGCTATCTGA	CTGCCGGTAA	GACCAAGAAG	600
	ATGCCCGACA	ATATCATGTT	TATGCAAGGA	GGGCGTTATA	CGACCTGCGA	CAATCACGAT	660
	CATCCTCACT	TCTATATCAA	TCTTTCCAA	GCAAAGGTGC	ATCCGGAGAA	AGACATCGTC	720
	ACAGGTCCGG	TCAATCTGGT	TATCGCCGAT	ATGCCGCTGC	CGATAGGTCT	TCCTTTGGGC	780
	TATTTTCCCT	TTTCCAACAA	ATACTCTTCC	GGTATATTGA	TGCCCACGTA	CGGAGAGGAC	840
55	AATCGCTATG	GATTTTATTT	GAGGAATGGT	GGATATTATT	TTGCCCTCAG	CGACTATATC	900
	GATTTGGCAT	TGCGTGGGGA	GATCTTTTCC	AAAGGGTCAT	GGGGCATTTT	AGCCCAATCG	960
	AAATATAAGA	AGAGGTATAA	GTACAACGGC	TCGTTGGAAG	CCAATTATCT	GGTATCGAAG	1020
	TCCGGCGACA	AATACGTGCC	CGGAGACTAC	AGCAAGACCA	CCAGTCTGAA	TATCCGATGG	1080
	ACACACAGTC	AGGATCCGAA	GGCCAATCCT	TTGCAAACTG	TGTGGGCCAA	TGTCAATTTT	1140
60	GCAACCGGGA	GCTATTTCCA	GAATTCGCTG	AATACCACCT	ATGATGTCAA	TGCCCGTACT	1200
	GCTACGACAC	GAAGTTCCGC	CGTGAGCTAT	TCGGCGAAGT	TTCCGGGTAC	TCCTTTTTCG	1260
	ATTACGGGTA	GCATGGATAT	CAGCCAGAAC	ATGCCGATA	CGACGGTGAG	CCTTACCTTG	1320
	CCGAATCTTT	CGATTAATAT	GTCCACGCGT	TATCCTTTCA	AGCCGAAGAC	CCGTGTAGGA	1380
	CCGAGCGGAT	GGTACGAGAA	STTGAGTGTG	GGCTATTCCG	GTGAGCTTCG	CAATAGTATC	1440
65	TTGACAAAG	AGAAAGATTT	GCTCCAGAGC	AATCTCGTGC	GCGATTGGAA	GAATGGTATG	1500
	CGTCATTCCG	TACGATCAG	TTTGACTGTC	CCTTTGTTGG	ATTATATCAA	TCTGACTATG	1560
	GGGGTTAACT	ACAATGAGTG	GTGGTACACG	AAAGGCATAC	GGAACTCGTG	GAATGAGGAT	1620
	AAGAAAACAT	TCCTGCCTTC	GGACACGACC	TATAAATTCC	GCAGACTGTA	CGATTACAGT	1680
	CTGTCCGAG	GCTTATCTAC	CACATTGTAC	GGTATGTTCA	AGCCTTGGAA	ACCTTTTTC	1740
70	TTCCGAGGCA	ATCTCATTAT	GATCCGTGAT	CGCTTCACGC	CCACTGTGAG	TTTCTCCTAT	1800
	ATGCCGAGCT	TCACGAAACG	CCGATATGGC	TTTTGGGAGC	TTCTTGAGCA	TACGGATCAG	1860
	AAOGCAAGC	TGCATACGCT	GCTCTACTCT	CCTTATTTTC	AGCAGATATT	CGGTGCTCCC	1920
	TCCATGGGCA	ATGCAAGATC	TGTCAATTTT	TCTTTTGACA	ACAACCTAGA	GGCCAAGATC	1980
	AAATCCAAAT	CGGATTGAC	AGGGATCAAG	AAGATCAGCC	TGATAGATCA	GTTACATGG	2040
75	TCTACATCCT	ATAATATGTT	TGCCGATTCC	ATCCGATGGA	GCAATATCTC	GGCTTCGCTG	2100

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5 GCACTTCGCC TCTCCAAGAG CTTTACCTTG CGCTTGTCCG GTCTGTTCGA TCCCTATTTC 2160  
 ACGAAGTATT ATCAGGGGAGA AGATGGGAAG ATCATTCCCT ATAAGAGCAA CGACCTGCGC 2220  
 ATTTTAAACG GCAAGGGATT GGCACGCTG ATCAGTACGG GTACTCTTT CAGCTATAGG 2280  
 CTCAACAAAG AGTCGCTCAG CGGATTGATA GCTCTTTCA GTGGCAAAA GGAGCGGAGA 2340  
 10 GATGAAAAA AAAACACAGG GGCTACTCCT CATGAAGGAG ACGATGCTGC CGATATACTT 2400  
 GAGGAGGAA GACCGCAAAA TGAAAGTGGG GGGTCGCTCC TCGAGCGCAA CCGTCAGGGC 2460  
 GGAGCAGTGG ATCAGGATGG TTAATTGCGA TATTGATCC CATGGAGCCT GTCCTTCGAC 2520  
 TATAGTTGGA ATATTGCTAC CGACTACAAT AGGTACAATG TCAATAAGAT GGAGCACTAC 2580  
 TACGGGTA CGCAGAACT GAGCTTTCGG GGCATATCC AGCCTACACC GAACTGGAGC 2640  
 15 TTGGGATTCA ATGCGAACTA CAATTTTCGAC TTGAAGAAA TAACATCGCT TACCTGCAAC 2700  
 GTCACTCGCG ACATGCACTG CTGGGCTATC TCGGCCAGTT TCATCCCTAT AGGAGCATAC 2760  
 AAGTCCCTATA ATTTCGTCAT ATCGGTGAAG AGTTCACCT TGCAGGATCT GAAGTATCAG 2820  
 CAGAGCAATC GTCCCATCAC GAATACTTGG TAT 2853

## (2) INFORMATION FOR SEQ ID NO:220

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3678 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3678

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

40 ATGATGAAAC GATATACAAT AATTCCTGCA GTTTTCTTT TATTCTGCAC GGTATTACC 60  
 TTTCAAAATA AAGCTCGCCC TTATGAAAGA TTTGCAGATG TAGAGAAGCC TTGGATTACG 120  
 AAACATTCAA TGGATTCTAA ATTGGTGCTT GCAAATAAGG GTAACCTAAT TCAAGCTGAA 180  
 ATTGTATACC AATCTGTTTC TGAACATAGT GACTTAGTTA TTTCACCTGT GAACGAAATA 240  
 AGGCTGCA ATCGTTTCCC TTGCGATAGG AAGTCTTTT TTGCAGAAA TCTACGGGCA 300  
 45 TCTCCCCCG TAGTTCCCGT TGCCGTCGAC AAGTATCGCG TACCGGTTGC CAATCCAATG 360  
 SATCCTGAAA ATCCCAATGC CTGGGATGTG ACGCTAAAA TCACTACTAA AGCGGTAACA 420  
 GTACCTGTGC ATGTGGTGAT GGTATCGAC CAGTCTTCGT CAATGGGAGG GCAAAACATT 480  
 GCCAGATTAA AGTCTGCCAT TGCATCGGGA CAGCGTTTTG TGAATAAAT GTTGCTAAG 540  
 GGGACGGCTA CAGAAGGGGT GCGTATCGCT CTGTGAGTT ATGACCATGA GCCTCATCGC 600  
 TTATCTGATT TTACCAAGA CACTGCTTTT CTCTGTCAA AATCCGGGC TTGACTCCT 660  
 50 ATTTGGGGAA CACATACCCA GGGGGGCTT AAAATGGCGA GAAACATTAT GGCCACTTCT 720  
 ACTGCTGTGG ATAAGCATAT CATATTGATG TCTGACGGGT TAGCGACGGA GCAGTATCCT 780  
 GTTAAAAATG TAACTACTGC AGACTTCATT GGCAAACTG GAAATGCGAA TGATCCCATT 840  
 GATTGTGTTA TACAAGGAGC AATTAAITTC CCTACAAAT ATGTTTCCAA CAATCCATCT 900  
 ACACCTCTTA CCCCAATTA TCCAACTCAT TCTTCTAAG TTGGACGGAG AAATCTGCG 960  
 55 GAATCCAAAT TCGATTATAG TAATCTGAGT GCAAGGATTA CTTTGTATGG TGTGTGTCG 1020  
 GCATTGGTCT ATGAACCGAG GTTTCCTCAT CCCTATTATT ATTATTCCC TTGTAACGCT 1080  
 GCTATCAATG AGGCTCAGTT TCGCAAAAAC TCTGGTTATA CAATCCATAC TATTGGCTAT 1140  
 GACCTGGGAG ATTTTGCTT GGCCAACAT TCGTTGAATC TAACGCTAC AGACGAGAAT 1200  
 60 CACTTCTTTA CGGCGACACC GGCCAATTTA GCTGCAGCGT TTGATAATAT TGCCCAAACT 1260  
 ATTAATATAG GTATACAGAG GGGGGAGGTG ACGGACTTTG TAGCTCCTGG TTTATCGTT 1320  
 AAAAATCTGA CGCAATCGGG AGATGTTACT CATTTGCTAA ATGTTTCAA TGGAACGGTG 1380  
 CACTATGATG TCTCTACTAA AAACTGACA TGGACTACTG GTACTATCCT GAGCTCATCA 1440  
 GAAGCTACCA TAACCTATCG TATTTATGCC GATTTGGATT ATATACAGAA CAATGATATT 1500  
 CCGGTAAATA CTACTTCTGC TATCGGCCG GATCTTGGTG GATTGCATAC CATACCGAG 1560  
 65 GCAAAATGA CCTATACCAA TTCCAATGGC GAACCGAATC AGCAGTTAAT TTTCCCACCT 1620  
 CCGACGGTTA AGTTAGGTTA TGGTGTATT AAGCGGCACT ATGTATTGGT AAATAAGAGC 1680  
 GGTCACCCCA TACAGGCAAA TGGAACAGTT GTCAGTTCCC TAAGCGAGGC TCATGTTCTA 1740  
 CAGTCACAAG ATTTCTTTT GCCCTCAGGT GGAGGTACATA TTGTTCCCAA ATGGATAAAG 1800  
 70 TTGGACAAAA CGACGGAAGC ATTACAGTAC TATTCCGTAC CGCGACTAA CAGGTCATC 1860  
 ACTACTGCCG ATGGTAAACG TTATCGTTT GTCGAAGTCC CAGGCTCCAC GCCGAATCCG 1920  
 GGCCAAATCG GTATCAGTTG GAAAAACCG GCAGGAAACG CTACTTTCG TTACAAGCTC 1980  
 CTCATTATT CGATGGGAGG AACACAGAC CAACAGAGTG AATGGGATGT GAGCTCCAAT 2040  
 TGGACAGGAG CCCAAGTACC GCTCACAGGA GAAGATGTAG AGTTTGAAC GACAGAAAAT 2100  
 75 TCGGTTCTC CGCGGTAGC CGATTGCAAT GTCCCGACAA CCAACCCAA AATTATCGGT 2160  
 AACCTATCA ATAATCCGA CAAGGATTTA GTTGTACCA CAAGCAGTCA ATTGACGATC 2220

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AACGGCGTGG TTGAGGATAA CAATCCGAAT GTCGGTACGA TCGTCGTGAA GTCGTCGAAA 2280  
 GACAATCCTA CGGGGACATT GCITTTTGCC AATCCGGGCT ATAATCAAAA TGTAGGGGGG 2340  
 ACCGTCGAGT TTTACAAATCA GGGATATGAT TGTGCCGATT GTGGTATGTA TCGCAGGAGC 2400  
 TGGCAGTATT TCGGTATCCC TGTCAATGAA TCAGGTTTTC CAATTAATGA TGTGGGCGGA 2460  
 5 AACGAGACCG TCAACCAATG GGTGAGCCT TTCATGGCG ATAAGTGGCG GCCAGCACCT 2520  
 TATGCACCTG ATACAGAGCT TCAAAAATTC AAGGGCTACC AGATCAGGAA TGACGTGCAG 2580  
 GCACAGCCTA CGGGAGTTTA CAGCTTCAAG GGTATGATTT GTGTGTGCGA TGCCTTCTCG 2640  
 AATCTGACAC GCAGCTCCGG TGTCAACTAC TCGGGCGCCA ACTTGATCGG CAACTCATAC 2700  
 ACTGGAGCCA TCGACATCAA GCAGGGTATT GTCTTCCGCG CGGAAGTCGA GCAGACGGTG 2760  
 10 TATCTGTTCA ACACGGGAAC ACACGACCGG TGGCGTAAGC TTAATGGAAG CACGGTTTCA 2820  
 GGCTATCGAG CCGGTACGTA CCTCTCTGTA CCTAAGAATA CAGCGGGTCA GGCAATCTT 2880  
 CCGGATCGTA TTCCATCGAT GCATTCCTTC TTGGTGAAGA TGCAGAACGG AGCGTCTTGT 2940  
 ACGTTGCAHA TCTGTACGA TAAGCTGCTC AAGAACACGA CTGTAAACAA CGGTAATGGT 3000  
 ACGGATGACA CATGGCGATC CGGCAACTCC GGATCGGCGA ATATGCCGTC ACTTGTGATG 3060  
 15 GATGTTCTTG GTAACGAGTC GGGCGACCGT TTGTGGATCT TTACCGATGG GGGTCTTCT 3120  
 TTGGATTTCG ACAACGGCTG GGATGGTCGC AAGCTGACTG AAAAAGGTTT GTCACAACTT 3180  
 TATGCGATGT CTGACATCGG TAATGATAAA TTCCAGTTG CAGGGGTTCC GGAGTTGAAT 3240  
 AACCTGCTGA TCGGCTTCGA TCGGATAAAG GATGGTCAAT ACACGTTGGA GTTGTCTCT 3300  
 TCGGATCATT TTGCGAAAGG GGCTGTTTAC CTGCACGATC TTCAGTCAGG AGCCAAACAC 3360  
 20 CGTATTACSA ATTCTACGTC GTATTCAATC GATGCCAAGC GGGGAGATTC CGGGGCTCGT 3420  
 TTCCGCTTGT CATATGGATG TGATGAGAAC GTAGATGATT CGCATGTGCT GAGTACAAAT 3480  
 GGCGGTGAAA TTATAATTCT GAATCAAGAT GCTCTTGACT GCACGTGAAC CTIATTCACA 3540  
 ATAGAAGGTA AGCTTCTTCG CCGCTTGAAA GTATTAGCTG GTCATAGAGA AGTCATGAAA 3600  
 25 GTGCAGACCG GAGGGGCTTA TATTGTGCAT CTTCAAAATG CTTTCACTAA TGATGTGCAT 3660  
 AAGGTGCTTG TTGAGTAT 3678

## (2) INFORMATION FOR SEQ ID NO:221

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3675 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3675  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

50 ATGAAACGAT ATACAATAAT TCTTGCAATT TTTCTTTTAT TCTGCACGGT ATTACCTTIT 60  
 CAAATAAAAG CTCGCCCTTA TGAAAGATTI GCAGATGTAG AGAAGCCTTG GATTTCAGAAA 120  
 CATTCAATGG ATTCTAAATT GGTGCCTGCA AATAAGGGTA ACTTAATTCA AGCTGAAATT 180  
 GTATACCAAT CTGTTTCTGA ACATAGTGAC TTAGTTATTT CACCTGTGAA CGAAATAAGG 240  
 55 CCGTCAAATC GTTTCCTTTC GCATAGGAAG TCTTTTITG CAGAAAATCT ACGGGCATCT 300  
 CCCCCGTTAG TTCCCGTTGC CGTCGACAAG TATGCGGTAC CGGTTGCCAA TCCAATGGAT 360  
 CCTGAAATTC CCAATGCCTG GGTGTGACG CTAAAAATCA CTACTAAAGC GGTAACAGTA 420  
 CTTGTGATG TGGTGATGGT TATCGACCAG TCTTGTCTCA TGGGAGGGCA AAACATTGCC 480  
 60 AGATTAAAGT CTGCCATTGC ATCGGGACAG CGTTTGTGTA AAAAAATGTT GCCTAAGGGG 540  
 ACGGCTACAG AAGGGGTGCG TATCGCTCTT GTGAGTTATG ACCATGAGCC TCATCGCTTA 600  
 TCTGATTTTA CCAAAGACAC TGCTTTTCTC TGTCAAAAAA TCGGGCTTTT GACTCCTATT 660  
 TGGGGAACAC ATACCCAGGG GGGGCTTAAA ATGGCGAGAA ACATTATGGC CACTTCTACT 720  
 GCTGTGATTA AGCATATCAT ATTGATGTCT GACGGGTTAG CGACGGAGCA GTATCCTGTT 780  
 65 AAAAAATGTA CTACTGACGA CTTTATGGC AAAACTGGAA ATGCGAATGA TCCCATTGAT 840  
 TTGGTTATAC AAGGAGCAAT TAATTTCCTT ACAAATTATG TTTCCAACAA TCCATCTACA 900  
 CCTCTTACCC CAAATTATCC AACTCATTCT TCTAAAGTTC GACGGAGAAA TCTGCCGGAA 960  
 TCCAAATTCG ATTATAGTAA TCTGAGTGCA AGGATTACTT TTGATCGTGT TGCTGGCGCA 1020  
 TTGCTCTATG AACCGAGGTT TCCTCATCCC TATTATTATT ATTTCCCTTG TAACGCTGCT 1080  
 ATCAATGAGG CTCAGTTTGC GAAAAACTCT GGTATACAAA TCCATACTAT TGGCTATGAC 1140  
 70 CTGGGAGATT TTGCCTTGGC CAACAATTGC TTGAAACTAA CCGCTACAGA CGAGAATCAC 1200  
 TTCTTTACGG CGACACCGGC CAATTAGCT GCAGCGTTTG ATAATATTGC CCAAACCTATT 1260  
 AATATAGGTA TACAGAGGGG GGAGGTGACG GACTTTGTAG CTCCTGGTTT CATCGTTAAA 1320  
 AATCTGACGC AATCGGAGA TGTACTCAT TTGCTAAATG TTTCAAATGG AACGGTGAC 1380  
 TATGATGTCT CTACTAAAAA ACTGACATGG ACTACTGGTA CTATCCTGAG CTCATCAGAA 1440  
 75 GCTACCATAA CTTATCGTAT TTATGCGGAT TTGATTATA TACAGAACAA TGATATTCCS 1500

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	GTAAATCTACTA	CTTCTGCTAT	CGGCCCGGAT	CTTGGTGGAT	TCGATACCAA	TACCGAGGCA	1560
	AAATTGACCT	ATACCAATTC	CAATGGCGAA	CCGAATCAGC	AGTTAATTTT	CCGACGTCGG	1620
	ACGGTTAAGT	TAGGTTATGG	TGTTATTAAG	CGGCACATG	TATTGGTAAA	TAAAGACGGT	1680
	CAACCCATAC	AGGCAAAATG	AACAGTTGTC	AGTTCCCTAA	CGCAGGCTCA	TGTTCTACAG	1740
5	TCACAAAGATT	TCTTTTGGCC	CTCAGGTGGA	GGTCATATTG	TTCCTCAATG	GATAAAGTTG	1800
	GACAAAACGA	CGGAAGCATT	ACAGTACTAT	TCCGTACOSC	CGACTAACAC	GGTCATCACT	1860
	ACTGCCGATG	GTAACGTTA	TCGTTTTGTC	GAAGTCCGAG	GCTCCACGCC	GAATCCGGGC	1920
	CAATTCGGTA	TCAGTTGGAA	AAAACCGGCA	GGAAACGCTT	ACTTCGCTTA	CAAGCTCCTC	1980
	AATTAATTGGA	TGGGAGGAAC	AACAGACCAA	CAGAGTGAAT	GGGATGTGAC	GTCCAATTGG	2040
10	ACAGGAGCCC	AAGTACCGCT	CACAGGAGAA	GATGTAGAGT	TGCAACGAC	AGAAAATTTC	2100
	GGTTCTCCGG	CGGTAGCCGA	TTTGATGTC	CCGACAACCA	ACCCCAAAT	TATCGGTAAC	2160
	CTTATCAATA	ATTCCGACAA	GGATTAGTT	GTTACCACAA	GCACTCAATT	GACGATCAAC	2220
	GGCGTGGTTG	AGGATAACAA	TCCGAATGTC	GGTACGATCG	TCGTGAAGTC	GTGAAAGAC	2280
	AATCCTACGG	GGACATTGCT	TTTTGCCAAT	CCGGGCTATA	ATCAAAATGT	AGGGGGGACC	2340
15	ATCGAGTTT	ACAATCAGGG	ATATGATTGT	GCCGATTGTG	GTATGTATCG	CAGGAGCTGG	2400
	CAGTATTTCG	GTATCCCTGT	CAATGAATCA	GGTTTCCAA	TTATGATGT	GGCGGAAAC	2460
	GAGACCGTCA	ACCAATGGGT	TGAGCCTTTC	AATGGCGATA	AGTGGCGGCC	AGCACCTTAT	2520
	GCACCTGATA	CAGAGCTTCA	AAAATTCAG	GGCTACCAGA	TCACGAATGA	CGTGCAGGCA	2580
20	CAGCCTACGG	GAGTTTACAG	CTTCAAGGGT	ATGATTGTG	TGTGCGATGC	CTTCCTGAAT	2640
	CTGACACGCA	CGTCCGGTGT	CACTACTCG	GGCGCCAAT	TGATCGGCAA	CTCATACACT	2700
	GGAGCCATCG	ACATCAAGCA	GGGTATTGTC	TTCCCGCCGG	AAGTCGAGCA	GACGSGTAT	2760
	CTGTTCAACA	CGGGAACACG	CGACCACTGG	CGTAAGCTTA	ATGGAAGCAC	GGTTTCAGGC	2820
	TATCGAGCGG	GTCAGTACCT	CTCTGTACCT	AAGAATACAG	CGGGTCAGGA	CAATCTTCCG	2880
25	GATCGTATTC	CATCGATGCA	TTCTTCTTG	GTGAAGATGC	AGAACGGAGC	GTCTTGACG	2940
	TTGCAHATCT	TGTACGATAA	GCTGCTCAAG	AACACGACTG	TAAACAACGG	TAATGGTACG	3000
	CAGATACAT	GGCGATCCGG	CACTCCGGGA	TCGGCGAATA	TGCGGTCACT	TGTGATGGAT	3060
	CTTCTTGGTA	ACGAGTCCGG	CGACCGTTTG	TGGATCTTTA	CCGATGGGGG	TCCTTCTTTC	3120
	GGATTGACGA	ACGCTGGGGA	TGGTCGCAAG	CTGACTGAAA	AAGGTTTGTC	ACAACTTTAT	3180
30	CGGATGTCTG	ACATCGGTAA	TGATAAATTC	CAGGTTGCAG	GGGTTCCGGA	GTGGAATAAC	3240
	CTGCTGATCG	GCTTCGATGC	GGATAAGGAT	GGTCAATACA	CGTTGGAGTT	TGCTCTTTCG	3300
	GATCATTTTG	CGAAAGGGGG	TGTTTACCTG	CACGATCTTC	AGTCAGGAGC	CAAAACACCGT	3360
	ATTACGAATT	CTACGTCGTA	TTCAATCGAT	GCCAAGCGGG	GAGATTCCGG	GGCTCGTTTC	3420
	CGCTTTGTCAT	ATGGATGTGA	TGAGAACGTA	GATGATTCGC	ATGTCGTGAG	TACAAATGGC	3480
	CGTGAAATTA	TAATTCTGAA	TCAAGATGCT	CTTGACTGCA	CTGTAACCTT	ATTGACAATA	3540
35	GAAGGTAAGC	TTCTTCCCGC	CTTGAAAGTA	TTAGCTGGTC	ATAGAGAAGT	CATGAAAGTG	3600
	CAGACCGGAG	GGGCTATAT	TGTGCATCTT	CAAAATGCTT	TCATAATGA	TGTGCATAAG	3660
	GTGCTTGTG	AGTAT					3720
40	(2) INFORMATION FOR SEQ ID NO:222						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 1275 base pairs						
45	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
50	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
55	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc feature						
60	(B) LOCATION 1...1275						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222						
	ATGGAAGTGA	AGAAAAACAC	AGTGGTGCTA	CGCCTTCTGA	TTTGGTTCGT	GGCCATTCTT	60
65	CTCTTCCACT	CCTCAGGCT	GTGGGGACAG	GAAGGGGAGG	GGAGTGCCCG	ATACAGATTTC	120
	AAAGGATTCTG	TGGATACCTA	CCATGCCGTA	CGCAGCTCTT	CTCCTTTTGA	TTTCATGAGC	180
	TCGCGTACGA	GAGTGAGAGG	TGAGCTGGAG	AGGTGCTTGG	GTAATTCGAA	AGTAGCCGTA	240
	TCGGTCAATG	CCACCTACAA	TGCTTACTG	AAAGACGAGA	CCGGCTTACG	TTTACGTGAA	300
	GCCTTCTTGG	AGCATCAGGA	AGAGCATTGG	GGGTTGCGCC	TCGGACGACA	GATTGTCAAT	360
70	TGGGGGCGTG	CCGACGGTGT	GCGCATCAGC	GATCTGATCT	CCCGGATGGA	TATGACCGAG	420
	TTTCTGGCAC	AGGATTACGA	TGATATTGCT	ATGCCGCTCA	ATGCATTGGC	TTTCTCTGTC	480
	TTCAACGAAT	CGATGAAAGT	GGAACTCGTG	GTAAGTCTG	TATTCGAGGG	GTACCGTCTG	540
	CCTGTGGATC	CTCGCAATCC	TTGGAATATC	TTCTCCCTTT	CGCCCATTCG	TCAGGGGATG	600
	AATATCGTCT	GGAAAGAAGA	AGCCGGCAAA	CCGGCCTTCA	AGGTTGCCAA	TATCGAGTAC	660
75	GSTGCGCGAT	GGAGCACTAC	GCTCTCCGGT	ATCGACTTCG	CTTTGGCTGC	ATTGCATACA	720
	TGGAAACAGA	TGCCCGTCAT	CGAAGTACAG	GGCATTGTGC	CGACGGAAAT	CATCGTTAGC	780

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5 CCGCGCTATT ATCGTATGGG ATTGTGCGGC GCGGACCTCT CCGTACCGGT CGGACAGTTT 840  
 GTTTTCAGGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC 900  
 GAGCAAGAGG GTTTCCAAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT 960  
 GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTCATC 1020  
 TCCCAAAGAC AACATTCTAC CCGTATTACT CTCAATGTTT CCAAGAAATT CTTCCGCGAGT 1080  
 ACACTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAAGGATG GTTCAGTCCG 1140  
 TTTGCAGCTG ACTATGCCCT GAACGATCAG ATACATCTGA TGGCCGGATA TGA CTGCTGTTT 1200  
 AGTAGTAAGG GCAGCGGTAT ATTCGATCGC TACAAAGACA ATTCGGAAT CTGGTTCAAA 1260  
 10 GCGCGCTACA GCTTC 1275

## (2) INFORMATION FOR SEQ ID NO:223

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1212  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

35 ATGTCTCTCT GTGAGGTGGC TTATTTTTC CTAAGCCGA TCGATCTGCA GAACATCCGC 60  
 GAACGGAATC ACTCTCCGA CATCGCGCTT TCCAATTTAT TAGACAATTC GAATCAGCTA 120  
 TTAGTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTCCAAT 180  
 TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 240  
 ATACTCCTGA CCACTGTTCT TTTGCTGTTT GGAGAGATTC TGCCGAAAGT GTATGCCGGG 300  
 40 AAGAATCCGC TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCGGTTAT CTATAAGATA 360  
 TTGTCACCGT TTTCAAATTT GCTGGTCAAA ACTACCGGCA TCGTTACCAG AGGTATCAGC 420  
 AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CGGTAGCCCT CACCACTACG 480  
 GAGGAGAGGC GGGAGGAGAA AGAAATGATT AACGAAATCA TCAAATTTCTA TAATAAGACA 540  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATTT 600  
 45 CGTAAGATGC TTGACTTCGT TGTTCGTCG GGTATTCCA GACTTCCCGT TTCAGAGGGG 660  
 TCAGAAGACA ATATCAAGG GGTGATTAC ATCAAAGATC TAATCCCA CAATGGATAAA 720  
 GCGATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTGTCCC CGAAAACAAG 780  
 CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCTC CATCGTTGTG 840  
 50 GATGAGTTTC GTGGCACTTG CGGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 900  
 GCGAGATTA CCGACGAGTA CGATGAGGAA GAACTCCCTT TTAAGGTTT GGGGATGGC 960  
 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCCGATGTTT GACACTATCT TGACCTTCCG 1020  
 GAAATGCTT TCGGTGAATT GGGGGACGAG GTAGATACGC TAAGTGGGCT CTTCTGGAA 1080  
 ATCAAGCAGG AACTCCCCCA TGTGGCGGAT ACAGCAGTGT ACGAGCCATT CCGCTTTCAA 1140  
 55 GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAAGA TTTCCCTTT CGAGCGCACT 1200  
 TGGAGGTCG AA 1212

## (2) INFORMATION FOR SEQ ID NO:224

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

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PCT/AU98/01023

154/ 490

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...780

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:224

5  
10  
15  
20

ATGAACTAT	TACTTTATCT	CCTATTGGTC	TTGTGACTC	TATCCCGAT	GTATTGCAA	60
ATGCTCTCT	CAGAGAATCT	CACAAATGA	ATAGACAGCA	CCAAAACCAT	ACAAGGAACG	120
ATATTGCCC	TACTGGATT	CAAAACCGAA	AVGGAAAATG	TGTTACCTT	CAAAAATACT	180
GCCAACTCA	ATCTGCTGAT	AAAGCACGGT	CAAGTAATCA	ACTTAATTAA	TAAAGCTTGAG	240
TTTTCTACCT	ATGGCAATAA	ACTAACCGTA	AGTGGAGGAT	ATGTACACAC	CGAATACCGC	300
TAITTTGTTG	ATCATGTTTT	TGAGGTTTAT	CCTTATGTCG	AGTCGCAATG	GGCAGAAAGT	360
ACAGGAATGA	AATATAAGGT	TTCTACGGGA	TTACAGTCGC	GTTATCGGCT	GGTAAATAGT	420
GATAACTGTC	TCATGTTTGC	AACATTGGGG	GTATTTTTCG	AAATCGAAAA	GTGGGAACAG	480
CCAGCCACTA	GCCTCTTTGC	AGGAACGTAT	GCATACAGCC	GAAGTATCAA	AAGCCACCTG	540
TCTATCAGTT	TCAGACATCG	GTTGGGTGAA	CATTGGGAAT	TTACAACTAC	GGCTATTTCAC	600
CAGGGAAGAG	CTGACAGTTA	TTTTAAGAAG	GCACGTTTTC	GAGGAGCTAT	CGACCTCAA	660
TACCATATCA	CACCTACGAT	AGGAATACGC	GGGCCTATC	GGATCATCTA	CGATACTGCC	720
CCTATTGTAC	CTGTGCGGAA	AGATTACAAC	ACCGTTGATG	TTGGTATCGA	TATTTGTTTT	780

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

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ATGAAACGAA	TCGTTTTATC	ATCTTTCTCG	TTCGTTCTGT	CCATACCTTC	TTTGATGGCA	60
CAGAACAATA	CCCTCGATGT	ACACATATCC	GGTACGATCA	AGGATGCTTC	CTCCGGGCGAA	120
CCAGTGCCCT	ATGCCACTGT	AAGCATCCGG	CTGACAGGAG	CAGATACCAC	ACAGGTGTTT	180
CGACAAGTGA	CTGACGGCAA	CGGCTACTTC	GTCTAGGCCC	TGCCGGCAGC	TCCCTCCTAT	240
CACCTGACAG	CTTCGTTTGT	AGGTATGAAA	ACCCATACCA	TGCACATTAG	TCGGGGAAAT	300
GGACAGCAGC	ACATCAAATC	CATCGACATT	TCTCTCGAAT	CCGAGGACAA	ACAACCTCTC	360
ACCGTCACCG	TATCGGCAGC	ACGACCACTG	GTGAAGATGG	AGATAGACCG	CCTGTCCTAT	420
AATATGAAAG	ATGACCCCGC	AGCCAAGACG	AACAACCTGC	TCGAAATGCT	GCGCAACGTT	480
CCTTTGGTAA	CGGTGGATGG	TCAGGGCAAT	ATCCAGGTGA	AAGGATCTTC	CAACTTCAAA	540
ATCCACCTCA	ATGSCAGGCC	CTCGACCATG	GTGAGCAGCA	ACCCGAAGGA	GGTCTTTCCG	600
TCCATTCTCT	CCCATACGAT	CAAAACGGTG	GAGGTCTATC	CCGATCCGGG	TGTAAAGTAC	660
GATGCGGAAG	GCACAAGTGC	CATCCTGGAC	ATCGTCACGG	AAGAAGGTAA	GAAGCTGGAA	720
GGATATTGAG	GTTCCATCAC	GGCCAGTGTC	ACCAACAATC	CCACAGCCAA	CGGTAGTATC	780
TTTCTGACGG	CAAAGTCCGG	CAAAGTCGGG	CTGACTACCA	ACTATAACTA	CTACGGTGGC	840
AAAACAAAGG	GCTCTCGCTA	CTTTACCGAA	CGTACTACAT	CCATGCTCCA	AACGATAGAA	900
GAAGGCAAGG	GGCAAGAAAC	CTTTGGCGGA	CACCTCGGCA	ATGCCCTCCT	CTCATTCGAG	960
ATAGATTGCG	TCAATCTCTT	TACGGTGGCC	GGCAATGTAC	GCCTTTGGGA	GATGACCACC	1020
GACCGGAACA	GCGTAGAAAA	AAGCTTTGCC	GSCAGCAACC	TCATGTCTTA	CATAGACAGA	1080
AAACTCAAAA	CACAGATGGA	TGCCGGATCA	TACGAGCTCA	ATGCCGACTA	TCAGCAGAGC	1140
ACTGCGCTGC	CGGCGGAATT	GCTCACCGTT	TCCTACCGCT	TCACTCAGAA	TCTTAATAAT	1200
AGCGAGACCT	TCATTGACCA	ATGGAAGCGC	GATCCGCTCA	ACACAGCTAA	TACGATCCAG	1260
TACGCGGSCC	AGCACTCCAA	ATCCGATGCG	GGCATGGACG	AACATACGGC	ACAAGTGGAC	1320
TATACAGCTC	CCTTAGGACA	AGCACATTCT	TTGGAAGCAG	GGCTGAGTA	CATCTATCGT	1380
CATGCCACGA	GCGATCCTCT	CTATGAGATA	CGACCATCCG	AAGATGCTCC	GTGGCAGCCC	1440
GGCTCTCTAT	ATGCACAGAA	TCCGTGGAAC	GAAAGTTTCC	GCCACGATCA	ATACATCGGA	1500
GLAGCCTATG	CGGGCTACAA	CTATCGTAAG	GATCAGTATT	CTTTGCAAAC	CGGCTCCGGA	1560
GTGAAABCA	GCAAGGTGAA	AGCACTCTTT	CCCGAAAACG	CAGCAGCAGA	TTTCTCCCA	1620
AACTCGTTTG	ACTGGGTGCC	ACAGCTCAGC	CTCGGCTATA	CCCCCTCGCC	CATGAAGCAG	1680
CTTAAGCTGG	CCTATAACTT	CCGAATCCAA	CGTCTTGCAA	TGGGCCAACT	GAATCCCTAC	1740
CGGCTACAGA	CCAACGATTA	TCAAGTACAG	TATGGTAAAT	CCGACCTAAA	GTCCGAGAGG	1800
CGTCACCAAG	TCGGTCTCTC	CTATAATCAA	TACGGAGCCA	AGGTATGCTT	TACAGCATCG	1860
CTGACTACG	ACTTCTGCAA	CAACGCCATC	CAGAATTACA	CCTTCTCCGA	CCCGGCCAAT	1920

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5 CCCATCTCT TCCACCAGAC CTATGGCAAT ATCGGACGAG AGCATTCTTT CAGCTTGAAT 1980  
 ACCTATGCCA TGTACACGCC GGCCGTATGG GTCAGGATTA TGCTCAACGG AAATATCGAT 2040  
 CGCACATTCC AAAAGAGCGA AGCACTCGGC ATTGATGTCA ATTCATGGTC CGGCATGGTA 2100  
 TACTCAGGCC TGAATGTTTAC CCTGCCGAAG GATTGGACTG TGAATCTCTT CGGAGGTTAT 2160  
 TATCATGGGG GAAGAAGCTA CCAGACGAAG TATGATGGCA ATGTATTCAA CAATATCGGT 2220  
 ATAGCCAAAC AGCTTTTCCA CAAAAATTG AGAGTCTGCG TGAGCGCAAA CAACATTGAT 2280  
 GCGAAGTATT CGACATGGAA GAGCCGGACC ATCGGCAATG GATTACTAT TTATTCGAA 2340  
 AATGCCGATA TACAACGGAG TGTTCCTCC AGCCTCACCT ACAGCTTCGG TAAGATGAAT 2400  
 10 ACACAAGTGC GCAAGGTAGA GCGTACGATC GTCAACGACG ACCTCAAGCA AACCTCATCC 2460  
 CAAGGACAGC AGGTGGCGG ACAAGGAAAT CCTACCGGCA AT 2502

## (2) INFORMATION FOR SEQ ID NO:226

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1197 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

35 ATGAGACTCT CTGCCATTCT TATCGCTTTG ATTGTGATGC TGCCTGCTGT GCTTAGCGGG 60  
 CAGCATTATT ATTCCATGCC GGGAGAGCGA CTGGAGACGG ACAGCATTCTG TCCGAACGAA 120  
 CTCTCGGCAT CGATCCGAAG TCGCTTTTC TTTGGGAACA ATCAATACAA TGCACGTTCTG 180  
 40 GTCAAAGGTT ATAGTGTGCC GGTGTCACGG GTTTCGGCTT TTGCTCTTA CTCGCTGCCG 240  
 GCAGCACATG GTGTGAAGCT TTCGCTCGGA GTATCTACCC TGAAGTACTG GGGGGCAAGT 300  
 CGCTATCCGG CCGGTATCGC TTATTCGGAT TTACCTTATT GAGCGGACTA TAACGACTAT 360  
 GTACGCTTGC GTATCCTGCC TTATGTACAG GCCATGCTGA AGCCGACGGC CACGACTGCT 420  
 CTCATGCTGG GCAATATAGC CGGTGGTACG GCTCACGGAC TGATCGAACC GATCTACAAT 480  
 45 CCTGAGTTGG ATTTGACGGC TGATCCTGAA GCCGGTGTGC AATTTCGGGG TGATTGGACA 540  
 CGTTTCCGAA TGGATGTTT GGTCAATTGG ATGAGCATGA TTTTCAAAA TGACAATCAT 600  
 CAGGAGTCGT TTGTCTTTGG CTGTCTCACT ACTTCGAAAT TGTATCGGG TGAAGGCAAA 660  
 TGGCGACTCG AACTGCCCTT GCAGGCTATT GCCACGCATC GCGGCGGGGA ATACAAGTGG 720  
 GCGCAGCAGG ATACCGTGCA TACATGGGTC AATGGAGCTG TCGGACTTAA GCTTTCTGAT 780  
 50 CGCCCTCGTA CCGACAAACC CATGCAGATT TGGGGATCTG CTTATGGTGT GGCAGCCTTG 840  
 TCAAGCGGAG GATACTTCCC TTACGAAAGA GGGTGGGGCG GTTATCTTTC TCTCGGAATC 900  
 GACTTGGAGC ACTTCGCTTT TCGTACCGAC TATTGGTACG GCAGGCATTA CGTTTCTCCC 960  
 TTTGCTGCAC CTTTCGCCAA TTCCCTGACG TATGACAAAC AGCCTCTTAC GAACGGTTGG 1020  
 GGGGATTATA TTGCTCTCTA TGCCGACTAT TCGTGGCGGA TGGCAGGAAG TGTTCGTTG 1080  
 55 GCGGCTGTTG CTCGGGTATG GTTCCAGCCT TCGGATCGTT TTGCGATGAG CCACGCCTTG 1140  
 GAAGTACGA TCGTATCGA TCCCAATTTC CCAATAGCTT TTCTGAAAGG CAATCAT 1197

## (2) INFORMATION FOR SEQ ID NO:227

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1146

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

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ATGAACAAAT	CGCTATTATC	ATTGGCATGC	CTCATCCTGT	GCGGTATGCC	GGCCATCGCC	60
CAACAGACAG	GACCGGCCGA	ACGCAGCGGC	GAGCCTTCTC	TGCCCGAAGC	TGTATTGGGT	120
CTGGAGCAGA	AGCAGAAAAA	GCTGAAGGTG	TACTTAGGCA	TACAGTCGTT	CTACGACCAG	180
CCGCTTGTGG	ATGAGGAATC	CCATATCGGA	CACTTCAAGG	TACAGGAGCT	GCGGATGTCT	240
GCTCATGGCG	AACTGAACCG	CCACCTCAGC	TTCGACTGGC	GACAACTCT	CAACCGTGCC	300
GCCGACGGCA	CTTCGTTTGC	CGACAATCTC	TCCAATGCCA	TCGACATCGC	AGGTGTGGAC	360
TGGCACCCGA	ACGACAAGGT	GTCCTTCTTC	TTCGGACGTC	AGTACGCGCG	TTTCGGAGGG	420
ATAGAATACG	ACATGAACCC	CGTAGAGATC	TACCAGTACA	GCGACCTTGT	GGATTACATG	480
ACCTGCTATA	CTTCGGGCGT	GAACTTCGCA	TGGAACTTCC	ACCCCGAACA	GCAGCTGCAG	540
CTACAGGTAC	TCAATGCTTA	CAACAACCGC	TTCGCCGACC	GCTACCAAGT	GACACCCGAT	600
GTCGCTACCG	CCACGAGCTA	CCCGCTCCTC	TACTCGGCAC	AGTGGAAAGG	TACCTCTCTC	660
GGAGGAGCAC	TGCATATGCG	TTACGCCGTG	TCGATGGGTC	ATCAGGCCCA	AGAGCGTAAT	720
ATGTGGTACT	TCAGTCGGGG	CAACCTGTTC	AATCCGGGCA	AACGGATCAA	CGGATACCTC	780
GACCTACCT	ACTCGATCGA	GGGATTGGAC	GACAAAGGCA	TTATGACTGC	TCGCTACGGC	840
AAGGGCAAGA	CCCTCAAGGA	CGTCAAGTAC	TATGCTCTGG	TATCGAAGTG	GAACCTCGC	900
ATTTTCGATC	AGGTCAATCT	CTTCCTCAAA	GGCATGTACG	AGAACGGCTA	TGGCCCTGCC	960
CAATACGGCG	AGAGCAGCCA	CACGCGCCAC	TCCTACGGCT	ATATGGGAGG	GGTGGAAATAT	1020
TACCTACGG	AGACCAACTT	CCGTCTGTTC	GTCACCTACA	TAGGACGGCA	TTACCGGTAC	1080
AGTGCGACCG	AGACGGAAAG	CACCAATGCT	CTTCGCGCCG	GTCTGATCTA	TCAGATACCT	1140
TTCTTA						1146

## (2) INFORMATION FOR SEQ ID NO:228

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(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 666 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...666

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

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ATGAACATT	TGTTTAAGTC	GACATTAGTA	CTTCCTTGTG	CTCTTCTTTT	TTCGGTACC	60
TATACCTTTG	CACAAGAAAA	TAATACAGAA	AAGTCACGAT	TGATTTTTTC	TGTTAGGCTG	120
GGACAGGGAT	ATATTGCAGG	TCAACTACC	AACCTGATGT	ATGGGTATAC	ATCTGCTAAC	180
GATAGACTTT	TGCTGGTGC	AATTTATCTG	GGCTTGACAC	CAAGTAAGAA	AGAAAATGCA	240
ACCGGCGTAG	CATTTCGTTT	CTTATGCCCC	TCCTCGGGTT	ATTATGTCGA	TATATCCGGC	300
AAAGAAAATA	CCTTGAATTA	TGCGTTTATC	GTTGTGCGAG	CATATAATAG	AATAGCCATT	360
CTTATACGCC	CTATCAAAAA	TTTTAATTTT	ATCTTCTCTA	CAGAACTCGG	AATGGCTTGG	420
ATGAGTCGTC	ATGAGCAAAAT	TTACAATTCT	ACTTCGCAGA	CTTGGGATAA	GCAGCGCAAG	480
TCGAGGTGGG	GACTGGATTT	TGGTCTCGGG	ATGCATCTGC	AATHCCACAT	TAATAAGACC	540
GTTTACTTTA	TGGCAGGAAC	CGATCTTAGG	TCTTGATGTG	TCGGAAGGAG	GATCAATGAC	600
TACCAGCAAA	AGGATCGAAC	CTTCATTGCA	CTTATCGACA	ACAGTATTGG	CATAGGATTA	660
AACCTC						666

## (2) INFORMATION FOR SEQ ID NO:229

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(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGATTATCA	AGAAATGCT	GAAAAATAAA	TTGGCCCCCT	TGGCCATACT	GTTCCTTTTT	60
GCTCCAAAGG	CTATGAAGGC	TCAGGAGCAA	CTGAATGTGG	TACACACCTC	TGTGCCATCG	120
CTGAATATCA	GTCCGGATGC	ACGTGCGGCC	GGTATGGGGG	ATATAGGTGT	GGCAACGACG	180
CCGGATCGGT	ATTCACAGTA	TTGGAATCCG	AGTAAATATG	CTTTCATGGA	TACGAAAGCC	240
GGTATTAGCT	TCTCATATAC	ACCTTGGCTG	TCCAAGCTGG	TCAATGATAT	TGCCCTGATG	300
CAGATGACCG	GTTTCTACAA	ATTGGGAACA	GACGAGAATC	AGGCTATTAG	TGCTTCTCTG	360
CGTTATTTC	CATTAGGAAA	GTTGGAGACT	TTGACGAAT	TGGGCGAATC	CATGGGAGAG	420
GCCCATCCCA	ATGAATTGCG	TGTCGATTTC	GGCTATAGCC	GCCAGTTGTC	GGAGAAGTTC	480
TCCATGGCTG	TTGCACTGCG	TTACATCCGC	TCAGACCAAA	GCACCTACAA	CACCGGAGAG	540
AATCAGGCCG	GAAATGCCTT	TGCGGCGGAT	ATAGCCGGTT	ATTTCGAGAA	GTATGTGCTA	600
CTGGGTAATG	CGGAGAGCTT	GTGGTCGTTG	GGTTTCAACG	TAAAGAATAT	CGGAACGAAG	660
ATCTCCTATG	ACGGAGGTGT	CACGAGTTTT	TTCAATCCCTA	CTTCGTTGAA	TCTCGGGACG	720
GGGCTGTTGT	ATCCGATCGA	TGACTATAAC	AGCATCAATT	TCAACCTTGA	ACTTAGCAAG	780
CTGCTTGTAT	CCACTCCTCC	TATCATGGAT	CAAAACGATC	AGGCGGGGTA	TGAGGCTGCA	840
CTCAAGAAAT	ATCAGGAAC	TTCTTCGATC	AGCGGTATAT	TCTCTTCTTT	CGGTGATGCG	900
CCGGGAGGAC	TCAAGGAAGA	ATTCCGTGAG	ATTACATGCG	GACTTGGGGC	TGAATATAGC	960
TATGACGATA	AATTTTTTGT	TCGTGCGGGA	TATTCATACC	TGCACCCAC	CAAAGGCAAT	1020
TTGCAGTACT	TCACGGCCGG	TGCCGGCTTC	AAAATGAACA	TATTCCGTAT	CGATGCTTC	1080
TACCTGTTGT	CTACGATCCA	GAGTAATCCG	TTGGATCAGA	CTCTGCGGTT	TACGCTTGCT	1140
TTGCATATGG	ATGGATTGCG	CAATTTGTTT	CAC			1173

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGAAAACAA	CAGTTCAACA	AATTATTCTG	TGCCTGECTT	TAATGATGTC	AGGTGATTG	60
GGCGGAAACG	CACAGAGCTT	TTGGGAAGAA	ATAGCTCCTC	CTTTTATCAG	TAATGAGCCT	120
AACGTCAAGT	ATATAATTCC	CAATATGGGG	ATTGATTCAA	AGGGAACAAAT	CTATGTAACC	180
GTGACAAAAA	GGATTACGCA	GGGAGCAAAAT	TATACTTCTG	AGCAATTGGG	TATGTACTAT	240
CGACCATTAG	GTGATAATGA	ACAGTGGTGG	AAACATGATC	CGTATTTTGA	TGACAAGATA	300
GTTGCGGATA	TTGAGACAGA	TGCATATGGC	AGAGTTTATG	TATGTACGAC	TTCTTCTCGA	360
GATCAAGAGT	ATCAACTTTA	TATAAACGAG	CAGAACGAAT	GGAGGTGTAT	ATTCAAAAT	420
TCTGTGTCTA	CATATGAGCA	TGGTATGGCT	GTTTTCGCT	CTTCGACAGG	GGTGACTTAT	480
ATAGGTACCA	GGCATCACAT	CTTCGCATCA	GGTGTAATG	ATTTCGAGTT	CAACACTATC	540
TATGAAGACT	CTACACCTAT	GAGCTGTGCG	TTTGACAGG	CTACGAATAG	TGGCACCATC	600
TATCTGSCAT	TGATGCATGA	AACCACAATG	TCTACGACTA	TCCTTACTTA	TCAAAACGGT	660
GAGTTCGTCG	ATATCTCGGA	AAGTGAATTG	AGTAACTCGA	TATTGTCATC	CATGTGCTCT	720
AATAAAGAAG	GTGATATAAT	AGCTCTTGT	ACTTCATAAT	CAGGATTAT	GAGTGAACCC	780
CTTGCGATCA	GAAAAGCAGA	TGAAGGCCAA	TGGCAACTTG	TTGGCGGAGA	TATACAGAAT	840
GCGATCGTTC	AAAATATATG	CATGATGGAC	GACAACAAGA	TTGCTTGTGA	AGTCTTCGGG	900
ACTCCTAAGC	GAGTAGATGG	TGGGACAAGG	GTTTGTGTTT	CTGACGCATC	TGTCTTTGAT	960
TTTGAGTGGT	ATGAAGATGA	AATATACGGA	GGCCTGATAT	TTGACACTTT	CTTCTATAGC	1020
CCTTGCGACA	AACTTCTTTA	TGCGAAATTT	GGTGGGATTA	TGCTCAGGAG	TAAAGAGTCT	1080

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TTTATAACCT CTTTCATTTC TCCGACAGTT GTACAAGGAG TGGATGTCTA TACTTTGGCC 1140  
 GGCAAGATAA GGATCGAAAG TGAAACTCCG GTGTCTGAGG TGTTCCTTTT CGACCTGGCT 1200  
 GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAAATCT ATTCGGACAT AGATACTAAC 1260  
 GGAATAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTCCGG ACAGGTATT 1320  
 5 AGTCATAAGG TGCAGGTA 1338

## (2) INFORMATION FOR SEQ ID NO:231

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 924 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...924

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

30 ATGATAATCC GGTGTCTTAT CCGTCGTCGG AGAACCSTCC TGTTCGGGTT GATATTCGTG 60  
 GTAGGTCTTT TCTCTGCGAT GGCACAAGAG AAAAAGGATA GTCTCTCTAC GGTCAGCCA 120  
 GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTTCTCT CCATTGATCA CCCCCTCCTG 180  
 CCCCCTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTTA GAGACAAACA TCTTCCGAT 240  
 35 GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAACCTAAC 300  
 TTCGCGCAG AGCGTCGGGA TTCTGTTTCT CCCCCTTTCG AAACCTGCCA CGCTGCCGGT 360  
 GTCCCTTCAT GCGGACCGAC CGATAGGATG CATTTTATA CATCGGGCAA TATCGSTCTT 420  
 GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC 480  
 40 TTGCTGACTC AAAATCTTAC GGCACATGTC CAAGGCGGTT GGCAGCAGAA TTTCGGCTTT 540  
 ATACCTATGA CCGCTGTCAA TGGCCAACTG CGTTGGCAAG CCACCGAGAG ATTGAGTTT 600  
 ACCACCGTA TCGATTATCG ACAGGTACAG TGGAAATGCT TCGATAATAG AACGTTCTCG 660  
 CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGTCAATGG ATTTGGCAGC 720  
 TATCCTCTCT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATT 780  
 45 GGCCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC 840  
 GGTATGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGCTTAT 900  
 CCTGTATTCT ATGGCGATAA GAAG 924

## (2) INFORMATION FOR SEQ ID NO:232

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

70 ATGAAAACGA ATAGACGATA CGCATTTGTT TTGCCGCTTC TGCTACTCAC CGGATTGTTG 60  
 GCATGGGGGC AGGATTCTTC CCAOGGTAGC AATACAGCGT TTGCAACTGA TTCTTCGAGT 120  
 75 AGAGAGTTGC CCACGGAGCA GTCCGCCTAC CGCATTCATT CTGCCTATAT GGTCGGTGGT 180  
 GCGGGAAGCA TAACGCGCGA CACCTATTG TCACCCCTTC GTTATGGAGC ATGGACACTG 240

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AATTTGTTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCCTTG GATGATCCGT 300  
 ACCGGGCATG AGCTGGATTI TGCCCTGATG GACAATCCGG CCAATAATGC TCATTTCTAT 360  
 TCCCTGCTGT ATAACGGTTC CGCTGCGGCT CTTTACCGCC TTGGCGGTAA GCATCTGCGA 420  
 GCGCGGTGGA TGGACATCT GCGCTTGCCA TTGGGCCCGG GCTTGGAAT CGGGCTTGGA 480  
 5 GGAATTTATA GTACACGCAA CGGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC 540  
 ATCGCCCAAG CCTCGATAGG ATACTACGTC CCCTCCGAAA CTTTCCOCT GTATTTTCGG 600  
 TTGCTCTCCC AGATCAATCT CTTCGGTATA GCCTATGGAA ATGGTTTGG TGAGAGCTAT 660  
 TACGAGAATT TTTTGCTCAA TAACGGCATT GCAGGCTCCC TGCAATTCAC TTATCCGGGC 720  
 10 AAGTTTACTC GGTTCACGAC ACTCATACG GCGGATATTC CCATTCCGAA CTTCTGTAGG 780  
 CTTCGTGTCG GTTATCGCTA TTCCCAATTT GGCTCTTCGC TTAACGCATT GGATACTCGA 840  
 ATCCACAGTC ATACGGCTTT TATCGGTTTC GTCACGGAGT TTTACCGATT CCGTGGGCGC 900  
 AAAGCCATGA ATACGGGTG GAGAACCACT CTTTACTATC ATGAT 945

- 15 (2) INFORMATION FOR SEQ ID NO:233
- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 25 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...855
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

ATGGTAGTGA CGTGCTCGT AATTGTCGGT ATTGTGGTAG TAGTGCGGTA CTCCTTGC GC 60  
 GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGCCA TATTGGCTT CATCCTCCTT 120  
 40 GGAAAGACCG TTCCATGCGA TACCCGTAAC TTCTTTTCTT CCGAAAGTGA TGAACCTGAG 180  
 AGCCGTGTIG CTACCGAAAT AGCCACCTG TGCGAAATAG GATTTCAGAT CCACGCTTCC 240  
 TCTATCCACG TAGCGTCCG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG 300  
 ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGGCGGAAAT GTGCGGAACG AACCTCCGCT 360  
 45 CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC 420  
 CCAAAAGCT CCGGCACCAT TGGTGGAAAT ACCCACACCT CGCTGCACCT GAAGGTCTTC 480  
 GATGGAAGAG CCGAAGTCGG GCATATTAC CCAAAAGACG GACTGAGATT CGGAGTCGTT 540  
 GAGGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA 600  
 GCGGGAATAT CCGATACCGG TACCGGCATC GCTGGTGGCT ACCACGGAGG GAGTCAGCAT 660  
 50 CAGCAGATAG GGGATGTCAC GACCATAATT GGAATTGGAA AGTTGGGCTT TCGGAACGTT 720  
 GGTGTAAGCG ACAGGGGTTT TCGCGTGGC GCGAGTAGCT ACGACCTGTA CCGTCTGGAG 780  
 CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGAGAGCG GGTGCTTGTG CCGTCAGGCA 840  
 GAAAGGCAGG ACGGC 855

- 55 (2) INFORMATION FOR SEQ ID NO:234
- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...1797
- 65 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...1797
- 70 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...1797
- 75 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...1797

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:234

5 ATGGAACAACT TAAAGAACAT TCAGCCCAAG GAGGATTTC AACTGGGAAGA GTTTGAGGCC 60  
 GGTGGCGTCC ATGCTGCCGT GAGTCGTGAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC 120  
 AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA 180  
 GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCGGCTAC 240  
 AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAAATTTATA TCGAGAATCA GGAAGATAAG 300  
 AAGGGCCAGC TCGTCTTGTC TCACCCGAAG GGTGCTGCCG CTCGCTCTTG GGAGCGCGTG 360  
 10 AACGAGGCTC TCGAAAAGA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT 420  
 GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCCTCC CGGGATCACA GATCGACGTG 480  
 CGCCCCATTC GCGACTACGA TGCATTCTGT GAGAAGACGA TGGAGTTCAA GATTGTGAAA 540  
 ATCAATCAAG AATATAAGAA TGTAGTTGTT TCCCAAGAGG TGCTCATCGA AGCAGAGCTC 600  
 GAACAACAGA AGAAGAAGAT CATCGGCAAG CTCGAAAAAG GGCAGGTACT CGAAGGTATC 660  
 GTCAAGAATA TTAATCTCTA CGGAGTATTT ATCGACCTCG GTGGAGTGGG TGGTCTTATC 720  
 15 CATATCACTG ACCTTTCATG GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT 780  
 CAGAAGATCA ATGTCGTTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA 840  
 CTCAAACAGC TGATGCCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT 900  
 AAGGTGAAGG GTAAAGTTGT GGTGATGGCA GATTACGGTG CTTCGTTGA GATTGCACAG 960  
 20 GCGCTTAGAG GTCTTATCCA CGTAAGCGAA ATGTCATGGA CACAGCACTT GCGTCTCTGT 1020  
 CAGGACTTCC TCCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA 1080  
 GAACGCAAAA TGTGCTCGG TCTGAAGCAA CTCAGCCGGG ATCCTTGGGC TGATATCGAA 1140  
 ACTCGTTTCC CTGTAGGCTC TCGTCACCAT GCTCGTGTTC GCAACTTCAC CAATTTCTGG 1200  
 GTATTCTGTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCCGA CCTTCTTGG 1260  
 25 ACGAAGAACA TCAACACCCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTCAG 1320  
 GTAATCGASA TCGACAAAGA AAACGTCGT CTCAGCTTG3 GTCACAAACA GTTGAAGAG 1380  
 AATCCTTGGG ATGTATTCTA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA 1440  
 ATCGAAGTGA TGGACAAGGG TGCTGTGCTT TCTCTGCTT AOGGTGTGGA AGGTTTTCGC 1500  
 30 ATCCGGAAGC ACATGGTGAA GGAAGATGCC TCACAGGCTG TACTCGAAGA GAAGTTACCT 1560  
 TTCAAGGTTA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA 1620  
 TTCGAAGATG AGCAGAAAT GGCTCAGCGT GAAGCCAATG CAGAGCGTAA GGCTGAAGCC 1680  
 AAAGCGGCTC AGAAAGAAGC TGCTGCCCAA GCTGCCAATC CTCACACAGC TGTAGAGAAA 1740  
 GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAAC 1797

## 35 (2) INFORMATION FOR SEQ ID NO:235

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1650 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 45 (iii) HYPOTHETICAL: NO  
  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1650

## 55 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:235

60 ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGAGG GTACAAATCG 60  
 GAAGGTGTGG TACCTGCAAC AGAATTCGCG TACAATCCCG AACTCAAAGT GGGAGACGAA 120  
 GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTCACCGC 180  
 AAGGTCGTG CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAAA AGACGAAATC 240  
 GTAAAGCGCT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTCAATGT ATTCGGTATC 300  
 GAGGCTTTCC TCCCGGGATC ACAGATCGAC GTGCGCCCA TTGCGGACTA CGATGCATTC 360  
 65 GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT 420  
 GTTTCCCAAC AGGTGCTCAT CGAAGCAGAG CTCGAACAAC AGAAGAAAGA AATCATCGGC 480  
 AAGCTCGAAA AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTT TACCGAGTA 540  
 TTTATCGACC TCGGTGGAGT GGATGCTCTT ATCCATATCA CTGACCTTTC ATGGGGTCGT 600  
 GTGGCTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTCTG TATCCTCGAC 660  
 70 TTTGATGAAG ATCGCAAGCG TATCGCTCTC GGAATCAAAC AGCTGATGCC TCATCCTTGG 720  
 GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGTTAAAGT TGTGGTATG 780  
 GCAGATTACG GTGCTTCTGT TGACATTGCA CAGGGCGTTG AGGGTCTTAT CCACGTAAAG 840  
 GAAATGTCTT GGACACAGCA CTTCGCTTCT GCTCAGGACT TCCTGCATGT AGGCGACGAA 900  
 GTGGAAGCCG TGATCTGAC GCTCGACCGC GAAGAACGCA AAATGTCTGT CGGTCTGAAG 960  
 75 CAACTCAAGC CGATCTCTG GGCTGATATC GAAACTCGTT TCCCTGTAGG CTCTCGTCAC 1020  
 CATGCTCGTG TTGCAACTT CACCAATTTT GGTGTATTCC TTGAGATCGA AGAGGGCGTA 1080

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5 GATGGCCTTA TCCATATTTC CGACCTTTCT TGGACGAAGA AGATCAAACA CCCAGCGAG 1140  
 TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAAACCGT 1200  
 CGTCTCAGCT TGGGTCAACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA 1260  
 TTCCTGTAG GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACAA GGGTGCTGTC 1320  
 GTTTCTCTGC CTTACGGTGT GGAAGGTTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT 1380  
 GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCAAGG TTATTGAGTT CAATAAGGAT 1440  
 GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTGGAAG ATGAGCAGAA AATGGCTCAG 1500  
 CGTGAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAAGCGG CTCAGAAAGA AGCTGCTGCC 1560  
 10 GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGGAGACCT CGGCGAGCTG 1620  
 GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC 1650

## (2) INFORMATION FOR SEQ ID NO:236

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1374

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

35 ATGATCGTCG ATGTATTGCG TATCGAGGCT TTCCTCCCGG GATCACAGAT CGACGTGCGC 60  
 CCCATTCCGG ACTACGATGC ATTCTGTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC 120  
 AATCMAGAAT ATAAGAATGT AGTTGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA 180  
 CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAAGGGC AGGTACTCGA AGGTATCGTC 240  
 40 AAGAATATTA CTTCTTACGG AGTATTATATC GACCTCGGTG GAGTGGATGG TCTTATCCAT 300  
 ATCACTGACC TTTTCATGGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG 360  
 AAGATCAATG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC 420  
 AAACAGCTGA TGCCCTCATCC TTGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCGATAAG 480  
 GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGGTGCTT TCGTTGAGAT TGCACAGGGC 540  
 45 GTTGAGGGTC TTATCCACGT AAGCGAAATG TCATGGACAC AGCACTTGGC TTTCTGCTCAG 600  
 GACTTCCTGC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA 660  
 CGCAAAATGT CGCTCGGTCT GAAGCAACTC AAGCCGGATC CTTGGGCTGA TATCGAAACI 720  
 CGTTCCCTG TAGGCTCTCG TCACCATGCT CGTGTTCGCA ACTTCACCAA TATCGGTGTA 780  
 50 TTCGTTGAGA TCGAAGAGGG CGTAGATGGC CTTATCCATA TTTCCGACCT TTTTGGACG 840  
 AAGAVGATCA AACACCCAG CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTCAGGTA 900  
 ATCGAGATCG ACAAGGAAAA CCGTCGTCTC AGCTTGGGTC ACAACAGTT GGAAGAGAAT 960  
 CCTTGGGATG TATTGAGAC GGTATTCACT GTAGGATCTA TCCACGAAGG AACGGTAATC 1020  
 GAAGTGATGG ACAAGGGTGC TGTGTTTCT CTGCCTTACG GTGTGGAAGG TTTTGCCACT 1080  
 55 CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC 1140  
 AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATTG TATCTCATAG CCGTGTATTG 1200  
 GAAGATGAGC AGAATATGGC TCAGCGTGAA GCCAATGCAG AGCGTAAGGC TGAAGCCAAA 1260  
 GCGGCTCAGA AAGAAAGCTG TGCCGAAGCT GCCAATCTG CACAGGCTGT AGAGAAAGCC 1320  
 ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

## (2) INFORMATION FOR SEQ ID NO:237

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 5 (A) NAME/KEY: misc feature  
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

10 ATGGAGTTCA AGATTGTGAA AATCAATCAA GAATATAAGA ATGTAGTTGT TTCCACAAAG 60  
GTGCTCATCG AAGCAGAGCT CGAACAACAG AAGAAAGAAA TCATCGGCAA GCTCGAAAAA 120  
GGGCAGGTAC TCGAAGGTAT CGTCAAGAAAT ATTACTTCTT ACGGAGTATT TATCGACCTC 180  
GGTGGAGTGG ATGGTCTTAT CCATATCACT GACCTTTCAT GGGGTCGTGT GGCTCATCCG 240  
GAAGAATACG TACAGCTGGA TCAGAAGATC AATGTCGTTA TCCTCGACTT TGATGAAGAT 300  
CGCAAGCGTA TCGCTCTCGG ACTCAAACAG CTGATGCCTC ATCCTTGGGA TGCTCTCGAC 360  
15 AGCGAGCTTA AGGTAGGCGA TAAGGTGAAG GGTAAAGTTG TGGTGATGGC AGATTACGCT 420  
GCTTTCTGTT AGATTGCACA GGGCGTTGAG GGTCTTATCC ACGTAAGCGA AATGTCATGG 480  
ACACAGCACT TCGCTTCTGC TCAGGACTTC CTGCATGTAG GCGACGAAGT GGAAGCCGTG 540  
ATCCTGACGC TCGACCGCGA AGAACGCAAA ATGTCGCTCG GTCTGAAGCA ACTCAAGCCG 600  
GATCCTTGGG CTGATATCGA AACTCGTTTC CCTGTAGGCT CTCGTACCCA TGCTCTGTTT 660  
20 CGCAACTTCA CCAATTTCCG TGTATTCTGT GAGATCGAAG AGGGCGTAGA TGGCCTTATC 720  
CATATTTCCG ACCTTTCTTG GACGAAGGAG ATCAAACACC CCAGCGAGTT TACGGAAGTA 780  
GGTGGCTGTA TCGAAGTTCA GGTAAATCGAG ATCGACAAGG AAAACCCGTC TCTCAGCTTG 840  
GGTCAACAAC AGTTGGAAGA GAATCCTTGG GATGTATTCC AGACGGTATT CACTGTAGGA 900  
TCTATCCACG AAGGAACGGT AATCGAAGTG ATGGACAAGG GTGCTGTCTG TTCTCTGCCT 960  
25 TACGCTGTGG AAGGTTTTGC CACTCCGAAG CACATSGTGA AGGAAGATGG CTCACAGGCT 1020  
GTACTCGAAG AGAAGTTACC TTTCAGGTT ATTGAGTTCA ATAAGGATGC CAAGCGAATC 1080  
ATTGTATCTC ATAGCCGTGT ATTGGAAGAT SAGCAGAAAA TGGCTCAGCG TGAAGCCAAT 1140  
GCAGAGCGTA AGGCTGAAGC CAAAGCGGCT CAGAAAGAAG CTGCTGCCGA AGCTGCCAAT 1200  
CCTGCACAGG CTGTAGAGAA AGCCACTCTC GGAGACCTCG GCGAGCTGGC CGCTTTGAAA 1260  
30 GAAVAGCTTT CAGAAAAC 1278

(2) INFORMATION FOR SEQ ID NO:238

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 720 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 45 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

55 ATGAAAAAAG CTATTCTTTC CGGAGCGGCC TTGCTCCTCG GCCTATGTGC CAACGCACAA 60  
AACGTGCACT TCGACTACGA TTTCCGGTCAT TCCATCTAAG ACGAACTAGA TGGACGTCCC 120  
AAACTGACTA CCACAGTGA AACTTTCACA CCGACAAAAT GGGGAAGCAC CTTCTTCTTC 180  
ATCGACATGG ATTACACGGG CAAGGGTATC CAGTCGGCCT ATTGGGAGAT TTCGCGCGAA 240  
60 CTGAAGTTTT GGCAAGCTCC CGTTTCCATT CATTGGAGT ACAACGGAGG CCTCTCCACA 300  
AGCTTTACTT TCGGACACGA TGCTCTAATC GGTGCCACCT ACACCTACAA CAACCCCTCC 360  
TTTACAGTGG GATTACGAT CACGCCCATG TACAAGCATC TGGGTGCGCA CGACTTCCAC 420  
ACCTATCAGA TCACCGGCAC TTGGTACATG CACTTTCTGG ACGGTCTGCT TACCTTCAAC 480  
GGCTTCCTCG ATCTTTGGGG TTTCGCCCAA GAGAACCCAA TCGGGGGGCC TGTGCTCAAA 540  
65 GAAGGGGATA AGTTCTGATT CCTGTCCGAA CGCAGTTCT GGATCAACCT CAATGCAATC 600  
AAAGGCATCG ACAAGGATTT CAATCTCAGC ATAGGGACAG AGATGGAAAT CAGCAGGAAC 660  
TTGCTCGCA TGGACAAATT CTCTGCATC CTAATCTTG CGGTCAAAAT GACTTTCAAC 720

(2) INFORMATION FOR SEQ ID NO:239

- 70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double
- 75

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...1302

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

20	ATGTATAAAG	ACTATAAGGG	TTGTATGCG	TGCTTCGGT	GGTATGCCCT	GATCATTGGG	60
	TTGCTATTGG	CAGCAGACGG	TATACAGGCT	CAGAACAACA	ACTTTACCGA	GTCCGCTTAC	120
	ACTCGCTTCG	GCCCTGGCCG	TCTCGGAGAA	CGGACGACTA	TTAGTGGGCA	TTCCATGGGA	180
	GGACTCGGGG	TGGCTCTGCG	TCAGGGACAA	TACGTCAATG	CCGTCAATCC	TGCTTCATAC	240
	TCGGCTGTGG	ATTCTGATGAC	GTTTATCTTC	GATTTCGGTG	CATCTACCGG	AATTACGTGG	300
	TATGCCGAGA	ACGGGAAAAA	GGACAATAGG	AAAATGGGAA	ACATTGAGTA	TTTCGCCATG	360
	CTTTTTCCTA	TTTCCAAATC	CATTGCTATG	AGTGGCGGAG	TGCTTCCTTA	CTCCGCATCC	420
25	GGGTACCACT	TCGGATCCGT	TGATCAAGTG	GAAGGAGGCA	GCGTCCAGTA	CACCCGTAAA	480
	TACTTGGGGA	CAGGCAATCT	GAACGATCTC	TATGTCGGTA	TAGGTGCAAC	CCCGTTCAAA	540
	AACCTCTCAA	TAGGAGCCAA	TGCTTCATCC	CTTTTGGGCG	GATTACACCA	CAGCAGGCAG	600
	GTAATCTTCT	CCACGGAGGC	TCCTTACAAT	CCCGTACATC	TCTCGAGGCT	GTACTTGAAG	660
	GCTGCCAAGT	TGCACTTCGG	TATGCAGTAT	CACCTTCTTC	TCAAATCAGA	TCGTTGCTTC	720
30	GTTATCGGTG	CCGCTCTATC	TCCGCGGGTG	AAGATGCATA	GCGAGCTGAC	TCAGATAAAG	780
	AATCAGGTTG	AGAACGGTGT	AGTAGTGGAG	AGCGAAACCC	AAGAATATAT	CAAGGGGAATG	840
	GACTATTATA	CCCTGCCTCA	TACATTGGGG	ATAGGTTTTT	CTTATGAAAA	GAAAGATAAA	900
	CTTCTCTTAG	GAGCAGACGT	CCAATATAGT	AAATGGAAAG	GCGAGAAATT	TTTAAATCC	960
	GATTGCAAAAT	TCCAGGACAG	AATACGGGTA	TCTCTCGGCG	GAGAGATCAT	ACCGGATATA	1020
35	AATGCCGTTG	GGATGTGGCC	TAAAGTTGCG	TATCGCTTCG	GTTTACATGG	TGAAAATTCT	1080
	TACCTGAAGA	TGCCGACTAA	AGGCGGTGTA	TATCAAGGAT	ACCATATCGT	AGGTGCTGTA	1140
	TTCCGTATAG	GAATCCCGCT	CAATGACAGA	CGTTGCTTCG	TAAATGCTTC	TCTTGAATAT	1200
	GACCGATTGA	TCCCGAAGGA	GGGTATGATC	AAAGAAAATG	CTCTGAAATT	GACCTTCGGC	1260
40	CTCAGGTTC	ACGAGTCAATG	GTTTAAAAAG	CTGAAACTGA	AC		1302

(2) INFORMATION FOR SEQ ID NO:240

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 2778 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

65	ATGCGATCGA	TTTATCAATT	ACTGTTGTCA	ATACTCCTTG	CTTCTCTTGG	TTTCGTGCGG	60
	CTGGAAGCCC	AACAAGCCGG	AGTAGCAGGT	AGAGTATTGG	ACGAAGAAGG	CAACCCCATG	120
	ATTCAAGCCA	ACGTACAGCT	TGTACAGAGT	ACCGGCCAAG	TAGCCGTTGC	CGCAGGTGCC	180
	ACTAATGAAA	AAGGGTTGTT	CAGCCTGAAA	ACGTACACAG	AGGGTGACTA	CATTCTGCGC	240
70	TTTCTATATG	TAGGTTACAC	TACCCACGAC	GAAAAAATAT	CTCTTAGAAA	CGGGCAAAAC	300
	ATTACGCTCA	AAGATATATC	CATGAACGAA	GATGCCCGTC	TTCTACAGAG	TGTGACGGTG	360
	CAGGCTAAAG	CGGCAGAGGT	CGTGGTACGC	AACGATACGC	TCGAATTCAA	TGCCGGATCC	420
	TATACCGTAG	CACAGGGAGC	TTCTATCGAG	GAAGTATCA	AGAAGCTACC	CGGAGCAGAG	480
	ATCGGATCCG	ATGGGAAGAT	CACCATCAAC	GGCAAGGACA	TTAGCAAGAT	CCTTGTGATG	540
	GGCAAGAGAT	TTTCTCCAA	AGATCCACAG	GTGGCAATAA	AGAATCTTCC	GGCCGATATG	600
75	GTCAATAAAG	TACAGGTACT	GAACAAACTG	AGCGAGCTGT	CGCGGATGAG	CGGTTTCGAT	660

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	GATGGAGAAG	AGGAGACCGT	AATCAACCTG	ACGGTGAAGC	CCGAAAAAAA	GAAAGGCCTC	720
	TTCCGAACGC	TTCCAGGCCG	CTACGGTACC	GACCAACGCT	ATATGGCCGG	AGGGAACGTC	780
	AATCGGTTCC	ATGGAAATAA	GCAATGGACA	TTGATCGGTA	GTGCGAACMA	TACGAACAAT	840
	ATGGGCTTTA	GCGAGATGGA	CAGCGAGATG	GGATCCATGA	CCTTCTTCTC	TCCCAAGGCG	900
5	GGTGGTCCGAC	GCGGCTTCGG	CAATAGTGGA	GGTGTACGT	CTTCGTGAT	GCTGGGCGGC	960
	AACTTCAGTG	TGGAATTCCT	CTCTGCCCTT	AATACAGGAG	GCGATGCACG	CTACGGATAC	1020
	AACGACAAGG	CCATAGAGAC	GACCAAACGC	GTGAAAATA	TCCTCGCCGA	AGGGAATACT	1080
	TATATGGACG	AAAATATATT	GGAACGCTCT	TTCTCTCACA	ATGGTCAGGC	GCGATTAGG	1140
	ATGCAATGGA	AAACCGTCCG	ACGTACCGAA	GTGGTATTGG	AGCGGATCT	TTGATATCC	1200
10	AAGATCGATG	GGTCTTTTAA	CGACACATAC	GAGACGAAAG	ATGCCACCGG	AATCTCTATC	1260
	AACAAGGTT	CTATCCACCA	AATACACAA	GGAAACAACT	TCAGACTGAA	CGGAGAATTG	1320
	GATATCAGTC	ACAAGCTCAA	CGACGAAGGC	CGTACGATCA	GTGCGTCCGT	CAGTGGCGGT	1380
	CTGACCGACG	AAGACGGAGA	TGGCATATAT	CAGGCTGTGC	TCCAAAGCGT	GGAGACGAAT	1440
	CAAAAGCAAT	TCAACGACAA	CTCCAACCTG	CAATATCGGC	TTGCGCTCTC	GTATGTGGAA	1500
15	CCGTTGGGTA	AAAACIACIT	CGCACAGCG	ATTCTGAACA	GACGTTTCTC	CCGTCGCAAT	1560
	TOGGATCGTC	AGGTGTACCG	ACTGGGCGAT	GACGGGCAAT	ACTCCATATT	AGACAGTCAG	1620
	TACGGACTCT	CTACAGTAA	CGAGTTCACC	CAGTATCGCA	TCGGACTCAA	CCTCAAGAAG	1680
	ATTGCCAAAA	CGTGGGACTA	CACCGTAGGA	TTCAATGTGG	ATCCCAACAG	AACGTGCAGC	1740
	TATCGGAGCG	TAGCCGGAGT	AGAGCAGGAC	AAACTGGCTT	TCAATCGTGT	CAATCTCTCC	1800
20	CGGATGCTCC	GAATCAACTA	CAAACCGAGC	AGGACTACCA	ACCTCCGAGT	GGACTACCGA	1860
	GGACGCACGA	CACAACCATC	CATCAATCAG	ATCGCTCCCG	TTCAGGACAT	CACGAATCCG	1920
	CTATTCTGTA	CGGAAGGCCA	TCCCGTCTG	AAGCCGAGCT	ATTCCAACAA	TGTGATGGCC	1980
	ATGTTCTCGG	ACTTCGATGC	CAAAAGTCAG	CGAGCTTTCA	ACATTGTTTT	CTTCGGCAAC	2040
25	TATACATTCC	ACGACATCGT	CCCCAATACG	CACTACGATC	CGTCTACAGG	GATCCGTACC	2100
	ACTCGTTACG	AAAACGCCCT	CGGTACGTGG	CAAGCGAATC	TTCATGGGAC	ACTATCGCTT	2160
	CCACTCAAGA	ACAGGGCATT	TTCTTTCAGG	ATGTCCTTGT	TCAACAGGTT	GGCCGAAGGA	2220
	CAAGCTTCA	TCAATGACGA	TAAGAACAAA	GCTCTCTCTT	TCCGAACGAG	GGAAACGCTG	2280
	ACGCTGACCT	ATCGCAVCAA	TGGATTCGAT	ACGAGTATCG	GTGGCAATAT	CGGATTCTAT	2340
30	ATGGCGAATA	ATAGTCTGAG	CGGACAGAAA	GATTCTCGCA	CATACGATTT	TGGCGGCAAT	2400
	TATCAAGTTG	CCCTAACGCT	TCCCTATGGA	TTCCGTATCG	ACACGCGATG	TGAATACAA	2460
	ACGAATCCCG	GTTACAGCGG	AGGATTCACT	CTGGACGAAT	GGCTTTGGAA	TGCTTCGCTT	2520
	TCATACAGCT	TCCTCCGTGA	CAAGCCCGGT	ACACTGCGTG	TCAATGGCTA	TGACATCCTC	2580
	GTCACGCGGT	CAAGTATCAG	CCGTCTGCT	TCGGCCATCA	ATATAGAAGA	GAGCATGTCC	2640
35	AATACGATCG	GACGCTACGT	GATGGTGGAC	TTTATCTACC	GATTCAACGC	CTTCAGTGGT	2700
	GGTGGATCTC	GCAGCGATCA	TCAGCGTGGC	AATATGAATC	GTCCGGGCCC	ACCTTTCCGG	2760
	GGTGGCAGAC	GACCGTCC					2778

- (2) INFORMATION FOR SEQ ID NO:241
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

	ATGTTATGA	AGCTGATTAA	AAGAAGTTTG	CTCCTGCTTG	GAGCGGTACT	GCTGATTACG	60
	CTTCTGCT	ACTCGCAGAA	TGATGACATC	TTCGAAGATG	ACATCTATAC	ATCGCGAAAA	120
	GAAATAGTA	AACAAAACCA	AGTTAAAGAC	TGGCAAAACC	AAGAGGACGG	ATACGGCGAC	180
65	GATACGGAAT	ATACAGTGGC	TTCCGATCGG	GACATTGACG	CCTACAAATC	TAGAGATGGC	240
	CAGTCCCTACG	ATGGGAAAAA	GTGTCCAAA	GACAAGAAAA	GAGACTCCAC	TCGTTCTTCT	300
	GTTCGCCGTC	GCTATAGTCG	CCGCTTGGCT	CGATTCTATA	AGCCGAATAC	GATCGTCATT	360
	TCAGTGGCG	ACAAATGTATA	TGTAAGTATG	GATGGTGAGT	ATTTCGTCTA	TGGAGACGAA	420
70	TACTATGATG	ACGCGTCGTC	TGTAACATT	TACATCAACA	GTCTTGGTG	CGATCCGTTT	480
	CCTTATACGT	CATGGTATCC	ATCTTTCTCC	GGCTGGTACA	ACTATACGTG	GAACTATCCA	540
	TGGTCTTACT	ACGGTAGCCA	TATCCGATGG	GGCGGTATT	ACCCCGGATA	TAATTGGTAT	600
	TGGAGCTACT	ACTATGATCC	TTTCTACAA	CCCTATGGAA	TCGGTATGGG	TTGGGGATAT	660
	CCTTATGGCT	GGGGCAGCTA	TTACGGTTGG	GGTGGCTATC	CGGGAGTGAT	ACATCACTAC	720
75	CACCACTACC	CCAAGAAGAC	CTATTCCAAT	GGTCAGCATT	CCGGAGCTTA	CTATTCTTAT	780
	GGCCGACCGA	ATCGTATCAA	AGGTGGAACG	TCCGTGCCA	AACCTGGGAC	AGGACGCTAC	840

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5 GATAGAATTC AAAATTCGTC TTCGCAAAAA AATAAGTTCS GATTGCAGTC GAACAAACCC 900  
 AATAATAATC TGCAAAATGT CAAGTCGGGA CGTACCGGCC GAGCCAATAG AGACCGAAAT 960  
 ATAGAAACGG TAACTCCAAA CAACGGGCAA AAGCAGAATC GTCCCGTATT CCAGCAGAAAT 1020  
 CAGTCCGGCA ATGACCGACC GACCGGACGG AATATCCGCA GCGAGAGACA GGGGGAAAAAT 1080  
 AACGATAGGA CATTTCGAC TCCTTCTCGT AGCAATAGTA ACGGTGGCTT CTCCACGCCT 1140  
 TCTCGCTCTT CTTCGGCTC TATGAGCGGA GGTGGCGGAC GTAGTGGCCG GGGACGCAAT 1200

10 (2) INFORMATION FOR SEQ ID NO:242  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1194 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...1194  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA TAAAAGAAG TTGCTCCTG CTGGAGCGG TACTGCTGAT TACGCTTCCT 60  
 GCGTACTCGC AGAATGATGA CATCTTCGAA GATGACATCT ATACATCGCG AAAAGAAATA 120  
 CGTAACAACA ACCAAGTTAA AGACTGGCAA AACCAAGAGG ACGGATACGG CGACGATACG 180  
 GAATATACAG TGGCTTCGGA TCGGGACATT GACGCCTACA ATCGTAGAGA TGGCCAGTCC 240  
 TACGATGGGA AAAAGTTGTC CAAAGACAAG AAAAGAGACT CCACTCGTTC TTCTGTTCCC 300  
 GGTGCTATA GTCGCGCTT GGCTCGATT TATAAGCCGA ATACGATCGT CATTTCAGGT 360  
 GCGACAATG TATATGTAAC TGATGATGGT GAGTATTTCT TCTATGGAGA CGAATACTAT 420  
 GATGACGGGT CGTCTGTAAA CATTTACATC AACAGTCCTT GGTGGCATCC GTTCCCTTAT 480  
 ACGTCATGGT ATCCATCTTT CTCCGGCTGG TACAACTATA CGTGGAACTA TCCATGGTTC 540  
 TACTACGGTA GCCATATCGG ATGGGGCGGT TATTACCCCG GATATAAATT GTATTGGAGC 600  
 TACTACTATG ATCCTTTCTA CAATCCCTAT GGAATCGGTA TGGGTGGGG ATATCCTTAT 660  
 GGCTGGGGCA GCTATTACGG TTGGGTGGG TATCCGGGAG TGATACATCA CTACCACCAC 720  
 TACCCCAAGA AGACCTATTC CAATGGTCAG CATTCCGGAG CTTACTATTC TTATGGCCGA 780  
 CGGAATCGTA TCAAGGTGG AACGTCCGGT GCCAACTTG GGCAGGAGC CTACGATAGA 840  
 ATTCAAATTT CGTCTTCGCA AAAAAATAAG TTCGATTGC AGTCGAACAA ACCCAATAAT 900  
 AATCTGCAAA ATGTCAAGTC GGGACGTACC GGCCGAGCCA ATAGAGACCG AATATAGAA 960  
 ACGGTAACTC CAAACAACGG GCAAAAGCAG AATCGTCCCG TATTCCAGCA GAATCAGTCC 1020  
 GGCAATGACC GACCGACCGG ACGGAATATC CGCAGCGAGA GACAGGGGGA AAATAACGAT 1080  
 50 AGSACATTTT CGACTCCTTC TCGTAGCAAT AGTAACGGTG GCTTCTCCAC GCCTTCTCGC 1140  
 TCTTCTCCG GCTCTATGAG CGGAGGTGGC GGACGTAGTG GCCGGGACG CAAT 1194

55 (2) INFORMATION FOR SEQ ID NO:243  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1743 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...1743  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

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5 ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 60  
 GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 120  
 TCITTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 180  
 CAGAGCGATA TGCTGCTTTC TACTGCCCCA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 240  
 TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 300  
 TATAAGCCCC TGCCCCGACA TGAACCGAG ATGGGGCGTG GGGTTCCTCA CATGTATGTG 360  
 AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 420  
 10 GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 480  
 GGAGGTATAG TACTCACTCC TTTTGATGGA GTGGGTGTCA AGGGTATTGC AGGACAGCAG 540  
 CGTAACCTACT TCGACCGCAC GGGCAAGGTA TTCAAITCCG GCCGAGGCTA CCTACTGGGT 600  
 TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGGCGGACAA TGACTATCAT 660  
 TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 720  
 GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 780  
 15 ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 840  
 CCTCGGCGAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCGCTCA 900  
 TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCCTTC 960  
 CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1020  
 CAAGCTCACA CTTATACGCT GCGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1080  
 20 TGGGCTTTCC AAGGTGAAGT GCGTTACAAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC 1140  
 TACGGTACCG GCTTGCCTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAGATGCTC 1200  
 AAAGAGATTC CCGACGAAGT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCCGCCATG 1260  
 GCGGACCTCT ATTATTCCGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1320  
 AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1380  
 25 GGAGAGAACC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1440  
 AGTAATAAGG TAGCCCTCGG TACCGAAGTG CAATATTTCG ACACGAAGCA GGATCAGGCT 1500  
 GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCTCT CTCTGATGCT TTCCCTCTCG 1560  
 GAGCAATATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1620  
 CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGAT GAAGTCTCTG 1680  
 30 GGAGGTGTAT GTCGTGTGGT CCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCAACCAAT 1740  
 CTG 1743

35 (2) INFORMATION FOR SEQ ID NO:244  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...717

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244  
 ATGCGTTCTT TATTTTGAG CGCGTIGCG AGCTCCTCTC TCCATGCTTC AGAGCGACGC 60  
 AGTCGGATAA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AATAAGGTT ATTCCATCTC 120  
 TCGGTATGCG CCCAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTG CATCGAATTC 180  
 60 GGGGCCATCG ACACAGACGA ATTTCTGTCTG TCCTCCACCG CTTATACGAC AAGCCCCACA 240  
 CATACCGGTG CCATCCACCA TAATTGTATT GACAGAAGCT ATGGTCGGTA TCTCGTAACG 300  
 TTTGTCAGG AGAGAAACGA ACTTCATCAT CACAGCCCGC CCGATCGTAA CGCAGAGGTC 360  
 TACCGTTTCC CGTTTGATAA CGCTTTCCAC TCCATCCGTT ACGAGGCCCT TCCTCCCAT 420  
 AGACCCATCG TCTGTATGA TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG 480  
 65 GATAACCGA TCTTTAGTTC TGGCAGCCAA TACGACAATT ACACGGTTGC CTGCTTTGTG 540  
 GAAAGCCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCTCCGG CACAAACCAC 600  
 TGTGCCGACC TTTTCGATAT GCGTACTCTG TCCAGCGGGA CCTACCATAT CCGTGATATA 660  
 70 GTCGCCGACT TCGAGTTCGG CCAATTTCTT GGAAGATTTG CCCACGGCCT GAACCCAC 717

(2) INFORMATION FOR SEQ ID NO:245  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

20	ATGTCATAAA	GGCAGAAAAT	AAGGTTATTC	CATCTCTCGG	TATGCGCCCA	AACGCATGAT	60
	CATCTCATCG	AAATCCACTT	GGTGTGCATC	GAATTCGGGG	CCATCGACAC	AGACGAATTT	120
	CGTCTGTCC	CCCACGCTTA	TACGACAAGC	CCCACACATA	CCGCTGCCAT	CCACCATAAT	180
	TGTATTGAGA	GAAGCTATGG	TGGTATCTCT	GTAACGTTTG	GTCAGGAGAG	AAACGAACCT	240
	CATCATCACA	GCGGCGCCGA	TCGTAAACGA	GAGGTCTACC	GTTCCTCGTT	TGATAACGCT	300
	TTCCACTCCA	TCCGTTACGA	GGCCTTTCGT	CCCATAAGAC	CCATCGTCTG	TCATGATGAT	360
25	CACTTCATCG	CTATTGGCTC	GCATTGTGTC	TTCAAGGATA	ACCAGATCTT	TAGTTCTGGC	420
	AGCCAATACG	ACAATACAC	GSTTGCTGTC	TTTGTGGAAA	GCCTCCACGA	TCGGGAGCAA	480
	AGGAGCCACA	CCCACACCGC	CTCCGGCACA	AACCACTGTG	CCGACCTTTT	CGATATGGGT	540
	ACTCTGTCCC	AGCGGACCTA	CCACATCGGT	GATATAGTCG	CCGACTTCGA	GTTGCGCCAA	600
30	TTTCTTGGAA	GATTTGCCCA	CGGCCTGAAC	CAC			633

(2) INFORMATION FOR SEQ ID NO:246

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

55	ATGGATCGTC	CTAAGCCTTC	ATATATTGTT	CGAATAGCAG	CCATTCTCTG	CTTGTCTTGC	60
	GGCAGGCCTT	TGTTTGCGCA	GAGCTATGTG	GAATACGTGG	ATCCGCTGAT	CGGGACGCTA	120
	AGTTCTTTTG	AGCTGAGTGC	GGGCAATACC	TATCCGGTGA	TGGTTTACC	GTGGGGGAATG	180
	AATAGCTGGA	CACCGATGAC	CGGTGTACCC	GGTGACGGCT	GGCAATATAC	CTACTCGGCA	240
	CACAAGATTU	GCGGATTCAA	ACAGACCCAC	CAACCCAGTC	CTTGGATCAA	CGACTACGGC	300
60	CAATTCTCCC	TTCTTCCCCT	TACGGCACCG	CAGAAGCCAT	CATCGAACGA	CTCCATAGCT	360
	CTGACTAAAT	GGTGCAAGCA	ACTCTTTTCG	GACGAACAGA	CCTCGTGGTT	CTCGCACAAA	420
	GCGGAGACGG	CGACGCCATA	CTATTATAGT	GTCTATTTCG	CCGATTACGA	CACACGGGTG	480
	GAGATGGCTC	CGACCGAGCG	TGCAGCTATC	TTTCGCATAC	GTTATTCCGG	CAATACCGAA	540
	AGTGGCTCCG	GTCGATGGCT	TCTCTTGAT	GCCTTTACCG	GTGGTTCCGA	GATTAGCATC	600
65	GTGGATCCTC	ACACCGTAGT	GGGCATATCT	CGCAAGAATA	GCGGAGGTGT	GCCGGCTAAC	660
	TTGCGCTGTT	ATTTCATCCT	GCAGTCCGAT	ACTCCTATGG	CGATGTCTCT	GCTTGAGACA	720
	GATACCGGCA	AGTCAGACGA	AGGCACAAGG	GCATGGGCAG	CCTGTCCGCT	CGATTCCGCA	780
	GAAGTTACCG	TCGGGTGGGC	ATCTTCTTTT	ATCAGTGTGC	AGCAGGCCGA	AAGAAATCTT	840
	GCGGAAGTCA	AAGGGCAGAG	TTTCGACCGG	ATCAGACTTG	CCGGTCCGCA	AGCTTGGAAAT	900
70	AAGGTGCTCG	GACGCATACA	TGTGGAGGGA	GGAACGAAGG	ATGAGCGCAC	TACATTCTAT	960
	TCGCACTCT	ATCGCTGTCT	GCTTTTCCC	CGTCGCTTCT	ATGAGGAGGA	TGCTTCCGGC	1020
	AATTTTGTGC	ATTACAGCCC	CTACAATGGA	GAGGTACTTC	CCGGTTATCT	CTATACCGAT	1080
	ACCGGATTTT	GGGACACTTT	TCGAGCCCTT	TTCCCTCTGC	TCAATCTGCT	GTATCCCGAT	1140
	GAAAACATTA	AAATTCAGGA	AGGTCTGCTG	AATGTATATC	GCGAGAGTGG	CTTTTCCGCC	1200
75	GAATGGGCCA	GTCCGGGCCA	TGGGATTGT	ATCATAGGCA	ACAACCTCTG	TTCTGTTCTG	1260

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5 GCGGATGCCCT ACCTCAACGG TGTTCGGGTA GAAGATACCC GTACACTGAT GAACGGACTC 1320  
 TTGCATGCTA CGAAAGCCGT CCATCCGAAA ATCTCCTCCA CGGGTCGCAA AGGTTGGGAG 1380  
 TGGTACAACCT CCTTAGGTTA TGTTCGGGCT GATGCAGGCA TCGACGAAAG TGCTGCCCGT 1440  
 ACGCTCGAAT ATGCTTATAA CGATTGGTGC ATCCTCCGAC TGGGGCGCAC ATTGGGTTGG 1500  
 GATAGAGCTG CATTGGACAC GTTGGCTCAT CGTTCGATGA ACTATCGTCA TCTGTTCGAT 1560  
 CCGGAAACCA AACTCATGCG CGGTAGAAAT CAGGATGGTA GTTTCGGGAC ACCTTTTTTC 1620  
 CCTTTCAAAT GGGGAGATGT ATTACGGAG GGCAATGCCT GGCACTACAC TTGGTCGGTC 1680  
 TTTCATGATG TGCAGGGGCT TATCGACCTG ATGGGAGGAG ATCGCCCGTT CGTGTCTATG 1740  
 CTCGATTCCG TATTCAATAC TCCTCTATG TTCGATCAGA GCTATTACGG ATTTGTCTATC 1800  
 10 CACGAATCA GAGAGATGCA AATAGCGGAT ATGGGCAATT ATGCTCATGG CAATCAACCC 1860  
 ATACAGCATA TGATATATCT GTATAATCAT GCCGGTCATC CATGGAAAGC TCAGGAGAGA 1920  
 CTACGCGAAG TGATGGGGCG GCTCTATCGT CCTACTCCGG ATGGGTATTG CGGCGATGAA 1980  
 GACAAACGAC AGACTTCGGC TTGGTACGTT TTCTCTGCTT TAGGCTTCTA TCCTGTTACA 2040  
 CCGCTACCG ATCAGTATGT GCTCGGTTCC CCGATTTTTT CCAAGGTAAT ACTCTCTTT 2100  
 15 CCGGACGGAC ACAAACCGGT GTTGCATGCT CCGGCCAACA GTGCCGATAC GCCTTACATC 2160  
 GCCTCGATCA GCGTAGAAGG AAAAGAATGG AGCTGCAATT ACCTGACTCA CGAACAGCTT 2220  
 CGCTCTTCTG CATCCATTCA ATGGATGATG GACACGAAAC CCAATTATAA TCGTGGTATG 2280  
 AAGGAAAGTG ACAGACCTTA TTCTTCTCC ACGGAGCAAC AGCGTCGGCG TAATCACACT 2340  
 AAT 2343

## (2) INFORMATION FOR SEQ ID NO:247

- 25 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...813  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

45 ATGATGAAAT CCATGCGCAG CGTGCTGTTG CTACTCTTTC CATTGTCTTT GATCACTGCT 60  
 TTGGGCTGTA GCAATAACAA AGCTGCCGAA TCGAAGTCTG TCTCTTTCGA TTCGGCCTAT 120  
 CTCGAACGCT ACATCCCTCT GCGGGCAGAC ATAGATACGC CATCGCTGCA TGTGATGATC 180  
 AGCTACGTCT ATCCTTCGGG AGATGATATG CTCACAGAGA TTTTCAACGG TTGCTCTTC 240  
 GGGACAGGCC TGATGGATTG CTCTTCGCGG GAGAATGCCA TGGAAGGCTA TGCACAGATG 300  
 50 CTGGGAGAAG ACTATCGCTC TAACAATGCC GAAGCCAATC TGCAAGGGCT TCCTTCTGAC 360  
 CTTTGGACT ATATCTACAA GCAGGAAAAT ACCATCGCTT ATTGCGATAC GGGATTGATC 420  
 TCCACGCGCA TCAATACATA TACTTACGAA GCGGTGCAC ATACGGAGAA TACAGTCCGG 480  
 TTTGCCAACA TCCTTCGCAC CACCGGCAAG GTGCTCGAAG AGCGAGATAT ATTCAAGATC 540  
 GACTATGCGG AAAGGCTGTC CGCACTCATC ATAGGACAAT TGGTGACGA TTTGGGCAAG 600  
 55 ACCACACCTG CCGAATTGGA TGCAATAGGT TTCTTCAACG CAGAAGAAAT ACAGCCCAAT 660  
 GGCAATTTTA TGATCGATGA CAAAGGTCTC ACATACTGTT TCAATGAGTA TCAGATAGCT 720  
 GCTTATGCCA GAGGTGCTGT CTATGTCCGT CTCGGATATG ACGTATTGGC TCCTTTGCTA 780  
 AGGGATGATT CCCCACTAAA GCGTTACTTG CCG 813

## (2) INFORMATION FOR SEQ ID NO:248

- 65 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...810

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

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10  ATGAAATCCA TGCGCAGCGT GCTGTTGCTA CTCTTTCCAT TGCTTTGAT CACTGCTTTG      60
    GGCTGTAGCA ATAACAAAGC TGCCGAATCG AAGTCTGTCT CTTTCGATTC GGCCTATCTC      120
    GAACGCTACA TCCCTCTGCG GGCAGACATA GATACGCCAT CCGTGCATGT GATGATCAGC      180
    TACGTCTATC CTTGCGGAGA TGATATGCTC ACAGAGATT TCAACGGTTT GCTCTTCGGC      240
    GACAGCCTGA TGGATTCCCTC TTCGCGGAG AATGCCATGG AAGGCTATGC ACAGATGCTG      300
    GGAGAAGACT ATCGCTCTAA CAATGCCGAA GCCAATCTGC AAGGGCTTCC TTCTGACCTT      360
15  TTGGACTATA TCTACAAGCA GGAATAACC ATCGCTTATT GCGATACGGG ATTGATCTCC      420
    ACGCGCATCA ATACATATAC TTACGAAGGC GGTGCACATA CGGAGAATAC AGTCCGGTTT      480
    GCCAACATCC TTCGCACCAC CGGCAAGGTG CTCGAAGAGC GAGATATATT CAAGATCGAC      540
    TATGCGGAAA GGCTGTCCGC ACTCATCATA GGACAATTGG TGCACGATTT CGGCAAGACC      600
20  ACACCTGCCG AATTGCATGC AATAGGTTTC TTCAACGCAG AAGAAATACA GCCCAATGGC      660
    AATTTTATGA TCGATGACAA AGGTCTCACA TACTGTTTCA ATGAGTATCA GATAGCTGCT      720
    TATGCCAGAG GTGCTGTCTA TGTCCGTCTC GGATATGACG TATTGGCTCC TTGCTAAGG      780
    GATGATTCCC CACTAAAGCG TTACTTGCCG                                     810

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(2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...801

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

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50  ATGCGCAGCG TGCTGTGCT ACTCTTTCCA TTGTCTTGA TCACTGCTTT GGGCTGTAGC      60
    AATAACAAAG CTGCCGAATC GAAGTCTGTC TCTTTGATT CGGCCTATCT CGAACGCTAC      120
    ATCCCTCTGC GGGCAGACAT AGATACGCCA TCGCTGCATG TGATGATCAG CTACGTCTAT      180
    CTTTCGGGAG ATGATATGCT CACAGAGATT TTCAACGGTT TGCTCTTCGG CGACAGCCTG      240
    ATGGATTCCCT CTTGCGCGGA GAATGCCATG GAAGGCTATG CACAGATGCT GGGAGAAGAC      300
    TATCGCTCTA ACAATGCCGA AGCCAATCTG CAAGGGCTTC CTTCTGACCT TTTGGACTAT      360
55  ATCTACAAGC AGGAAAATAC CATCGCTTAT TGCGATACGG GATTGATCTC CACGCGCATC      420
    AATACATATA CTTACGAAGG CGGTGCACAT ACGGAGAATA CAGTCCGGTT TGCCACATC      480
    CTTGCAACCA CCGCAAGGT GCTCGAAGAG CGAGATATAT TCAAGATCGA CTATGCGGAA      540
    AGGCTGTCCG CACTCATCAT AGGACAATTG GTGCACGATT TCGCAAGAC CACACCTGCC      600
    GAATTGGATG CAATAGGTTT CTTCAACGCA GAAGAAATAC AGCCCAATGG CAATTTTATG      660
60  ATCGATGACA AAGGTCTCAC ATACTGTTTC AATGAGTATC AGATAGCTGC TTATGCCAGA      720
    GGTGCTGTCT GTTCCGTCTC CGGATATGAC GTATTGGCTC CTTTGCTAAG GGATGATTCC      780
    CCACTAAAGC GTTACTTGCC G                                     801

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(2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTT	GGGTCTCTCG	60
GCCAAATGCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCCAC	TTTCAGTTCTG	120
GCCACGGCCG	GAAATGGTTT	TGSGTGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGGTACACC	ACAGCATTCT	GCCCGAAGGG	TTGGATTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCAG	AAGACTTTT	TGACAAAAA	360
GCTCTCGGCC	GCTTCCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATTCTT	TTCTCACCGA	TACCCAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGACTTTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTCACC	GGGGATCGGA	CTCAAAAGTT	CTATTTGGTG	GAAAAATGCC	600
ATCAAGAGCA	AATATGATTT	TGGCCTCGGT	TTCAGCTGG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATTT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACTTTACCG	TGGGTCTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...3798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAGAGC	TAAGTACCGC	TATTGGCTTT	TTCTTTCTG	TTCCGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGACG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTGATCT	CTCCTCACAA	180
GAAGGGATAA	GCTGGTCGGT	AAATAGATAT	TTCAAGCAAG	ATTCTCTCGG	TGCAGTCGTT	240
GAGCTTTGCT	TGCCAGAAATG	TCAGATAGAA	AGCATGACTT	GGCTTATGTA	TTTTCTTGCT	300
CTAAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAACGTCCT	360
ACTTCGTAA	CAAAACTTCG	TCTAAGAAAT	AACCAATCC	GTAAGCTAGA	GGGCTCGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAT	CAGTAACTA	540
GAGGCTCTGG	AACGTCTCAC	GTCTTAGCA	ACGCTTGAAC	TATCGGGTAA	CCAAATCOGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAACATATC	GGTAACCAA	660
ATCCGTAAGC	TAGAGGGTCT	GGAACTCTC	ACTTCGTAA	CAGAGCTTCG	TCTAAGAAAT	720
AACCAATCA	GTAAGCTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACCTA	780
TCGGGTAACC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	840
GAACCTGTCG	GTAACCAAT	CAGTAAGCTA	GAGGGTCTGG	AACGTCTCTC	TTCGTTAACA	900
AAGCTTCGTC	TAAGAAGTAA	CCAGATCAGT	AACTAGAGG	GCCTGGAACG	TCTCACCTCG	960
CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAACGTCCT	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AACCAATCC	GTAAGCTGGA	GGGCTGGAA	1080
CGTCTCACCT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGGATAGTC	TCACCTCGCT	AACAAAACCT	TCTCTCTCG	ATAACCAAT	CAGTAACTA	1200
GAGGGCTCGG	AACGTCTCAC	GTCTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGG	GTCTTGATGG	TCTTGCTTCC	TTAACAAAGC	TTAGTCTAAG	GGGCAACCAA	1320
ATCAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTTGA	GAAAACCTGA	TGTTTCGGGC	1380
AATGATATTC	AATCTATTGA	TGATATTAAG	CTATTGGCTC	CGATTCTGGA	GCAAACTTTA	1440
GAAAAACTGA	GAATCCATGA	CAATCCATTT	GTTCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500
TATGATAATC	ATTTCGGCGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAACAGAAA	1560

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5 AAGACTTCAG TTGAATATCA CCCATTTTGC AAAGTAATGC TATTGGGAAA TCATTCTTCG 1620  
 GGTAAAACAA CATTTCCTTAG TCAATACGAT ACAAATTATA CGTATCAGAA AAATACACAT 1680  
 GTGTGTGCGA TACATCGAAG CAATAACCCT AATGCCATCT TTTACGACTT TGGGGGACAG 1740  
 GACTATTATC ATGGGATTTA CCAAGCCTTT TTTACCACCC AATCGTTATA CCTTCTCTTT 1800  
 TGGGATGCTA AGAAGGATCG AAACCTTTGTG AGCGTAGATG ATAAAGAATA TCAGACTCTT 1860  
 AATTTCATTC GCCCCTATTG GTTAGGACAG ATAGCCTATG CCTGCAATCG TTGTATGTCC 1920  
 GTTGGAGGAA ATCCTGATGG CAAGGACACA CCACAGACCA CAGACGATAC AATTATCATT 1980  
 CAGACTCATG CCGATGAAAC GGGGCGTAAG CAGCAATCCT TAGGCTGTGC AGCCGAGAAT 2040  
 GGAGTATTGG AAGAAATCTA TGTATCCTTA GAGCCCAAGG CGAATAGTGC CGTACATGCG 2100  
 10 CTCAACTATC TGAATGAGCG GGTGCGAGAA GTTGTGCGAA GCAGGAGTAA ATCAATTTCAG 2160  
 ATCAGAGAAA AAGATAAGGG ATTGTACGAA GCTCTTCCCA CAATCGCCGG TGATAATAAA 2220  
 CACATCCCTA TCTCTCTCGA AGCTCTTGGG GCTCAATTGA ATAAGGGAAG AGCTGAAAT 2280  
 GATCTTTACA CCATAGAGTA TCTACAGACC GAATTGAACC AGCTTAGTCT GCGAGGGGAG 2340  
 GTGCTTACT ATCGTGAGAA TGAGAAGCTG AACAATTATG TCTGGTTAGA TCCGGCAGCT 2400  
 15 TTTGTCCAAA TGATTTCATG AGAAATCCTC CAAAAAGACA ACATCAATAG AGGAACAGTT 2460  
 CCTAAGNCA TTTTGAATG CAAACTGCAAT AATCTAAGTT CCGGAAGTAT ATTTGAAGAA 2520  
 CAGTACGAAA ATGGTAATAT GATCTTGCAAG CTATTATTGG AAGAGCTGAT CGTATATGAA 2580  
 GATAAGGACT GCTATGTGAT ACCGGGCTAT CTCCTTTTGC ATTCCGATGA CGAAGCCTAT 2640  
 AAATGGCTTA CTTTGGGATT CGAGAGGCC CAAATTTGTCC TCAAAATCGA ACGTTTTATC 2700  
 20 CCCTTTGGCC TGATCAACCA GATTATAGCC TACTATGGCC GGGAGAAGG TGCTCTAAAG 2760  
 CGGTATTGGC GAGATCAGGT CATCTTCACA GCAGGCCGTG AGATGGATAG GCAACCGTT 2820  
 GAGCAAGAAA AAGAGAAAGA GGGTTTGGCC AAGACGAATG CCGAGGATTA TCAGATCTGG 2880  
 ATCAAGCTCG ACTTTACCGA CTTGGCCATA TCCGTATTCA TCAAAAGACA GAGAAAGACA 2940  
 TCAGCTAAGG ATATGACGG GAAAGAGGCT ACTATCCTCA GTGATATGTT GGATATGTAT 3000  
 25 TGGAACAATA TCCCTCCGAG GGAGCAAATA GGAGATAAGG ATACGGAGCA AACGAGAAGC 3060  
 ACTATTCGTG AAACAACAG AAAGAAGAGA CCCATCCAGG ATCTCTACCT CTCTGTGCC 3120  
 CAAGCGGATA AAGATTGAC GGAGTCTCAT TATATCCATT TGGGCACGCT GGACGATGAA 3180  
 AGCAAGACTA CGGCGAGGAT TGCAGCCTAT CCGTTGAAGA ACGGCGTTAT CGATAAAGAG 3240  
 CGGGTCCGAG AAGTATCGAC TCGTCCCTAC AAACATCTTT CCGTCAATA AAATCTGGCT 3300  
 30 ACTGCAAAAC AGATCTTTAT TTCCTATTCC AAAGAGGATC AGACTGAACT GGAGACCTGT 3360  
 CTGCAATTTT TCAAAACCTT GGAGAAGAAAT GGTGAGATCG AGATCTACTA TGATAAGTTG 3420  
 ACTAAGTTT AAACAACCTAT TCACCCTGAA ATAAAGAAAG GTATTGTGCA AGCCGACTGT 3480  
 ATAATCGCTT TGATCAGCCA ACGTATCTCG GCCACGGATT ACATCCTGGA TCATGAGTTG 3540  
 35 CCTGTATTTC GGGAGTATTA CAAGACCATA GTGCCGATAT TGATCAAGCC TTGTACATTC 3600  
 GAAGACGATG AGTTCTCTCG GGAGAAATAT TTTGCTCAGA AAGCTCAAT AATCAATCTT 3660  
 GGAAGAGAGG GAAAAACCAT TAAAGCTTAT GATAGTATTA CGGCATCAGC CCATCGTGAT 3720  
 GAAATTTGGG TGGCAGTAGT CAGAGAGTTC AAAGAGAAGA TATTAAGAAT AACAAAACAG 3780  
 GAGGTAAATA CAGATGAA 3798

(2) INFORMATION FOR SEQ ID NO:252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...3696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

65 ATGACAACCA AGAAACCCCA AGCCATTTTA GACTTAGAGA AGGCCTATAA CATTGAAATT 60  
 CCTGATCTCT CCTCACAAGA AGGGATAAGC TGGTCGGTAA ATAGATATTT CAAGCAAGAT 120  
 TCCTCCGGTG CAGTCGTTGA GCTTTGCTTG CGAGAATGTC AGATAGAAAG CATGACTTGG 180  
 CTATTGATT TTCTGCTCT AAAAAAGCTT GATCTATCGT ATAAACCAAT CAGTAAGCTA 240  
 GAGGGTCTAG AACGTCTTAC TTCGTTAACA AAACCTCGTC TAAGAAGTAA CCAATCCGT 300  
 70 AAACCTAGAGG GCCTGGATAG TCTCACTCG CTAACAAAAC TTTCTCTCTC CGATAACCAA 360  
 ATCAGTAAGC TAGAGGGTCT GGAACGTCTC ACCTCGTTAG CGGAGCTTTA TCTTTGGAT 420  
 AACCAATCA GTAACCTAGA GGGTCTGGA CTTCTCACGT CCTTAGCAAC GCTTGAACCTA 480  
 TCGGGTAACC AAATCCGTAA GCTGGAGGGT CTGGAACGTC TCACGTCCTT AGCAACGCTT 540  
 GAACTATCGG GTAACCAAT CCGTAAGCTA GAGGGTCTCG AACGTCTCNC TTGTTAACA 600  
 75 AAGCTTCGTC TAAGAAGTAA CCAATCAGT AAGCTAGAGG GTCTGGAACG TCTCAGTCC 660  
 TTAGCAACGC TTGAACATC GGGTAACCAA ATCCGTAAGC TGGAGGGTCT GGAACGTCTC 720

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5 ACGTCCTTAG CAACGCTTGA ACTGTCGGGT AACCAAATCA GTAAGCTAGA GGGTCTGGAA 780  
 CGTCTCTCTT CGTTAACAAA GCTTCGTCTA AGAAGTAACC AGATCAGTAA ACTAGAGGGC 840  
 CTGGAACGTC TCACCTCGCT AACAAAATT TCTCTCTCCG ATAACCAAAT CAGTAAGCTA 900  
 GAGGCTTGGG AACGCTCTCAC CTCGTTAGCG GAGCTTTATC TTTTGGATAA CCAAAATCCGT 960  
 AAGCTGGAGG GCCTGGAACG TCTCACCTCG TTAACAAAGC TTCGCTAAG AAGTAACCAA 1020  
 ATCAGTAAC TAGAGGGCCT GGATAGTCTC ACCTCGCTAA CAAAACCTTC TCTCTCCGAT 1080  
 AACCAATCA GTAACCTAGA GGGCCTGGAA CGTCTCAGT CCTTAGCGGA GCTTTATCTT 1140  
 TTGGATAACC AAATCCGTAA GCTGGAGGGT CTTGATGGTC TTGCTTCCTT AACAAAGGCT 1200  
 10 AGCTAAGGC GCAACCAAAAT CAGTAAGCTG GAAGGACTAG ACAGACTAAA GGTTTTGAGA 1260  
 ATTCTGGAGC AAACCTTAGA AAAACGAGA ATCCATGACA ATCCATTTGT TGCAATCA 1320  
 GGCTTGATAC TCTCTCCTTA TGATAATCAT TTGCCGAGA TTAAGCTCT TCTTGAAAAA 1380  
 GAAAAAGAAA AACAGAAAAA GACTTCAGTT GAATATCACC CATTTTGCAA AGTAATGCTA 1440  
 15 TTGGGAAATC ATTCTTCGGG TAAAAACA CAATTCAGTT AATACGATAC AAATATACG 1500  
 TATCAGAAA ATACACATGT GTTGTGATA CATCGAAGCA ATAACCTTAA TGCGATCTTT 1560  
 TACGACTTTG GGGGACAGGA CTATTATCAT GGGATTAC AAGCCTTTT TACCACCAA 1620  
 TCGTTATACC TTCTCTTTG GGATGCTAAG AAGGATCGAA ACTTTGTGAG CGTAGATGAT 1680  
 AAGAATATC AGACTCTTA TTCAATCGC CCTATTGGT TAGGACAGAT AGCCTATGCC 1740  
 20 TGCAATCGTT STATGTCCT TGGAGGAAAT CCTGATGGCA AGGACACACC ACAGACCACA 1800  
 GACGATACAA TTATCATTC GACTCATGCC GATGAAACGG GCGCTAAGCA GCAAACTTAA 1860  
 GGCTGTGCG CCGAGAAATG AGTATTGGA GAAATCTATG TATCCTTACA GCGCAAGCG 1920  
 AATAGTGCCG TACATGCGCT CAACATCTG AATGAGCGGG TCGAGAAAGT TGTGCAAGC 1980  
 AGGAGTAAT CAATTGAGT CACAGAAAA GATAAGGGAT TGTACGAAGC TCTTCCACA 2040  
 25 ATCGCCGGTG ATAATAACA CATCCCTATC TCTCTCGAAG CTCTTGGCGC TCAATTGAAT 2100  
 AAGGSAAGAG CTGAATATG TCTTTACACC ATAGAGTATC TACAGACCGA ATTGAACAG 2160  
 CTTAGTCTGC GAGGGGAGGT GCTTTACTAT CGTGAGATG AGAAGCTGAA CAATTATGTC 2220  
 TGGTTAGATC CGGAGCTTT TGTCCAAATG ATTCATGGAG AAATCCTCCA AAAGACAC 2280  
 ATCAATAGAG GAACAGTTC TAAAGACATT TTTGAATGCA AACTGCATA TCTAAGTTCC 2340  
 GGAAGTATAT TTGAAGAAGA TGGCCAAAT GGTAAATATG TCTTGCAGCT ATTATTGGAA 2400  
 30 GAGCTGATCG TATATGAAGA TAAGGACTGC TATGTGATAC CGGGCTATCT CCTTTGCAT 2460  
 TCCGATGACG AAGCCTATAA ATGGCTTACT TTGGGATTG AGAGGCCCAA TTTTGTCTC 2520  
 AAATTCGAAC GTTTTATCCC CTTTGGCCTG ATCAACCAGA TTATAGCCTA CTATGGCCG 2580  
 GAAGAGGTG CTCTAAAGCG GTATTGGCGA GATCAGGTCA TCTTCACAGC AGGCCGTGAG 2640  
 35 ATGGATAGGC AAACGCTTGA GCAAGAGAA GAGAAAGAGG GTTTGCCCAA GACCAATGCC 2700  
 GAGGATTATC AGATCTGGAT CAAGCTCGAC TTTACCGACT TGGCCATATC CGTATTATC 2760  
 AAGAGCAGA GAAAGACATC AGCTAAGGAT ATGCAGCGGA AAGAGGCTAC TATCCTCAGT 2820  
 GATATGTTGG ATATGATTG GAACAATATC CCTCCGAGG AGCAAAATAGG AGATAAGGAT 2880  
 ACGGAGCAAA CGAGAAGCAC TATTCGTGAA ACAACAGAA AGAAGAGACC CATCCAGGAT 2940  
 40 CTCTACCTCT CCTGTGCCCA AGCGGATAAA GATTGACGG AGTCTCATT TATCCATTG 3000  
 GGCAGCTGG ACGATGAAAG CAAGACTACG GCGAGGATTG CAGCCTATCC GTTGAAGAAC 3060  
 GGCGTTATCG ATAAAGAGCG GGTGCGAGAA GTATCGACTC GTCCTACAA ACATCTTCC 3120  
 GTCATAAAA ATCTGGCTAC TGCAAAACAG ATCTTTATTT CCTATTCCAA AGAGGATCAG 3180  
 ACTGAACCTG ASACCTGTCT GCAATTTTTC AAACCTTGG AGAAGATGG TCAGATCGAG 3240  
 45 ATCTACTATG ATAAGTTGAC TAAGTTTGAA ACACCTATTC ACCCTGAAAT AAGAAAGCGT 3300  
 ATTGTGGAAG CCGACTGTAT AATCGCTTGG ATCAGCCAAC GCTATCTGGC CACGGATTAC 3360  
 ATCTGGATC ATGAGTTGCC TGTATTTGGG GAGTATAACA AGACCATAGT GCCGATATTG 3420  
 ATCAAGCCTT GTACATTGCA AGACGATGAG TTCCTTGGG AGAAATATTT TGCTCAGAAA 3480  
 GCTCAATATA TCAATCTTGG AAAAGAGGGA AAAACCATTA AAGCTTATGA TAGTATTACG 3540  
 50 GCATCAGCCC ATCGTGATGA AAATTGGGTG GCAGTAGTCA GAGAGTTCAA AGAGAAGATA 3600  
 TTAAGATAA CAAACAGGA GGTAAATACA GATCAA 3660

## (2) INFORMATION FOR SEQ ID NO:253

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAIDEDNESS: double  
 (D) TOPOLOGY: circular  
 60  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 65 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3525  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253



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	ATGACTTGGC	TTATTGATTT	TUCTGCTCTA	AAAAAGCTTG	ATCTATCGTA	TAACCAATC	60
	AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTTAACAA	AACCTCGTCT	AAGAAGTAAC	120
	CAAAATCCGTA	AAC TAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180
	GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
5	CTTTTGGATA	ACCNAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	300
	CTTGAACAT	CGGGTAACCA	AATCCGTAA	CTGGAGGGTC	TGGAACGCT	CACGTCTCTA	360
	GCAACGCTTG	AACTATCGGG	TAACCAATC	CGTAAGCTAG	AGGGTCTGGA	ACCTCTCACT	420
	TCGTTAACAA	AGCTTCGTCT	AAGAACTAAC	CAAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
	CTCACGTCTCT	TAGCAACGCT	TGAACATACG	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
10	GAACGTCTCA	CGTCTTAGC	AACGCTTGAA	CTGTCGGSTA	ACCAATCAG	TAAGCTAGAG	600
	GGTCTGGAAC	GTCTCTCTTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
	CTAGAGGGCC	TGGAACGTCT	CACCTCGCTA	ACAAAACCTT	CTCTCTCCGA	TAACCAATC	720
	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCAC	TCGTTAGCGG	AGCTTTATCT	TTTGGATAAC	780
	CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
15	AGTAACCAAA	TCAGTAAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTCT	900
	CTCTCCGAT	ACCAATCAG	TAACTAGAG	GGCCTGGAAC	GTCTCACGTC	CTTAGCGGAG	960
	CTTTATCTTT	TGGATAACCA	AATCCGTAA	CTGGAGGGTC	TTGATGGTCT	TGCTTCTCTA	1020
	ACAAGGCTTA	GTCTAAGCG	CAACCAATC	AGTAAGCTTG	AAGGACTAGA	CAGACTAAAG	1080
	GTCTTGAAG	AACTTGATGT	TTGGGCAAT	GATATTCAT	CTATTGATGA	TATTAAGCTA	1140
20	TTGGCTCCGA	TTCTGGAGCA	AACCTTAGAA	AACTGAGAA	TCCATGACAA	TCCATTGTGT	1200
	GCATCATCAG	CCTTGATACT	CTCTCTTAT	GATAATCATT	TGCGGAGAT	TAAAGCTCTT	1260
	CTTGAAAGAG	AAAAAGAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
	GTAATGCTAT	TGGGAATCA	TTCTTCGGGT	AAAAACAAT	TTCTTAGTCA	ATACGATACA	1380
	AAATATACGT	ATCAGAAAA	TACACATGTG	TTGTCGATAC	ATCGAAGCAA	TAACCTTAAT	1440
25	GCGATCTTT	ACGACTTTGG	GGGACAGGAC	TATTATCATG	GGATTACCA	AGCCTTTTTT	1500
	ACCACCCAAT	CGTTATACCT	TCTCTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
	GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCC	CCTATTGGTT	AGGACAGATA	1620
	GCCTATGCCT	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
	CAGACCCAG	ACGATACAA	TATCATTGAG	ACTCATGCCG	ATGAAACGGG	CGCTAAGCAG	1740
30	CAAACTTAG	GCTGTGCAGC	CGAGAATGGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
	CCCAAGGGGA	ATAGTGCCGT	ACATGCGCTC	AACTATCTGA	ATGAGCGGGT	GCGAGAAGTT	1860
	GTCCGAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
	CTTCCCAAA	TCCCGCGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGCGGCT	1980
	CAATTGAATA	AGGGAAGAGC	TGAAAATGAT	CTTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
35	TTGAACACG	TTAGTCTGCG	AGGGGAGGTG	CTTTACTATC	GTGAGAATGA	GAAGCTGAAC	2100
	AAATTCGCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTCTGGGAGA	AATCCTCCAA	2160
	AAAGACAAAC	TCAATAGAGG	AACAGTTCTT	AAAGACATTT	TTGAATGCAA	ACTGCATAAT	2220
	CTAAGTTCCG	GAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGCAGCTA	2280
	TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
40	CTTTTGCAAT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTCGA	GAGGCCCAAT	2400
	TTTTGCTCCG	CAATCGAACG	TTTTATCCCC	TTTGGCCTGA	TCAACCAGAT	TATAGCCTAC	2460
	TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCAT	CTTCACAGCA	2520
	GGCCGTGAGA	TGGATAGGCA	AACGCTTGAC	CAAGAAGAAG	AGAAAGAGGG	TTTGCCCAAG	2580
45	ACGAATGCCG	AGGATTATCA	GATCTGGATC	AAAGCTCGACT	TTACCGACTT	GGCCATATCC	2640
	GTATTTCATCA	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGCTACT	2700
	ATCCTCAGTG	ATATGTTGGA	TATGTATTTG	AACAATATCC	CTCCGAGGGA	GCAAAATAGGA	2760
	GATAAGGATA	CGGAGCAAA	GAGAAGCACT	ATTCGTGAAA	CAACAGAGAA	GAAGAGACCC	2820
	ATCCAGGATC	TCTACCTCTC	CTGTGOCCAA	GCGGATAAAG	ATTTGACGGA	GTCTCATTAT	2880
50	ATCCATTGCG	GCACGCTGGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
	TTGAAAGACG	GCGTTATCGA	TAAAGAGCGG	GTGCGAGAG	TATCGACTCG	TCCCTACAAA	3000
	CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCTTTATTTC	CTATTCCAAA	3060
	GAGGATCAGA	CTGAACCTGGA	GACCTGTCTG	CAATTTTTC	AACCTTTGGA	GAAGAATGGT	3120
	CAGATCGAGA	TCTACTATGA	TAAGTTGACT	AAGTTTGAAA	CACCTATTCA	CCCTGAAATA	3180
	AGAAGCGGTA	TTGTGCAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAAAG	CTATCTGGCC	3240
55	ACGGATTACA	TCCCTGGATCA	TGAGTTGCCT	GTATTTCCGG	AGTATAACAA	GACCATAGTG	3300
	COGATATTGA	TCAAGCCTTG	TACATTGGA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
	GCTCAGAAAG	CTCAAAATAT	CAATCTTGGA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
	AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCAG	AGAGTTCAAA	3480
60	GAGAAGATAT	TAAGAATAAC	AAAACAGGAG	GTAATAACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 687 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (11) MOLECULE TYPE: DNA (genomic)
- (111) HYPOTHETICAL: NO
- (117) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

10	ATGATGAAAA AAGCATTGTG TTTCTACTA CTGGTTTGCC TATCTCCTC GTTCAGCAGT	60
	TCCGCCCAAA CAACGACGAA CAGTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG	120
	AGTTTGAAC TAGGGGTCCC CCCGTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG	180
	AACGGTCTCC CTTTCGAAAT ACCTATCTCT TTCAGTCGTT TCAACAGCCA GGGAGATATA	240
15	GCTACCACTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA	300
	CACCCGGGCG GCATCGTGAG GGTAGAAGGT CGTTTTTGA AAATGACTTA CAACATACCA	360
	ACCTACAATG CAGTCTGCAC CCGGATTACA TTCGAAAATC AAGAAATAGA AGGAACGATC	420
	GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCAIC	480
	CGAACCGAAG CCGGGAGGGA ATTTATCCTT TCGGAAGAAG ACGACACCTT TGTGTCTCAC	540
20	GATGGTAACG AAGTAACGAT AGGCGGTAAC CCTTCTTGC TCAATACCAA CGTAAAGATT	600
	GTGGGGGACG TATCTCAAAA GTATGCCGTG GGGGTAGGAG AAATTCGATT CTGCAGATT	660
	TGTGCCCAAA CAGTATCACA ACAAAAA	687

(2) INFORMATION FOR SEQ ID NO:255

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 684 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...684

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

50	ATGAAAAAAG CATTGTGTTT CGTACTACTG GTTTGCCTAT TCTCCTCGTT CAGCAGTTCC	60
	GCCCAAAACAA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT	120
	TTGAACCTAG GGGTCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC	180
	GGTCTCCCTT TCGAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT	240
	ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC	300
	CCGGGCGGCA TCGTAGGGT AGAAGGTCGT TTTTGGAATA TGACTTACAA CATACCAACC	360
	TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AAATAGAAGG AACGATCGTC	420
55	TTGATACCCA AGCCCAAAGT CTGCTGCCCT CATGTGTGCG AATCGGTGCC TTGCATCCGA	480
	ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTTGT GTCTCAGCAT	540
	GGTAACGAAG TAACGATAGG CGGTAACCT TTCTTGCTCA ATACCAACGT AAAGATTGTG	600
	GGGGACGTAT CTCAAAAGTA TGCCGTGGGG GTAGGAGAAA TTCGATTCTT GCAGATTGTG	660
60	GCCCAACAG TATCACAACA AAAA	684

(2) INFORMATION FOR SEQ ID NO:256

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (Rule 26) (RO/AU)

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

10 ATGAAGACAA AAGTTTACG CAAATTCGTG GTGGCGGCTT TCGCGGTCCG AACCTCTGT 60  
CCTCTCGCCC AAGCGCAGAC GATGGGAGGA GATGATGTCA AGGTGGTCCA GTACAATCAG 120  
GAAAAACTGG TACAAACCAG GATGAGTGTG GCGGACAACG GATGGATCTA TGTAAAGACC 180  
CACAGTGGAT ACGACACCGG CAATAGCAAT GTGAAGATCT TCGCTCCAA AGACCAAGGT 240  
GCCACATACC AAAAGTTGAG GGATTGGGAT CCATCGGATG ATTATCAGTT TCAAGACTTC 300  
GATATCGTGG TAACGGGTAA GAATGAATCC GACATCAAGA TTTGGTGGT AGAGCTCATG 360  
15 AATAAGCCCG GAGGATATAA GAGTAGAGT GCGGTCTTCA GTCGCGATGC CAACGCGCAG 420  
AATGCGAAGC TCGTGATATA GGAAGACTTC TCCAATGTGC AGTTGTACGA TGTGGATATA 480  
GCCTCCAAC ATCGTTCGCC TTCTTCTCT AACATGGTG GCAACCCCTT TGCCTTGGCT 540  
TTCGCTTACA CCGGCTTCAA CAATACGCAC AAAATAAGTT TTGTGGACTA TGTGTTCTCT 600  
CTGAATGGAG GGCAAAATTT CAATAAAAC TTACTCTTCA GTCAAGATGG AGAGAAGAAA 660  
20 ATTGACAAGG TGGATCTCTC ATTGGGTAGC ACCTCTGAAT CCATGGGTCA CAATGCCTGG 720  
CCGCTAATGG GTGTGGTATT CGAAATGAAT AAACAAGGGG GAAAAAGCGA TATCGGTTTC 780  
TTGTGGAAC TTGTGCAAA TGATCCCGAA TTTCAGTGGT CAGGCCCTAT AAAAGTGAGT 840  
GAAAGCGACA TCTCGTTCAG CCCCAAAATC CAAATGTTGC TGGACGAGGA TAACATACG 900  
ATCAATGGGG AGAGTTGCCA CAATTCATG ATTACGTACA GCGATTATGA TTCTGAATAT 960  
25 TCGGATTGGG ACATTGGTA TGTATATCCC AAGAAATCGT TCAAGTATGA AAAAGGAAAA 1020  
ACTCGGACTA TGGGTATGCT GGTGGAAGCT TTCCTTACAG CTTCGTACCA GAGTGAGACC 1080  
AATCGGSGC TGGGGTATGA CAAGAAGGCC AATCACTACC TGATTACATA TGCCAAAAAA 1140  
GAAGAGAACG GTACGAACAC GCTGAAATAC CGCTGGGCCA ATTATGACAA GATTCTAATC 1200  
30 AAAGATTGTG GGAAGCGAC ATTACGTAT ACATCATCTG CCAATGCTCT CTACACACCT 1260  
CAAGTAGACA TCAATCCGAC CAAGGGTCTC GTGTGCTGGT CATGGGTGGA ATATCTGCGG 1320  
GGCAAAACGA TCGTTTGGTC TGATACGCG TGGACCCATG CCAACGGTGT AGAAGACATC 1380  
GTAATGCAAG AAGGCAGCAT GAAGCTCTAC CCGAATCCGG CTCAGGAATA TGCTGTGATT 1440  
AGCTGCGCA CGGCAGCAAA CTGCAAGGCT GTTGTTCAG ATATGCAAGG CAGAGTAGTC 1500  
35 CGTGAGGCTT CTTTCTCCGG CAACGAATAC AGGCTGAACG TGCAAGCACT GGCTAAGGGT 1560  
ACGTACATAC TCAAGGTCGT ATCCGATACG GAGCGTTTCG TAGAGAAGCT CATCGTGGA 1620

(2) INFORMATION FOR SEQ ID NO:257

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
45 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
50 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

60 ATGCTGACGA TCCGAACTT CCTCCTCTT TGTGTCTGT CGCTGATAGC GTTGTCTGCC 60  
GATGCACAAA GCTCTGTCTC TTCGGGTAGA CGACTGACAG AATATGTCAA TCCCTTTATC 120  
GGAACGGCCA ATTACGGTAC CACGAATCCG GAAGCAGTAT TGCCCAATGG GTTGATGAGC 180  
65 GTTACCCCTT TCAATGTGAG CGGATCGACA GAGAATCGCT TCGACAAAGA TTCGCGTTGG 240  
TGGAGTGGCG CTTATTCGGC CGACAATAGT TACTGCAATG GTTTCAGCCA TGTGAATCTG 300  
AGTGGAGTAG GCTGTCCGGA ACTGAGTGGC ATACTGCTGA TGGCCACTTC CGGCACATTC 360  
GATCCTGATT ATGCTGCTA TGGCTCTTCG CTCAGTCCAG AATATGCGCG CCCGGGAGAA 420  
TACAAAGGCTG TATTGGACAA ATACGGTATA GATGCAGCCG TGACCGTAAC CGAGCGGACT 480  
GCTTTGACCG AATTGCTTT TCCGGAAGGA GAAGGCCATA TCCTGCTGAA CCTGGGACAG 540  
70 GCCCTAAGCA ATGAATCGGG AGCCTCTGTT CGATTCTTAA ACGACTCCAC AGTCGTGGC 600  
AGCAGGCTGA TGGGACGTT CTGCTACAAT CCGCAAGCAG TTTTTCGTCA GTATTTCTGA 660  
CTTCAGGTGA GTGCGGACCG GATCTCTGCC GGCTATTGGA AGAAGCAGCC TCCTATGACA 720  
GTGGAAGCCC AATGGGATTC GACTGCAGGG AATATAAGC AGTACGACGG CTACAAGCGT 780  
GAGATGACCG GTGATGACAT CGGTGTCGGA TTCTGTTCA ACTGCGATCA GGGGGAAAAG 840  
75 ATCTATGTAC GATCGGCCGT TTCATTCGTC AGCGAAGCCA ATGCGCTCTA TAATCTGGAA 900

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5 GCGGAGCAAG AAGAGGTGTT CAAAAGTGTC GGAGGGAATC CGGCCAAGCC TTTCTCCGCT 960  
 ATACGCTCTC GCGCTATAGA GCGTTGGGAG GAAGCCCTCG GTACGGTGGA AGTGAAGGA 1020  
 GGCACACCGG ATGAAAAGAC GATATTCTAT ACCGCACTCT ATCACCTGCT GATACATCCG 1080  
 AATATCCTAC AAGATGCCAA TGGAGAATAT CCTATGATGG GCAGTGGCAA AACGGGTAAT 1140  
 ACGGCTCAGC ACCGCTACAC CGTGTCTCTT CTTTGGGACA CGTACCGCAA TGACACCCG 1200  
 CTGCTCTGCC TCCTCTATCC GGAGAAGCAG TTGGATATGG TACGGACACT GATCGACATG 1260  
 TACCGAGAGA GCGGGTGGCT GCCGAGATGG GAGCTGTACG GACAGGAGAC CCTGACGATG 1320  
 GAGGGCGACC CCTCGCTTAT CGTCATCAAT GACACTTGGC AAAGGGGCGT TCGTGTCTTC 1380  
 10 GATACGGCAA CGGCCATGA AGCCATGAAA AAAAATGCTT CTTCGGCAGG AGCGACCCAT 1440  
 CCGATCCGTC CTGACAACGA CGACTATCTC ACCCTCGGCT TCGTACCGCT TCGCGAACAG 1500  
 TAGGACAATT CGGTATCGCA TCGCTGGAA TACTATCTGG CCGACTGGAA TCTGTCCCGG 1560  
 TTTGCCACCG CACTTGGGCA TAAAGAAGAC GCAGCTCTAT TCGGAAAACG CTGTTG3GC 1620  
 TACAGCACT ATTATAATAA GGAGTATGGT ATGCTGTGTC CATTGTCTCC GGATGGATCA 1680  
 15 TTCTCACTC CTTTCGATCC CAAACAGGGT GAAAACCTCG AGCCTAATCC CGGTTTCCAC 1740  
 GAGGGCAGTG CTATATACTA TGCCCTTTTC GTTCCCGACG ATATACAAGG GCTTGCCCGG 1800  
 CTGATGGGAG GAGCAAAGGT TTTTTCGGAA AGGTTSCAGA AAGTCTTGA TGAAGGATAT 1860  
 TATGATCCGA CCAACGAGCC GGACATCGCC TATCCTTACC TCTTCTCCTA TTTCCCAAG 1920  
 GAAGCATGCC GAACGCAGAA ATTGACCCCG GAGTTGATAG ACAAACATTT TTGCAATGCT 1980  
 20 CCTAACGGCT TGCCCGGTAA TGACGATGCC GGTACGATGA GTGCTTGGCT TGCTATATCC 2040  
 ATGCTGGGAT TCTACCCCTGA CTGTCCGGGC AGCCCCACT ATACACTGAC CTGCGCGGTA 2100  
 TTCCCGGAG TTAGGATTCG GCTCAATCCG CAGTATTATC CTCAGGGGGA GTTGATCATT 2160  
 ACGACCAATA CAGAGAATCA ACCGACAGAT TCCATTTACA TCCATACGGT TTCTCTTGGC 2220  
 AATAAAACAC TTCCGATGG AACAAAGGAT ATCAGCCATG CCGATTGGT GCGCTGCGGT 2280  
 25 CACCTCCGTT ACGAACAAAG CAATCGTCCT CGA 2313

## (2) INFORMATION FOR SEQ ID NO:258

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2328

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

50 ATGTGCAAAA TAAGATTCAG CCTCTTGCAG GCTCTGTGCG TCTGCTTATT GTTCACCTCT 60  
 TTTCTCTCC AAGCTCAAGA GGAAGGTATT TCGAATACCC TCTTGGCTAT CCACAAGACG 120  
 GAAAAAGCCG TAGAAACGCC CAAGAAAGTC TTTGCCGTAG CCACCGGAGT ACTTTACTCG 180  
 GTGGGCAAG AAGCTCCCCA TGAGGCAAG ATCTTCGACC GTATCAGCGG ACTCAGCGAT 240  
 55 ACATCGGTAA GCAGCATAGC CTACTCCGAG CAACTAAAAT CCTTGGTCAT ATACTATGCA 300  
 TCAGGCAATA TCGACATCTT GGACGAAGCA GGCGGTGTGA CCAACGTACC TGCATTGAAA 360  
 GACAATATCG ATCTGATAGA CAAAACGCTC AATCGCCTTT TGATCGTAGG CAACAGGGCT 420  
 TATTTGGCAG GAGGATTCGG CCTCTCCGTT CTGATGTGCG CCGAAGCTCG CATACCGGCT 480  
 ACCTACGCCA AGGGAACATA GGTGACCGAT GTGGCTAAGT TGGACAATGA TCGCTTGCTG 540  
 60 ATGCTGAAAG AAGGACAGCT CTTTCATCGA AAAGAGACCG ATAACCTGCA AGATCCGGCC 600  
 GCATGGACAG CCTTGTCTTT GAATTTGCCG ATGGGCTCGG TCACCGGTCT GGGCATTGTC 660  
 GGGGAAGACA TCTGTTTCTT GCTCGCGGAT GGCGGTGTAT ATGTGCTGTC AAACCAATCG 720  
 TTTGAGCCGG AGCTATTGCT CTCTTCTCC GCGATTACAC GACTGTATGT GACGGATCGT 780  
 GGTCTGTTC TCTGTGCCGA GAATCGAATT TATTTCATAG AAAAAGGTG CAAAACGACA 840  
 65 CAATTTCTTA TAGCCGACGT CTTTGGGTGTC GGTGCCATGA ACGAAAGCAA TACGGCATA 900  
 ATAGCATTGG GAGAAGAAGG TTTGGCTTCA CTTCTTCTCG CAGAGGGAAG TACGGCCGAA 960  
 CCCATGCCG TAGCATTCTGA CCGACCGGGG GACAATGATT TCTACGAGAT GCGGTTTAGT 1020  
 CACGGACGTC TGTATGCAGC CAGCGGACTC TGGGGACAAA ACCTGATGGG ACATGCCGGT 1080  
 ATGGTGAAGC TATACGACGG CAACCGATGG ACTAATCTCG ACAGAAGAC CGTACAGGAA 1140  
 70 CAGTTGGGCG GCGGATTCTG TTTCAATGAT GCTATCGATA TAGCTGTTTC CAACGGAGAC 1200  
 CCCGATCACT TTTTGTCCG TACATGGGGA AAGGGTCTGT TCGAATTCAA GGATGGCAA 1260  
 GCGATAGCTC GCTATTCCGG AAACGAAACT GCTATCGCAG AATGTAATCC CCGAGATGCC 1320  
 CGTGTGAAGC CGATTGCTT TGACAATAAG GGCAACCTCT GGGGACGCT CGGTGCCGTA 1380  
 GGCAGGAACA TCTTCATGTA CGATCCGCGAG AGTAGCACAT GGCATTCTTT CAGCTATCCG 1440  
 75 GATGTAGCCA ATCTGGCCTC CTTGGCAAT ATGATTATCC TACCAACGG AGACAAATGG 1500  
 GTAAATATCC TTCACCGTAG TGGCGGATCC ACGCGCAAG GTGTCTTGAT CTTCAACGAT 1560

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CGGGGTACAC CGGAAACGAC TTCGGACGAC AGCCATCTTT ACGTCGAGCA GTTTGTCAAT 1620  
 CGCCTCGGG CAGCCATAGG ACATAAGACT ATCTATGCAA TGGCCGTCGA TCATAACGGC 1680  
 TCTGTCTGGA TGGGATCGGA TATAGGCATT TTCGGCGTCT ACAATGCAGC CGGAGTATTG 1740  
 TCCTCGACTT CTACCCCTAT CGCTGTTCCG CCGGTCGGAG GAGAAGAACC CAATTTGTAC 1800  
 TATGTGCTGG ACAAGGTGAC GGTGACAGAC ATCGTCGTGG ACAAACTCAA TCACAAATGG 1860  
 GTTGCCACCC AAGGGACAGG ACTCTATCTC CTTTCGGAAG ATTGCAGTAA GATCCTCGCG 1920  
 CAATTTACCG TAGAAAACAG CCCTTTGCTT TCTAACAACTACTATCCCT GGCCTTAAT 1980  
 GACGATAACG GACTGCTGTA CATCGGTACG GCGGACGGAC TGATGAGGTT CCAAAACGGG 2040  
 ACCGGGAGTG GATCAGCTTC CGAACTGGAC GCGCTCTATG TATACCCCAA TCCGCTAAGG 2100  
 CCGGAATATC CCGATGGCGT CACCAATTGCC GGAAGTGAAG CCGGCTGTAG TGTCAAAATC 2160  
 ACCGATACCA CCGGCAGACT GCTATACCAG ACTGAGAGCG TAACCAACCGA AGTCAAAATG 2220  
 AATGCTCGAG GTGCCGATGG CAATAGGGTA GCTTCGGGCG TATATGCCGT TGCAGTGTAC 2280  
 GATCCGGTAT CGAAAAAGTC CAACTAATT CGCTTCGCAG TGATTTCG 2328

## (2) INFORMATION FOR SEQ ID NO:259

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...3474

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGAACGAA TACTTCCAAT AGTCGCATTC CTTCTCTCT TCCTTGCCCT TGCTTTGCCT 60  
 GCGAAAGCGC AACGAGCTAT GGGGAAGACG GCCGACCGTT CGCTAATGGC TTCGGGACAT 120  
 TGGGTCAAGA TACGTGTGGA TGCAAGTGGG GTGTATCGCC TTACGGACGA ACAGCTCCGT 180  
 GCCAATGGCT TCTCCGATCC GTCCAAGGTA GGTGTGTTCC GTTATGGTGG AGGGGTGCTT 240  
 CCUGAAGATC TGAGCCGGAT CACGACAGAC GATTTCCTC CGGTACCGGT ACTCCGTCAG 300  
 GGCAATGGCG TGTATTCTTA TGCCGTGGGC CCGGTGACAT GGTTCCTACAA TCCGGCCAAA 360  
 ACCACCATGG AGCATAAGGT GAATACATAC AGTACGGATG GCTACTACTT CCTGTCCGAT 420  
 GCTCCCGSAG CACCTTTGCA GATGTCCCAA TATACGGGTG GAGGTGCGTC GGCCGAGGCT 480  
 TTGATCGACT ACTACGATGA GCTGATGCTC CATGAACAGG AATTGTATTG GCCCAAAGAA 540  
 TCGGACGAG ATCTGTATGG CGAGTCTTTC AGTGCAGTCA ATACCGGTAC GGTCAAGTTC 600  
 CCTTTGAGGG GCAACACCCG CTGCTCTGGC GAAGTCCGTA CCGTATTCTC ATACATAGCC 660  
 AAGGCCAGAT CGGCCGGTGG CCGCCGTGAG ATGTCCGTCT CGGCGAATGG CATCTGATC 720  
 TTCAGCGATC CTTTTTCCAT GACATCGAAT GAAGTCTCCA ATTCTTATTI GGCCGGCAAG 780  
 AAGCGTCGTC TCTATCACAG TACGCCGATG AACAGCTTGG TCAATGAGTT GCGCTTGGAC 840  
 GCGAATATA GCAATGACAGG AGATGCGGTC AATCTGGATT TCATAGAGGT GGCTACACAG 900  
 AACGACCTCC GGTACGATGG CGCACCCATG CATATCAGGC GGTTTTCCAA TTTGCCCGTT 960  
 TTGGGGGGGG AGTCTTGCCG GTTGGTTATC AGTGAGGTGC CGGAGTCTCT GGTGGTTTGG 1020  
 CAGGCCAATT CTTCCCTGAC AGCATCGCTT GTTCCCGTTA AGACTGTCCG GGATAAGACC 1080  
 ATTGAGTTCC TGGCTCCGCC GAAGGGTCAG GATCGTAGGA CTATCAATAC GTTTTATGCC 1140  
 GTGGACTTGT CACAGGCTTC TGCTCCGGAG ATCCTCGGAG CGGTACCCAA TCAAAACCTG 1200  
 CATGGAGAGG AATCCCTGA TCTGATCATT GTCTCTACTC AGGCGCTCCT CTTGAGGCT 1260  
 GATCGACTGG CCACCTATCG TAGAGAGAAA AACGGGCTGA AGGTTTTGGT CGTGTTCAG 1320  
 GAACAGGTGT TCAACGAGTT TTCGGGTGGA ACTCCCGATG CTACAGCATA CCGCCTCTTT 1380  
 GCCAAATGT TCTACGACAG ATGGAAGGCA AATGCACCTG TGGGAGAGAC CTTCCCGATG 1440  
 CAAATGCTTC TCTTCGGTGA TCGGGCTCAT GACAACAGGA AGGTCTCCGT AGCTTGGCAG 1500  
 AAACCGTATC TCCAACAAAC GGAGTTCTTG CTGACATTCC AAGCGTCAA TTCCAGCAAC 1560  
 GTAAACAGTT ATGTGACGGA TGATTACTTC GGCTTGCTCG ATGATCAGCC GGCCTCGGT 1620  
 AATATCGSTT GGCCTAATTA TAATATGGCT GTAGGGCGAT TCCCGTACG TACTCCGGCC 1680  
 GAAGCTCGCA TCGCAGTGGG CAAGACCATC CGATATGAGG AGGATCGAGA GAGTGGTGCC 1740  
 TGGCGTATTC GTGCTGTTT TCGGGCAGAC AACGGGGACA AGCACGCAAC CGAGACTTCC 1800  
 CGTTTGATCG ATACCGTCAA GCGTTATGCT CCGCCATCA TCGCGGTACG CGCCTTTGAG 1860  
 GACGTATATC CGCATGTCT CGAGAACGGG TTGCACAGCA TTCGGGTGTC AAAGAAAAAG 1920  
 ATGCTGGAAC CCCTTCAGTC GGGTATTATC CTGCTTAATT ATGCTGGTCA TGGCGGTCT 1980  
 GCCGGATGTT CGGACGAGCA TTTGCTGACG CTCACGATA TACACAAATT CAATTATAAG 2040  
 CATATGCCCA TTTGGATTAC TGCCACGTGC GACTTTGCCA ACTATGACAG TCAGACGACC 2100  
 TCGGCGGGG AGGAGGTTTT CCTCCATGAG AAGAGTGGCA CTCGATCAT GTTCTCGACT 2160  
 ACGCGTGTG TTTACAATAC GCAGAATGAG AAGATCAATG GTTTTATGCT TCGGCGTATG 2220

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5 TTCGAGAAAG CTAAGGATGG GCGTTATCGT ACGATGGGCG AGATTATCCG ATCGGCCAAA 2280  
 CAGGGGATGC TCAGTACTGT TTCCCGGAT TCGATCAACC AGTTGAGTTT CTTTCTGATG 2340  
 GGTGATCCGT CCGTGCGTAT GAATCTTCCT ACCCACAAG TGCAATTGAC CGCAATCAAC 2400  
 GGGCAGGATC CCGAAGGGCA GTATGGAAC ATTATGCTCA AGTCTTTGGA ACGGGTAGCT 2460  
 CTGAAGGGTA AGGTAACCGA TGAAGAGGGG ACATTGCGAG AGACATTGAG TGGCAAGGTT 2520  
 TTCCTGACCG TCTTCGATGG CAGAAAGAAA ATGACAGCTT TGAAGAGGA GGGAAACGAT 2580  
 CTCTCTCTTG TATATTATGA CTATCCTAAC GTGATGTATG CCGGTATTGC CGAGGTGAAA 2640  
 GACGGAATCT TCGAAACTTC GTTTATCGTA CCCAAGGATG TGAATATTG CGAGCAGGAA 2700  
 10 GGCCCGATCA ATCTTTATGC TTATAACGAG AGCACAAGG CGGAAGCCAT GGGGGTAGAC 2760  
 TTCTCCATCA GAGTCCAACC GGGTATTCTT GATGAGGTAA CGGAAGATA TACACCGCCT 2820  
 GAAATCATAA GCTGCTTCCT CAATGACAGT ACATTCCGAT CGGAGATGA GGTAAATCCT 2880  
 ACTCCTCTGT TTATGGCCGA AGTATTCGAC TTGAATGGAA TCATATCAC GGGTAGCGGA 2940  
 GTAGGCGATG ATATTACGCT TTGTATCGAT GGGCGTGCCG ACCTGACCTA CAACCTCAAT 3000  
 GCATATTCCA CAAGTTCGGC TACGGATGCA GGTGTGGGCA CTATTCTCTT CATGATACCG 3060  
 15 GCTTTGGCCG AAGGAGATCA TACTGCCCGA CTGACGGTTT GGGACATTTT CAATAATGCG 3120  
 GTCCATCATG ACTTTTCATT CAGAGTGGTA GATGGCATTG CTCGGGATGT GGTGATGTTG 3180  
 ATTCTATTC CGAATCCGCT ACAGGAGAGT GCTACGTTCC GAATCTTCCA CAATCGCCCG 3240  
 GGAAGCGATT TGAACGTGGC CCGTGGAGATC TATGACTTCA CCGGTCTGCT TGTGAACAGT 3300  
 20 TTGCCAGTCA AGACCTATTC GTCTTCCTAC GGAGAACCTA TAGAGATCAA GTGGGATCTG 3360  
 ACCTCCAAAT ACGGAGTGAA GATCGGAAAC GGATTCTACC TCTATCGTTG TGTGGTGAAC 3420  
 TCTCCCGGAG GACAGACGGC CTCATGCGCC AAGAAAATGA TCGTGTAGG ACAA 3474

## (2) INFORMATION FOR SEQ ID NO:260

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2883

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:260

50 ATGAAGAAAC TTTTCCCAT ATTATTACTC ATATTGTGCA TTTTGGTGGG ATGTGGAAAA 60  
 AAAGAAAAAC ACTCTGTAAC TGAATCGGCC GGAGAGAAAA AGGTATTATC TGCAATTGCTG 120  
 TACGAAAAAG AACTCCCCAC TGATCTCTGT AAACAGCTTT ACGAGAACAG CGTACAGAAC 180  
 AAGAACCTTG TGGGACAAAT GTTATTCCGG ATCGAGGTGCG GCAAACGGAT CCGTAATATG 240  
 TCCCAATACA CAGATGCGAT GCTATATCAC CAAAAAGGGT TGAACGCTGC ATTGAATCTA 300  
 AGGGACACCA TCGTAGCCGC ACAAGCATGG AATCATCTCG GAACGGATAG CCGTCTGATC 360  
 GGTGCTTTGG CAGAAGCTTC GGATTATCAT TACAAGGCTC TTTCTTGAT AGAATCTTTT 420  
 55 AGCGGAATCC AGAATAGGCC TGUGATCAAA GCCAGATCGG CGGCCCTGAA CGGCATCGGC 480  
 AACATCAATC TTGAGTTAGG ATACCATGAT GAGGCCGAAA AGAATTTCTT GAAAGCACTG 540  
 CAAGGTGAGA AAGAATCGCA CAGTCCCTCT GGGCAAGCTA TCAACTATGC GAACCTCGGA 600  
 CGTATCTATC GACAACGCAA AGAATACGAC AAGGCTCGTA CCTACTCTCT CTGTCTCTG 660  
 GAGCAGAAAC ATATGGCAGA GAATCTGATG GGTATCGGAC TCTGTAGCAT CAATCTCGGA 720  
 60 GAAGTAGACG AAGAAAAAGG GGATTATCAA AAGSCTTTGC AAGAGTATGC CACGGCATAC 780  
 AAATCTGATG AACAGTTGTC CGATCGATGG CACTGGCTGA ATTCTGTAT CCCGATGGCA 840  
 CGTATCAATC TCAACAAGG TAACGAAAGG CTCTACCAGC ATTTCTTTT TTTGGCCGAA 900  
 GGGACTGCGA AAGAAATTA TCGCACTTCA CATCTGATAG AAATATACAA TCTTCAATAC 960  
 GAGATCTCG AGCGTAAAAA AGAATACAAA CAAGCCCTCG AAGCATTTCT TCTGAGCAAG 1020  
 65 ACGTTGAGCG ACAGCATGTC CATTGCGCAC AAGGTGAGCA GCATACAGA AACCGGATTC 1080  
 AACTACGAGA GAAACAAGTC CCAAAAAGAG CTTGAAGAAA TACAGCAAGT AAGCAAGGCA 1140  
 AAACAAGAGA AATCGAAGTT TATCCTCTTG AGCACTCTTT TTGCCCTTTT CATCTCGATT 1200  
 CTTTGTGATT CTGTTCTGAC ATATGCATAC CGTCAGGGCA AGAAGCATAA CAAGCTGATC 1260  
 AAAGAGACGG ATAACTTCG CTCGGCTTTT TTCACCGGTA TTACACACGA ATTTCTGACG 1320  
 70 CCTATCACCG CATACAGAG TTTGAATGAG AAAATGAGTT CAAGTCTGTA TCTCCAAGCA 1380  
 TCGGACAGAA CCGAGCTGCA CAAGATAATA GACAGACAGA GTAGCCATAT GCTGAATTG 1440  
 GTGAACGAGC TGTGATATAT TTGCAAGATC AGAAGCGGAG TATCCACGCC CGAATGGGCG 1500  
 AATGGCGACA TCGTCTCCTT CGTACAGATT CTCATCGATT CGTTTGACCC ATACGCACAG 1560  
 GCTCAAGACA TAACCTTGA GCTACAACCC GAGAGCAAAC CTATTGTCGT GGACTTCGTC 1620  
 75 CCTCCTACT TGCAAAAAAT CATATCCAA CTTTGTGCA ATGCCATCAA GTATTCTTTA 1680  
 GCGGAGGGA GAGTGGTCA ATCTCTGGA AAAACCAAGA ATGAAAAAA TCTGATCATA 1740

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5	CGCGTTGCAG	ACAATGGCAT	AGGAATAGAT	AAAACATGATC	AGGLTCATAT	CTTCGACATC	1800
	TTCTATCGAG	GACAGTCCGC	TACCGAAAAG	CATGGATCAG	GGGTCCGACT	CTCGTTTACC	1860
	AATATACTGG	TCGAAAACCT	TCGAGGTACG	ATCAAAGTGG	AAAGCCAGCC	GGGGAAGGA	1920
	AGTGCCTTCA	CCATCAGTAT	TCCTACACAA	AACCAATCCT	CTTCGGCAGA	GATTCTTCCT	1980
	TGGGTACCTT	CCTCGATGA	CATTGTCTATG	CCTGTCCACA	TCGGGCCGGA	TGACTCACCG	2040
	ACATCTCCGA	TGGTAGCAGC	TCTGAATCAT	CGCTTCGAGG	ACGAACGTCC	GACCATACTG	2100
	CTCCTCGAGG	ACAAATAAGGA	TATCAACCTG	CTCGTCAAAC	TACTCCTTTG	CGATCGCTAC	2160
	ATGTGTCTAT	CCGCCGCAAA	CGGAAAAGAG	GGTATAGCCC	TCGCTACOGA	GCATATTCCC	2220
10	GACATTATCA	TTACGGATAT	TATGATGCCG	ATAATGGATG	GGATAGAAAT	GACAAATCCG	2280
	ATGAAGCAAT	CGCTCTGCT	CTGTACATT	CCCATTTGTCG	CTTTGACGGC	CAAGAGTACC	2340
	GAACAGGACA	GATTGGAAG	AATCAAAAGC	GGTGTAGTCT	CTTATCTATG	CAAGCCATTG	2400
	TCCTCCGAGG	AGCTTTTGTAT	GCGGATCGAG	CAGCTTCTGA	AAGACCGTGA	GTTGCTCAAG	2460
	AAGTTCTATA	TGCAAAAACCT	CATGCTGGAT	CGGAAGCCGG	AGGAGGAGCC	TCAACCGATA	2520
15	GATGACAGCA	GTATGCAGTT	TCCTCTTGT	GCCAAAGATG	CAGTGTCCGG	TGGAATCAAA	2580
	CAAAATCCGG	ATTTTCCCGC	TCAAGACTTG	GCCGAAAAAA	TGTGCATGAG	TCCATCCCAA	2640
	CTCAACAGAA	AGCTCACGAG	TGTCGTAGGT	TGCTCCACCA	TCGGGTACAT	ACAGCAGATG	2700
	AAGATAAAAT	TGGCCTGCAG	GCTCCTTGCC	GATGAGAGCA	AAAACATCTC	CGACATTAGG	2760
	ATTGAGGCAG	GCTTTTCGGA	TCGGGCTTAC	TTCTCTCGCA	CCTTCAAACG	CTACATGAAC	2820
20	TGCTCTCCCT	CCCAATATCG	GCAAAAACCT	CTTGCCATGC	GGGGGAGCGA	CAAGGAGACA	2880
	GTT						2903

## (2) INFORMATION FOR SEQ ID NO:261

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1668 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1668
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

45	ATGAAAAAGC	TTTACAGGC	TAAAGCCTTG	ATTCTGGCAT	TGGGACTCTT	CCAATGCCCC	60
	GCAATCGCCC	AAACGCAAAAT	GCAAGCAGAC	CGAACAAACG	GTCAATTTGC	AACAGAAGAG	120
	ATGCAACGAG	CATTCCAGGA	AACGAATCCG	CCTGCAGGTC	CTGTGGGTGC	TATCGCTGAG	180
	TACGAACGCT	CTGCAGCCGT	TTTGGTACGC	TACCGGTTGG	GTATCCOGAT	GGAAATGATC	240
50	AAAGAGCTGG	CCAAGAACGA	CAAGGTGATT	ACCATTTGTT	CGAGTGAAAG	CCAAAAAAC	300
	ACCGTTATAA	CCCAAGTACAC	CCAAAGCGGT	GTGAATCTCT	CTAATTGGCA	TTTCATCATT	360
	GCGAAAACCT	ACTCTTACTG	GACACGCGAC	TATACCGGTT	GGTTGCGAAT	GTACGATACG	420
	AACAAAGTAG	GTCTCGTGGG	CTTTATTTAT	AACCGCCCTC	GTCTTAACGA	TGATGAATTC	480
	CCCAATACG	AAGCACAATA	TCTGGGCATC	GAGATGTTGG	GGATGAAGCT	CAAGCAGACC	540
55	GGTGGCAACT	ACATGACGGA	CGGATATGGA	TCGCTGTGTC	AGTCACATAT	CGCATATACG	600
	GAGAATCCTT	CTCTGTCTCA	AGCTCAAGTA	AATCAAAAGA	TGAAGAGCTA	TCTCGGCATC	660
	ACACATCATG	ATGTGGTACA	AGATCCGAAC	GGCGAATATA	TCAACCATGT	GGACTGTTGG	720
	GGCAAGTATT	TGGCACCGAA	CAAAATCCTC	ATCAGGAAG	TGCCTGACAA	TCACCTCAG	780
60	CACCAAGCCC	TGGAAGATAT	GGCAGCCTAC	TTCGCAGCAC	AGACCTGCGC	ATGGGGAACG	840
	AAGTACGAGG	TATATCGCGC	TTTGGCCACC	AATGAACAAC	CGTACACGAA	CTCTCTGATT	900
	CTGAACAACA	GGGTATTTGT	TCCTGTCTAT	GGCCCGGCTT	CCGTGGACAA	CGATGCTCTG	960
	AACGTCTATA	AGACGGCAAT	GCCCGGTTAC	GAATTTATAG	GTGTCAAAGG	GGCTTCACGA	1020
	ACACCTTGGT	TAGGAACAGA	TGCCCTGCAT	TGTCGTACTC	ACGAGGTAGC	GGATAAGGGC	1080
65	TATCTCTATA	TCAAGCACTA	CCCGATACCT	GGCGAACAGG	CAGGCCCTGA	TTATAAGATC	1140
	GAAGCAGATG	TCGTCTCATG	CGCCAATGCT	ACTATCTGCG	CGGTACAATG	TTACTATCGT	1200
	ATCAATGGTT	CCGGTAGCTT	TAAGGCTGCT	GATATGACGA	TGGAATCAAC	AGGTCACTAT	1260
	ACTTATAGCT	TTACAGGTCT	TAACAAGAAAT	GATAGGTTAG	AATACTATAT	CTCTGCGGCT	1320
	GACAAATAGT	GTGCGAAAGA	GACTTATCCC	TTTATCGGCG	AACCTGATCC	TTTCAAGTTT	1380
70	ACGTGTATGA	ACGAACCAA	TACATGTACT	GTGACCGGAG	CTGCCAAAGC	TCTTCGTGCA	1440
	TGGTTCAACG	CCGGTCGTTT	AGAACTGGCT	GTTTCGGTAA	GTTTGAATAT	TGCCGGCACA	1500
	TATCGGATAA	AGCTTTATAA	CACCGCAGGA	GAAGAAGTCG	CTGCAATGAC	CAAGGAATTA	1560
	GTAGCAGGGA	CGAGTGTCTT	CAGTATGGAT	GTGTATTCTC	AGGCTCCGGG	CACATATGTT	1620
75	CTGGTTGTTG	AAGGAAATGG	AATCCGTGAG	ACAAATGAAA	TTCTCAAA		1668

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## (2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

25 ATGAACTTT CATCTAAGAA AATCTTAGCA ATCATTCCAT TGCTGACGAT GGGACATGCT 60  
 GTGCAGGCAC AGTTTGTTC GGCTCCACCC ACAGGGATTG GCATGTCTGT CACTACAACC 120  
 AAGGCCGTAG GCGAAAAAT CGAATTGTTG GTTCATTCCA TAGAGAAGAA AGGCATCTGG 180  
 ATCGATCTCA ATGGGATGTC CACTTACCAA CAAGGAGAGG AAATAACCGT ATTCGATGAG 240  
 GCATACCAAG AATACACGAT CGGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA 300  
 TTGGGCTGTC GATCTACCGG TGCAACGGCT GTCSATGTAA CGAAAAACCC TAATCTGACC 360  
 TATCTCGCAT GCCCGAAAAA TATCTGAAA TCATTGGACT TGACGCAAAA CCCAAAGCTG 420  
 CTGCGAGTTT GGTGCGACTC TAACGAATA GAAAGTTGG ACCTGAGTGG CAATCCGGCT 480  
 TTGATCATCC TCGGCTGTGA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC 540  
 AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAAC CAGTGCCAAT 600  
 CCTCGTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC 660  
 35 AATCCTCTAT TGCTAACACT TTGGTGCACT GACAATGAGC TTTOGACCTT GGATCTTTCC 720  
 AAGAAATCGG ACGTTGCTTA CCTTTGGTGT TCATCGAACA AACTTACATC CTGPAATCTG 780  
 TCGGGGGTGA AGGGAATGAG TGTTTGGTTT TGTCATTCCA ATCAGATCGC AGGTGAAGAA 840  
 ATGACGAAAG TGGTGAATGC TTTGCCACAC CTATCTCCCG GCGCAGGCGC TCAGAGCAAG 900  
 TTGTCGTTG TAGACCTCAA GGACACTGAT GAGAAGAATA TCTGTACCGT AAAGGATGTG 960  
 40 GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTTGACTTCA ACGGTGATTC TGACAATATG 1020  
 CTTCCATACG AAGGAATCC GACATCGAAC TTGGCAGTAG ATGCTCCAC TGTCAGGATA 1080  
 TATCCCAATC CGGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTTAGGGCAG 1140  
 GAAGCTGCTT TATACGATAT GAATGGGGTA AAAGTCTATA GTTTCGGCGT AGAGTCTCTT 1200  
 45 CGTCAGAAC A TTGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC 1260  
 TATACCACTA AGCTCATCAA ACAG 1284

## (2) INFORMATION FOR SEQ ID NO:263

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 930 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

70 ATGAGAAAA CAATAATTT CTGCTTGTG CTGCGCCTAT TTGGCTGTTT TTGGGCACAA 60  
 GAAAGAGTCG ATGAAVAGT ATTCTCCGCA GGAACAAGTA TTTTATGGGG CATCCTTGAA 120  
 AAGGTGAAAG CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC 180  
 75 GAGGATTTCT TTTTATACT TCCCGTTACG GATGACCTCA CTCCGCTGCT TTTCTATAAC 240  
 CGTCTTACAA ACGAACCCCTG CTTTGTGTCA GAUCAAGGAA TAACTGAGTA TTTCAAATTC 300



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5 GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTCATGGC GAATCTTTTC 360  
 TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATGTA AGGTGTTGTG 420  
 AGCAAGACGG GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TAGGGGTTGT AAACATCACT 480  
 GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG 540  
 GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC 600  
 CCAACCAATT GCTATCCGCT CAGCACGAAA CCCGTTGCAG GAGACGATGA GGTTTTGTG 660  
 AAACAACAAG GCAGGCAAAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA 720  
 TACGATCTTG AGGGGAAAAG TGTTTTTCGC AAAAGAATGA CCGAAAACGC TTATACCCTA 780  
 10 TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AATTTCGATT 840  
 ATCAATAAAA AACTTAATGT TACACAGCTA 900  
 930

## (2) INFORMATION FOR SEQ ID NO:264

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

35

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1215

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

ATGAAAAAAA CAACCATAT TTCTTTGATT GTCTTCGGTG CTTTCTTTGC AGCCGTGGGC 60  
 CAAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT 120  
 40 TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGCT TCTTACAGCG 180  
 ACGGTCTCCA CAAACCAAGT TGCAGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT 240  
 ATCGCTCGTG ACATAAAAGC CAATGGGGTA AGAAAATCCA CGGACTCCAT TTAATACGAT 300  
 GCCAACGGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA 360  
 CTCGACACCC GATTCAAGTA CACCTATGAT GACGAGGAA AGATGACCGT GAGGGAAGTA 420  
 45 TTCTATGCTGG TAATGGATCC GAATACACCT ATCTCACGCT TGGAAATATCA TTATGATGCA 480  
 CAGGSCAGAC TGACCCACTG GATTTCTTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG 540  
 TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA 600  
 ACCTATTTCAG ACACCGGCAA AACGGAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG 660  
 GCOGATTAAT TCGTCGTCCA GCAAGGAAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC 720  
 50 ACCTATGAGG ACAATATCTG CATAAATAT TTGGCTATTA ACGGTACCGA CACAAGGATG 780  
 TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATGTCATTGA CATTCCGTCA 840  
 ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAACG CAAAGCGACT GAAAGAGACT 900  
 TATTCCTCCT ACGAAGGAGA TGTGGCTACT CCTATATTCT ACTATATCTA TACGTACAA 960  
 GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG 1020  
 55 TCAACGGACC GGTTAGTGAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG 1080  
 CAGGGTAAAG TTATCCGTGA TTGTGCTTGG AGCGGCCATA AGGTGGAAT GGGTGTCCGA 1140  
 TCTTTGACCA AAGGGACATA CCTGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA 1200  
 AAGTCGTGA TTCCA 1215

60

## (2) INFORMATION FOR SEQ ID NO:265

65

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 454 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

75

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

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(B) LOCATION 1...454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

5 Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu  
 1 5 10 15  
 Asn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln  
 20 25 30  
 10 Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro  
 35 40 45  
 Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu  
 50 55 60  
 Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser  
 65 70 75 80  
 15 Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser  
 85 90 95  
 Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val  
 100 105 110  
 20 Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu  
 115 120 125  
 Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val  
 130 135 140  
 Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe  
 145 150 155 160  
 25 Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu  
 165 170 175  
 Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Gly  
 180 185 190  
 30 Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn  
 195 200 205  
 Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly  
 210 215 220  
 Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp  
 225 230 235 240  
 35 Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr  
 245 250 255  
 Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala  
 260 265 270  
 40 Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala  
 275 280 285  
 Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile  
 290 295 300  
 Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe  
 305 310 315 320  
 45 Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp  
 325 330 335  
 Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser  
 340 345 350  
 50 Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr  
 355 360 365  
 Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser  
 370 375 380  
 Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu  
 385 390 395 400  
 55 Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly  
 405 410 415  
 Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp  
 420 425 430  
 60 Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met  
 435 440 445  
 Leu Tyr Lys Glu Met Asn  
 450

(2) INFORMATION FOR SEQ ID NO:266

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

5  
 10 Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu  
 1 5 10 15  
 Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met  
 20 25 30  
 Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Glu Lys Ala Pro  
 35 40 45  
 15 Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met  
 50 55 60  
 Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu  
 65 70 75 80  
 Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser  
 85 90 95  
 20 Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr  
 100 105 110  
 Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly  
 115 120 125  
 25 Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro  
 130 135 140  
 Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro  
 145 150 155 160  
 30 Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly  
 165 170 175  
 Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe  
 180 185 190  
 Ile Ile Glu Leu Leu Ser Ile Asn Lys  
 195 200

(2) INFORMATION FOR SEQ ID NO:267

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

55  
 60 Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala  
 1 5 10 15  
 Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile  
 20 25 30  
 Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile  
 35 40 45  
 Gln Val Cys Gly Glu Leu Ala Glu Gln Val Asp Cys Ile Gly Thr Gly  
 50 55 60  
 65 Asn Ser Ala Ile Ile Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu  
 65 70 75 80  
 Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly  
 85 90 95  
 Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr  
 100 105 110  
 70 Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn  
 115 120 125  
 Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr  
 130 135 140  
 75 Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys  
 145 150 155 160

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Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser  
 165 170 175  
 Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala  
 180 185 190  
 5 Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys  
 195 200 205  
 Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr  
 210 215 220  
 10 Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val  
 225 230 235 240  
 Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu  
 245 250 255  
 Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala  
 260 265 270  
 15 Lys Ser Ile Lys Leu Ala Ile  
 275

## (2) INFORMATION FOR SEQ ID NO:268

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...157  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu  
 1 5 10 15  
 40 Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala  
 20 25 30  
 Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala  
 35 40 45  
 45 Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp  
 50 55 60  
 Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln  
 65 70 75 80  
 Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr  
 85 90 95  
 50 Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala  
 100 105 110  
 Val Tyr Asp Met Arg Gly Arg Arg Val Ser Ala Arg Thr Val Asp Ser  
 115 120 125  
 55 Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met  
 130 135 140  
 Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:269

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 562 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...562  
 75

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

5 Thr Arg Asn Val Ser Leu Ile Lys Met Pro Arg Ile Met Lys Leu Lys  
 1 5 10 15  
 Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile Val Leu Phe Ser  
 20 25 30  
 Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp Asp Val Leu Ile  
 35 40 45  
 10 Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp Phe Tyr Tyr Lys  
 50 55 60  
 Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met Leu Asp Phe Ser  
 65 70 75 80  
 15 Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser Lys Asp Gly Gly  
 85 90 95  
 Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu Val Pro Tyr Asp  
 100 105 110  
 Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly Lys Asp Glu Asp  
 115 120 125  
 20 Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu Tyr Val Gly Gly  
 130 135 140  
 Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His Asp Ala Asp Ile  
 145 150 155 160  
 25 Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro Asn Asn Arg Leu  
 165 170 175  
 Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro Ser Pro Tyr Gly  
 180 185 190  
 Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val Ser Gly Ser Gly  
 195 200 205  
 30 Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu Asp Gly Gly Val  
 210 215 220  
 His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln Lys Leu Thr Ile  
 225 230 235 240  
 35 Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro Ser Leu Gly Phe  
 245 250 255  
 Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Asn Leu  
 260 265 270  
 Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val Asp Tyr Asp Pro  
 275 280 285  
 40 Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu Asp Cys Gly Trp  
 290 295 300  
 Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu Ile Gln Met Met  
 305 310 315 320  
 45 Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu Arg Ser His Asn  
 325 330 335  
 Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro Lys Gln Ser Phe  
 340 345 350  
 Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp Leu Val Phe Lys  
 355 360 365  
 50 His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys Glu Gly Asp Arg  
 370 375 380  
 Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg Tyr Arg Trp Ile  
 385 390 395 400  
 55 Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser Trp Pro Tyr Val  
 405 410 415  
 Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg Pro Gln Val Ala  
 420 425 430  
 Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp His Thr Arg Lys  
 435 440 445  
 60 Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro Val Ile Ile Lys  
 450 455 460  
 His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala Leu Asp Val Gly  
 465 470 475 480  
 65 Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala  
 485 490 495  
 Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly Gly His Glu Ala  
 500 505 510  
 Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys Val Ser Phe Ser  
 515 520 525  
 70 Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser Lys Gly Thr Tyr  
 530 535 540  
 Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val Glu Lys Ile Ile  
 545 550 555 560  
 75 Val Glu

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## (2) INFORMATION FOR SEQ ID NO:270

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...391

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Ala Gly Leu Val Ala  
 1 5 10 15  
 Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val  
 20 25 30  
 His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser  
 35 40 45  
 Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr  
 50 55 60  
 Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile  
 65 70 75 80  
 Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe  
 85 90 95  
 Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly  
 100 105 110  
 Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr  
 115 120 125  
 Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro  
 130 135 140  
 Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr  
 145 150 155 160  
 Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln  
 165 170 175  
 Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu  
 180 185 190  
 Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu  
 195 200 205  
 Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr  
 210 215 220  
 Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr  
 225 230 235 240  
 Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser  
 245 250 255  
 Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro  
 260 265 270  
 Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser  
 275 280 285  
 Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp  
 290 295 300  
 Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys  
 305 310 315 320  
 Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln  
 325 330 335  
 Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala  
 340 345 350  
 Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro  
 355 360 365  
 Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile  
 370 375 380  
 Arg Ala Lys Val Ser Leu Arg  
 385 390

## (2) INFORMATION FOR SEQ ID NO:271

75 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 428 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...428  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271  
 20 Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile  
 1 5 10 15  
 Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu  
 20 25 30  
 Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys  
 35 40 45  
 25 Gln Ser Glu Arg Tyr Val Val Leu Ser Leu Asp Gly Phe Arg Pro  
 50 55 60  
 Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln  
 65 70 75 80  
 Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe  
 85 90 95  
 30 Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His Gly  
 100 105 110  
 Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile  
 115 120 125  
 35 Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro  
 130 135 140  
 Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe  
 145 150 155 160  
 Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp  
 165 170 175  
 40 Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val  
 180 185 190  
 Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met  
 195 200 205  
 45 Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu  
 210 215 220  
 Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly  
 225 230 235 240  
 Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp  
 245 250 255  
 50 Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys  
 260 265 270  
 Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met  
 275 280 285  
 55 Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu  
 290 295 300  
 Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg  
 305 310 315 320  
 Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu  
 325 330 335  
 60 Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala  
 340 345 350  
 Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln  
 355 360 365  
 65 Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg  
 370 375 380  
 Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu  
 385 390 395 400  
 Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu  
 405 410 415  
 70 Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
 420 425

(2) INFORMATION FOR SEQ ID NO:272

75 (1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 282 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...282

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile  
1 5 10 15  
20 Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile  
20 25 30  
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn  
35 40 45  
25 Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser  
50 55 60  
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln  
65 70 75 80  
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu  
85 90 95  
30 Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser  
100 105 110  
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg  
115 120 125  
35 Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys  
130 135 140  
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe  
145 150 155 160  
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu  
165 170 175  
40 His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val  
180 185 190  
Arg Arg Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys  
195 200 205  
45 Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu  
210 215 220  
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile  
225 230 235 240  
Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met  
245 250 255  
50 His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile  
260 265 270  
His Ala Val Glu Ile Leu Ala Ala Asn Leu  
275 280

55 (2) INFORMATION FOR SEQ ID NO:273

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...251

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

75

Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu



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1      5      10      15
Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
20      25      30
5  Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
35      40      45
Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
50      55      60
Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
65      70      75      80
10 Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
85      90      95
Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
100      105      110
15 Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
115      120      125
Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
130      135      140
Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
145      150      155      160
20 Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
165      170      175
Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
180      185      190
25 Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
195      200      205
Ser Thr His Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu
210      215      220
Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
225      230      235      240
30 Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
245

```

## (2) INFORMATION FOR SEQ ID NO:274

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...238
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

```

Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
1      5      10      15
55 Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
20      25      30
Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
35      40      45
60 Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
50      55      60
Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
65      70      75      80
Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
85      90      95
65 Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
100      105      110
Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
115      120      125
70 Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
130      135      140
Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
145      150      155      160
Leu Ser Gly Gly Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
165      170      175
75 Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp

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180 185 190  
 Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg  
 195 200 205  
 5 Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg  
 210 215 220  
 Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:275  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...604  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

30 Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met  
 1 5 10 15  
 Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe  
 20 25 30  
 Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser  
 35 35 40 45  
 Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu  
 50 55 60  
 His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp  
 65 70 75 80  
 40 Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala Val  
 85 90 95  
 Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile Phe  
 100 105 110  
 Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu Leu  
 115 120 125  
 45 Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val Ser  
 130 135 140  
 Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile Ala  
 145 150 155 160  
 50 Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly Ile  
 165 170 175  
 Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly Val  
 180 185 190  
 Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu Pro  
 195 200 205  
 55 Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr Thr  
 210 215 220  
 Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu Ser  
 225 230 235 240  
 60 Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly Glu  
 245 250 255  
 Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp Glu  
 260 265 270  
 Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser Gln  
 275 280 285  
 65 Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val Leu  
 290 295 300  
 Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val Leu  
 305 310 315 320  
 70 Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe Asp  
 325 330 335  
 Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys Ala  
 340 345 350  
 Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn Ser  
 355 360 365  
 75 Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val Ala

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370 375 380  
 Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val Ala  
 385 390 395 400  
 Ala Ser Gly Gly Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val Ala  
 405 410 415  
 Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe Pro  
 420 425 430  
 Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val Val  
 435 440 445  
 10 Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met Thr  
 450 455 460  
 Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr Asp  
 465 470 475 480  
 15 Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala Gln  
 485 490 495  
 Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala Leu  
 500 505 510  
 Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile Lys  
 515 520 525  
 20 Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu Tyr  
 530 535 540  
 Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Ser Ser Ser Ala  
 545 550 555 560  
 25 Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro Glu  
 565 570 575  
 Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly  
 580 585 590  
 Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr  
 595 600  
 30  
 (2) INFORMATION FOR SEQ ID NO:276  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35  
 (ii) MOLECULE TYPE: protein  
 40  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 45  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...324  
 50  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276  
 Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile  
 1 5 10 15  
 Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Phe Gly Thr Ala Ile  
 20 25 30  
 55 Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln  
 35 40 45  
 Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala  
 50 55 60  
 60 Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser  
 65 70 75 80  
 Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys  
 85 90 95  
 Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu  
 100 105 110  
 65 Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser  
 115 120 125  
 Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg  
 130 135 140  
 70 Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala  
 145 150 155 160  
 Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr  
 165 170 175  
 Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys  
 180 185 190  
 75 Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys

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195 200 205  
 Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr  
 210 215 220  
 5 Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe  
 225 230 235 240  
 Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp  
 245 250 255  
 Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala  
 260 265 270  
 10 Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser  
 275 280 285  
 Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr  
 290 295 300  
 15 Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile  
 305 310 315 320  
 Leu Arg Leu Arg

## (2) INFORMATION FOR SEQ ID NO:277

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...533

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

40 Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr  
 1 5 10 15  
 Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val  
 20 25 30  
 Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe  
 35 40 45  
 45 Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu  
 50 55 60  
 Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Val Ile Pro  
 65 70 75 80  
 50 Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys  
 85 90 95  
 Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu  
 100 105 110  
 Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile  
 115 120 125  
 55 Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn  
 130 135 140  
 Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln  
 145 150 155 160  
 60 Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg  
 165 170 175  
 Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu  
 180 185 190  
 Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln  
 195 200 205  
 65 Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe  
 210 215 220  
 Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys  
 225 230 235 240  
 Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu  
 245 250 255  
 70 Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val  
 260 265 270  
 Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp  
 275 280 285  
 75 Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala

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290 295 300  
 Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp  
 305 310 315 320  
 Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu  
 325 330 335  
 5 Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile  
 340 345 350  
 Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met  
 355 360 365  
 10 Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile  
 370 375 380  
 Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala  
 385 390 395 400  
 15 Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val  
 405 410 415  
 Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys  
 420 425 430  
 Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp  
 435 440 445  
 20 Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser  
 450 455 460  
 Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys  
 465 470 475 480  
 25 Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg  
 485 490 495  
 Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala  
 500 505 510  
 Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His  
 515 520 525  
 30 Ala Thr Gln Gln Arg  
 530

(2) INFORMATION FOR SEQ ID NO:278

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 720 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...720  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro  
 1 5 10 15  
 55 Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys  
 20 25 30  
 Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg  
 35 40 45  
 60 Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly  
 50 55 60  
 Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn  
 65 70 75 80  
 Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser  
 85 90 95  
 65 Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly  
 100 105 110  
 Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro  
 115 120 125  
 70 Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu  
 130 135 140  
 Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val  
 145 150 155 160  
 Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg  
 165 170 175  
 75 Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr

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180 185 190  
 Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu  
 195 200 205  
 Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly  
 210 215 220  
 Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser  
 225 230 235 240  
 Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Gln Arg  
 245 250 255  
 Pro Glu Val Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu  
 260 265 270  
 Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val  
 275 280 285  
 Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg  
 290 295 300  
 Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr  
 305 310 315 320  
 Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg  
 325 330 335  
 Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile  
 340 345 350  
 Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg  
 355 360 365  
 Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp  
 370 375 380  
 Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser  
 385 390 395 400  
 Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln  
 405 410 415  
 Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala  
 420 425 430  
 Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile  
 435 440 445  
 Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Leu Gly His Asn  
 450 455 460  
 Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly  
 465 470 475 480  
 Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile  
 485 490 495  
 Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu  
 500 505 510  
 Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg  
 515 520 525  
 Leu Ala Ile Ile Arg Leu Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu  
 530 535 540  
 Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys  
 545 550 555 560  
 Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp  
 565 570 575  
 Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp  
 580 585 590  
 Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr  
 595 600 605  
 Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu  
 610 615 620  
 Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp  
 625 630 635 640  
 Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg  
 645 650 655  
 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu  
 660 665 670  
 Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala  
 675 680 685  
 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala  
 690 695 700  
 Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly  
 705 710 715 720

(2) INFORMATION FOR SEQ ID NO:279

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*
- 10 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279
- 15 Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys  
1 5 10 15  
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Asp Thr  
20 25 30  
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn  
35 40 45  
20 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr  
50 55 60  
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His  
65 70 75 80  
25 His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val  
85 90 95  
Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu  
100 105 110  
30 Pro Val Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser  
115 120 125  
Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile  
130 135 140  
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu  
145 150 155 160  
35 Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln  
165 170 175  
Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro  
180 185 190  
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys  
195 200 205  
40 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe  
210 215 220  
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys  
225 230 235 240  
45 Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu  
245 250 255  
Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr  
260 265 270  
Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr  
275 280 285  
50 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr  
290 295 300  
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu  
305 310 315 320  
55 Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu  
325 330 335  
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg  
340 345 350  
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro  
355 360 365  
60 Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr  
370 375 380  
Met Asn  
385
- 65 (2) INFORMATION FOR SEQ ID NO:280
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 655 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- 75 (iii) HYPOTHETICAL: YES

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...655

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

10 Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met  
 1 5 10 15  
 Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser  
 20 25 30  
 15 Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys  
 35 40 45  
 Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg Lys  
 50 55 60  
 Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr  
 65 70 75 80  
 20 Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser  
 85 90 95  
 Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn  
 100 105 110  
 25 Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile  
 115 120 125  
 Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu  
 130 135 140  
 Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn  
 145 150 155 160  
 30 Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu  
 165 170 175  
 Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr  
 180 185 190  
 35 Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu  
 195 200 205  
 Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val  
 210 215 220  
 Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp  
 225 230 235 240  
 40 Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln  
 245 250 255  
 Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys  
 260 265 270  
 45 Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr  
 275 280 285  
 Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His  
 290 295 300  
 Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg  
 305 310 315 320  
 50 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala  
 325 330 335  
 Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser  
 340 345 350  
 55 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys  
 355 360 365  
 Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala  
 370 375 380  
 Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu  
 385 390 395 400  
 60 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val  
 405 410 415  
 Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser  
 420 425 430  
 65 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His  
 435 440 445  
 Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly  
 450 455 460  
 Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln  
 465 470 475 480  
 70 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr  
 485 490 495  
 Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala  
 500 505 510  
 75 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala  
 515 520 525



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Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys  
 530 535 540  
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys  
 545 550 555 560  
 5 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr  
 565 570 575  
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala  
 580 585 590  
 10 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly  
 595 600 605  
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro  
 610 615 620  
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro  
 625 630 635 640  
 15 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 467 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...467  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr  
 1 5 10 15  
 40 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly  
 20 25 30  
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu  
 35 40 45  
 45 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile  
 50 55 60  
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala  
 65 70 75 80  
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu  
 85 90 95  
 50 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala  
 100 105 110  
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala  
 115 120 125  
 55 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr  
 130 135 140  
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly  
 145 150 155 160  
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr  
 165 170 175  
 60 Trp Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu  
 180 185 190  
 Val Ile Ile Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe  
 195 200 205  
 65 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile  
 210 215 220  
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr  
 225 230 235 240  
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val  
 245 250 255  
 70 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile  
 260 265 270  
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln  
 275 280 285  
 75 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr  
 290 295 300

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Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp  
 305 310 315 320  
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu  
 325 330 335  
 5 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr  
 340 345 350  
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val  
 355 360 365  
 10 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val  
 370 375 380  
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu  
 385 390 395 400  
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu  
 405 410 415  
 15 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr  
 420 425 430  
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg  
 435 440 445  
 20 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu  
 450 455 460  
 Ala Gly Gly  
 465

(2) INFORMATION FOR SEQ ID NO:282  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...945  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

45 Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu  
 1 5 10 15  
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro  
 20 25 30  
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu  
 35 40 45  
 50 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe  
 50 55 60  
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Asp Ser Gln Ser  
 65 70 75 80  
 55 Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn  
 85 90 95  
 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg  
 100 105 110  
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr  
 115 120 125  
 60 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys  
 130 135 140  
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His  
 145 150 155 160  
 65 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg  
 165 170 175  
 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met  
 180 185 190  
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val  
 195 200 205  
 70 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp  
 210 215 220  
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val  
 225 230 235 240  
 75 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala  
 245 250 255

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Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp  
 260 265 270  
 Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln  
 275 280 285  
 5 Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly  
 290 295 300  
 Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr  
 305 310 315 320  
 10 Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro  
 325 330 335  
 Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln  
 340 345 350  
 Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala  
 355 360 365  
 15 Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln  
 370 375 380  
 Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu  
 385 390 395 400  
 20 Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn  
 405 410 415  
 Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile  
 420 425 430  
 Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln  
 435 440 445  
 25 Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro  
 450 455 460  
 Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala  
 465 470 475 480  
 30 Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg  
 485 490 495  
 Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu  
 500 505 510  
 Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp  
 515 520 525  
 35 Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val  
 530 535 540  
 Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala  
 545 550 555 560  
 40 Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser  
 565 570 575  
 Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala  
 580 585 590  
 Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro  
 595 600 605  
 45 Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu  
 610 615 620  
 Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn  
 625 630 635 640  
 50 Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn  
 645 650 655  
 Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser  
 660 665 670  
 Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys  
 675 680 685  
 55 Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr  
 690 695 700  
 Asn Glu Arg Phe Ala Asp Ala Gly Asp Phe Met Phe Phe Ile Gly  
 705 710 715 720  
 60 Asn Leu Asp Glu Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala  
 725 730 735  
 Ser Leu Pro Asn Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val  
 740 745 750  
 Pro Ala Ala Arg Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met  
 755 760 765  
 65 Asp Thr Pro Ser Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu  
 770 775 780  
 Tyr Thr Leu Lys Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met  
 785 790 795 800  
 70 Asp Gln Val Tyr Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr  
 805 810 815  
 Ser Val Ala Ala Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala  
 820 825 830  
 Leu Met Gln Ile Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met  
 835 840 845  
 75 Asn Ala Ile Val Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro

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850 855 860  
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His  
 865 870 875 880  
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala  
 885 890 895  
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu  
 900 905 910  
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu  
 915 920 925  
 10 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala  
 930 935 940  
 Gln  
 945  
 15 (2) INFORMATION FOR SEQ ID NO:283  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 686 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...686  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283  
 35 Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile  
 1 5 10 15  
 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu  
 20 25 30  
 40 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr  
 35 40 45  
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val  
 50 55 60  
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg  
 65 70 75 80  
 45 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile  
 85 90 95  
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys  
 100 105 110  
 50 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met  
 115 120 125  
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala  
 130 135 140  
 Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu  
 145 150 155 160  
 55 Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp  
 165 170 175  
 Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu  
 180 185 190  
 60 Gly Lys Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys  
 195 200 205  
 Gln Glu Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln  
 210 215 220  
 Ile Asn Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys  
 225 230 235 240  
 65 Asp Glu Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu  
 245 250 255  
 Glu Pro Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu  
 260 265 270  
 70 Thr Gly Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln  
 275 280 285  
 Arg Asn Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu  
 290 295 300  
 Val Gln Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile  
 305 310 315 320  
 75 Asp Ser Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser

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325 330 335  
 Asp Ala Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala  
 340 345 350  
 5 Asp Arg Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu  
 355 360 365  
 Lys Trp Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp  
 370 375 380  
 Glu Lys Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met  
 385 390 395 400  
 10 Asp Gly His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly  
 405 410 415  
 Val Gln Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp  
 420 425 430  
 15 Lys His Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr  
 435 440 445  
 Ser Val Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu  
 450 455 460  
 Leu Glu Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp  
 465 470 475 480  
 20 Thr Ile Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu  
 485 490 495  
 Ser Asp Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu  
 500 505 510  
 25 Pro Arg Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly  
 515 520 525  
 Ala Glu Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg  
 530 535 540  
 Met Arg Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu  
 545 550 555 560  
 30 Leu Pro Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile  
 565 570 575  
 Asp Arg Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr  
 580 585 590  
 35 Glu Leu Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu  
 595 600 605  
 Leu Asp Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr  
 610 615 620  
 Lys Glu Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly  
 625 630 635 640  
 40 Ser Ile Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile  
 645 650 655  
 Gly Gln Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly  
 660 665 670  
 45 Glu Ala Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu  
 675 680 685

(2) INFORMATION FOR SEQ ID NO:284

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 482 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...482  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

Asp Ile Arg Gln Lys Arg Pro Cys Phe Asn Ala Asn Leu Tyr Phe Tyr  
 1 5 10 15  
 70 Arg Ala Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val  
 20 25 30  
 Ala Val Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn  
 35 40 45  
 Pro Val Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn  
 50 55 60  
 75 Pro Asp Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe

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65 Ser Leu Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Leu Glu Lys Met 80  
 85 Gln Ile Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser 95  
 100 Ile Pro Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile 110  
 115 Gly Lys Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala 125  
 130 Leu His Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser 140  
 145 Asp Arg Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp 155  
 165 Pro Cys Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys 175  
 180 Glu Arg Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr 190  
 195 Gly Glu Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg 205  
 210 Gly Ser Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly 220  
 225 Ile Pro Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly 235  
 245 Ala Phe Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala 255  
 260 Asp Gly Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly 270  
 275 Asn Gln Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro 285  
 290 Leu Gly Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala 300  
 305 Thr Asn Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu 315  
 325 Asp Leu Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu 330  
 340 Arg Glu Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu 345  
 355 Ala Phe Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu 360  
 370 Ala Met Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu 375  
 385 Leu Lys Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu 395  
 405 Ile Ser Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala 410  
 420 Asp His Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile 425  
 435 Arg Glu Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg 440  
 450 Ala Leu Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr 455  
 465 Gly Leu 470 475 480

- 55 (2) INFORMATION FOR SEQ ID NO:285
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- 65 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...263
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285  
 75 Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys



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165 170 175  
 Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly  
 180 185 190  
 5 Gln Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr  
 195 200 205  
 Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile  
 210 215 220  
 Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe  
 225 230 235 240  
 10 Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn  
 245 250 255  
 Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp  
 260 265 270  
 15 Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn  
 275 280 285  
 Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile  
 290 295 300  
 Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr  
 305 310 315 320  
 20 Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn  
 325 330 335  
 Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln  
 340 345 350  
 25 Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro  
 355 360 365  
 Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp  
 370 375 380  
 Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser  
 385 390 395 400  
 30 Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala  
 405 410 415  
 Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg  
 420 425 430  
 35 Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys  
 435 440 445  
 Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:287  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...373  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

60 Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg  
 1 5 10 15  
 Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr  
 20 25 30  
 Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys  
 35 40 45  
 65 Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys  
 50 55 60  
 Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser  
 65 70 75 80  
 70 Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg  
 85 90 95  
 Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile  
 100 105 110  
 Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val  
 115 120 125  
 75 Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser



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130 135 140  
 Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala  
 145 150 155 160  
 Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys  
 165 170 175  
 5 Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile  
 180 185 190  
 Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp  
 195 200 205  
 10 Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp  
 210 215 220  
 Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly  
 225 230 235 240  
 15 Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala  
 245 250 255  
 Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu  
 260 265 270  
 His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu  
 275 280 285  
 20 Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu  
 290 295 300  
 Gly Asp Phe His His Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys  
 305 310 315 320  
 25 Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met  
 325 330 335  
 Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly  
 340 345 350  
 Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His  
 355 360 365  
 30 Ser Gln Asn Ser Arg  
 370

## (2) INFORMATION FOR SEQ ID NO:288

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val  
 1 5 10 15  
 55 Gln Gln Ile Lys Gln Arg Phe Gly Ile Ile Gly Ser Ser Pro Leu Met  
 20 25 30  
 Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser  
 35 40 45  
 60 Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln  
 50 55 60  
 Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val  
 65 70 75 80  
 Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly  
 85 90 95  
 65 His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr  
 100 105 110  
 Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu  
 115 120 125  
 70 Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly  
 130 135 140  
 Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg  
 145 150 155 160  
 Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly  
 165 170 175  
 75 Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu

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180 185 190  
 Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg  
 195 200 205  
 Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg  
 210 215 220  
 Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly  
 225 230 235 240  
 Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu  
 245 250 255  
 10 Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala  
 260 265 270  
 Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr  
 275 280 285  
 15 Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr  
 290 295 300  
 Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met  
 305 310 315 320  
 Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser  
 325 330 335  
 20 Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly  
 340 345 350  
 Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu  
 355 360 365  
 25 Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu  
 370 375 380  
 Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly  
 385 390 395 400  
 Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu  
 405 410 415  
 30 Tyr Arg Lys Ile Glu Tyr Gly Leu Glu  
 420 425

(2) INFORMATION FOR SEQ ID NO:289

- 35 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 653 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...653  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg  
 1 5 10 15  
 55 Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg  
 20 25 30  
 Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro  
 35 40 45  
 60 Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala  
 50 55 60  
 Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr  
 65 70 75 80  
 Lys Gly Asn Leu Gln Ile Gln Ser Ser His Gly His Arg Leu Thr  
 85 90 95  
 65 Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu  
 100 105 110  
 Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His  
 115 120 125  
 70 Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg  
 130 135 140  
 Tyr Glu Arg Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala  
 145 150 155 160  
 Asn Tyr Asp Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg  
 165 170 175  
 75 Leu Leu Met Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe

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180 185 190  
 Trp Lys Glu Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser  
 195 200 205  
 Val Ala Leu Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe  
 210 215 220  
 Phe Glu Pro His Ala Asp Glu Glu Leu Met Gln Ala Val Arg Pro Asp  
 225 230 235 240  
 Ala Ile Ile Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys  
 245 250 255  
 10 Ile Glu Ala Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Val Arg  
 260 265 270  
 Pro Pro Leu Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu  
 275 280 285  
 15 Arg Arg Ala Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser  
 290 295 300  
 Gly Phe Thr Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met  
 305 310 315 320  
 Tyr Arg Leu Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu  
 325 330 335  
 20 Pro Ser Gly Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu  
 340 345 350  
 Glu Asp Ala Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro  
 355 360 365  
 25 Asp Val Thr Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro  
 370 375 380  
 Glu His Glu Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val  
 385 390 395 400  
 Thr Leu Pro Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu  
 405 410 415  
 30 Val Pro Arg Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln  
 420 425 430  
 Gly Gly Val Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala  
 435 440 445  
 35 Thr Gln Thr Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile  
 450 455 460  
 Ile Gly Thr Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val  
 465 470 475 480  
 Gly Ala Ile Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn  
 485 490 495  
 40 His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly  
 500 505 510  
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe  
 515 520 525  
 45 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser  
 530 535 540  
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly  
 545 550 555 560  
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu  
 565 570 575  
 50 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile  
 580 585 590  
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala  
 595 600 605  
 55 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu  
 610 615 620  
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile  
 625 630 635 640  
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu  
 645 650

(2) INFORMATION FOR SEQ ID NO:290

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
 70 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...451

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:290

5  
1 Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly  
1 5 10 15  
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu  
20 25 30  
10 Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile  
35 40 45  
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val  
50 55 60  
15 Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His  
65 70 75 80  
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser  
85 90 95  
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu  
100 105 110  
20 Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn  
115 120 125  
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val  
130 135 140  
25 Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro  
145 150 155 160  
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu  
165 170 175  
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu  
180 185 190  
30 Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys  
195 200 205  
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu  
210 215 220  
35 Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys  
225 230 235 240  
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile  
245 250 255  
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val  
260 265 270  
40 Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys  
275 280 285  
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu  
290 295 300  
45 Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala  
305 310 315 320  
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile  
325 330 335  
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro  
340 345 350  
50 Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala  
355 360 365  
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly  
370 375 380  
55 Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu  
385 390 395 400  
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile  
405 410 415  
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu  
420 425 430  
60 Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala  
435 440 445  
Arg Lys Gln  
450

65 (2) INFORMATION FOR SEQ ID NO:291

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

70 (11) MOLECULE TYPE: protein

75 (111) HYPOTHETICAL: YES

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...489

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

10 Met Asn Ser Gln Lys Lys Glu Ala Phe Asn Met Lys Arg Ile Gln Leu  
 1 5 10 15  
 Thr Leu Ile Ala Leu Phe Ala Ala Val Ala Gly Leu Val Ala Gln Asn  
 20 25 30  
 15 Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile Ser Leu Asp Lys Thr Gly  
 35 40 45  
 Asn Lys Val Val Leu Asn Gly Ala Ala Asp Met Ser Asn Leu Lys Leu  
 50 55 60  
 Lys Ser Thr Gln Met Ile Ile Val Thr Pro Ile Leu Arg Ser Glu Asp  
 65 70 75 80  
 20 Gly Thr Ser Arg Val Glu Phe Pro Ser Val Val Ile Thr Gly Arg Asn  
 85 90 95  
 Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala Phe Ser Ser Ala Leu Pro  
 100 105 110  
 25 Gln Ala Lys His Ala Ala Gln Tyr Ile Arg Arg His Asn Gly Lys Ser  
 115 120 125  
 Glu Gln Phe Ala Phe Thr Gly Glu His Ala Tyr Ala Ser Trp Met Met  
 130 135 140  
 Asp Ala Lys Phe Val Val Arg Glu Glu Val Arg Gly Cys Ala Lys Cys  
 145 150 155 160  
 30 Pro Val Gly Leu Ser Ser Asn Ile Val Pro Phe Asp Pro Leu Phe Asn  
 165 170 175  
 Pro Ala Glu Ala Pro Tyr Leu Leu Ala His Ile Thr Pro Ala Glu Glu  
 180 185 190  
 35 Val Glu Lys Gln Arg Glu Ser Ser Phe Asp Ala Tyr Ile Asn Phe Lys  
 195 200 205  
 Val Asn Lys Ala Asp Val Leu Pro Glu Tyr Arg Asn Asn Lys Ala Glu  
 210 215 220  
 Leu Glu Lys Ile Lys Glu Phe Val Ser Thr Val Lys Ala Asn Pro Asn  
 225 230 235 240  
 40 Tyr Ser Val Asn Lys Met Ile Ile Glu Gly Phe Ala Ser Pro Glu Ala  
 245 250 255  
 Ser Ile Ala His Asn Lys Ala Leu Ser Glu Arg Arg Ala Lys Arg Leu  
 260 265 270  
 45 Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys Thr Leu Pro Asn Ile Thr  
 275 280 285  
 Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly Leu Lys Leu Ala Ile Glu  
 290 295 300  
 Lys Ser Asp Ile Ala Asp Arg Asp Arg Val Leu Glu Ile Ile Asn Ser  
 305 310 315 320  
 50 Asp Lys Tyr Ala Asp Asp Ala Arg Glu Gln Ala Leu Lys Gln Leu  
 325 330 335  
 Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile Tyr Pro Asn Leu Arg Arg  
 340 345 350  
 55 Asn Thr Ile Thr Met Gly Tyr Ile Val Arg Asp Tyr Thr Leu Glu Glu  
 355 360 365  
 Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys Glu Leu Ser Glu Ala Glu  
 370 375 380  
 Met Tyr Arg Val Ala Met Ser Tyr Pro Glu Gly His Gln Glu Arg Leu  
 385 390 395 400  
 60 Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe Pro Glu Ser Val Thr Gly  
 405 410 415  
 Arg Ile Asn Leu Ala Val Ala Ala Phe Asn Gly Gly Asp Val Gln Gln  
 420 425 430  
 65 Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr Glu Lys Gly Val Ser Asn  
 435 440 445  
 Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly Asp Phe Ala Arg Ala Glu  
 450 455 460  
 Thr Phe Phe Arg Lys Ala Val Ala Glu Gly Asp Ala Asn Ala Gln Arg  
 465 470 475 480  
 70 Asn Leu Asp Met Leu Leu Gly Lys Lys  
 485

## (2) INFORMATION FOR SEQ ID NO:292

75

## (1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...384

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys  
 1 5 10 15  
 20 Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile  
 20 25 30  
 Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His  
 35 40 45  
 25 Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys  
 50 55 60  
 Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala  
 65 70 75 80  
 Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser  
 85 90 95  
 30 Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser  
 100 105 110  
 Asp Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu  
 115 120 125  
 35 Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu  
 130 135 140  
 Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly  
 145 150 155 160  
 Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His  
 165 170 175  
 40 Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met  
 180 185 190  
 Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile  
 195 200 205  
 45 Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu  
 210 215 220  
 Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln  
 225 230 235 240  
 Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn  
 245 250 255  
 50 Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile  
 260 265 270  
 Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu  
 275 280 285  
 55 Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala  
 290 295 300  
 Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu  
 305 310 315 320  
 Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln  
 325 330 335  
 60 Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp  
 340 345 350  
 Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr  
 355 360 365  
 65 Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:293

70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu  
 1 5 10 15  
 Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met  
 20 25 30  
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala  
 35 40 45  
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr  
 50 55 60  
 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg  
 65 70 75 80  
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln  
 85 90 95  
 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala  
 100 105 110  
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro  
 115 120 125  
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala  
 130 135 140  
 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr  
 145 150 155 160  
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln  
 165 170 175  
 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr  
 180 185 190  
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys  
 195 200 205  
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser  
 210 215 220  
 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val  
 225 230 235 240  
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp  
 245 250 255  
 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala  
 260 265 270  
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala  
 275 280 285  
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys  
 290 295 300  
 Ala Thr Ser Ala Arg  
 305

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Arg Lys Glu Leu  
 1 5 10 15  
 Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg

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20 25 30  
 Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln  
 35 40 45  
 Pro Ile Arg Phe Gly Ser Leu Ala Asn Pro Gln Gln Leu Ser Arg  
 50 55 60  
 Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg  
 65 70 75 80  
 Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly  
 85 90 95  
 10 Asn Ser Leu Leu Arg Thr His Ala His Ala Ser Arg Leu Gly Ala Gly  
 100 105 110  
 Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr  
 115 120 125  
 15 Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr  
 130 135 140  
 Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Gly Ala Val Leu Ile  
 145 150 155 160  
 Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser  
 165 170 175  
 20 Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala  
 180 185 190  
 Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu  
 195 200 205  
 25 Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met  
 210 215 220  
 Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile  
 225 230 235 240  
 Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly  
 245 250 255  
 30 Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val  
 260 265 270  
 Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu  
 275 280 285  
 35 Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile  
 290 295 300  
 Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe  
 305 310 315 320  
 Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly  
 325 330 335  
 40 Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala  
 340 345 350  
 Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln  
 355 360 365  
 45 Leu Asn Leu Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu  
 370 375 380  
 Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu  
 385 390 395 400  
 Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met  
 405 410 415  
 50 Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg  
 420 425 430  
 Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe  
 435 440 445  
 55 Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val  
 450 455 460  
 Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu  
 465 470 475 480  
 Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp  
 485 490

- 60 (2) INFORMATION FOR SEQ ID NO:295
- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 763 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 75 (ix) FEATURE:



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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...763

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:295

5  
His Phe Leu Val Thr Ile Met Arg Thr Lys Thr Ile Phe Phe Ala Ile  
1 5 10 15  
Ile Ser Phe Ile Ala Leu Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys  
20 25 30  
10 Ala Val Leu Thr Gly Ser Val Ser Asp Ala Glu Thr Gly Glu Pro Leu  
35 40 45  
Ala Gly Ala Arg Ile Glu Val Lys His Thr Asn Ile Val Ala Gly Ala  
50 55 60  
15 Asp Ala Gly Gly His Phe Glu Ile Lys Asn Leu Pro Ala Gly Gln His  
65 70 75 80  
Thr Ile Ile Cys Ser Leu Gly Gly Tyr Gly Gln Lys Glu Glu Val Val  
85 90 95  
Ala Ile Glu Ala Gly Gln Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu  
100 105 110  
20 Arg Thr Asn Asn Leu Glu Glu Val Val Val Thr Gly Thr Gly Thr Arg  
115 120 125  
Tyr Arg Leu Val Asp Ala Pro Val Ala Thr Glu Val Leu Thr Ala Lys  
130 135 140  
25 Asp Ile Ala Ser Phe Ser Ala Pro Thr Ser Glu Ala Leu Leu Gln Gly  
145 150 155 160  
Leu Ser Pro Ser Phe Asp Phe Gly Pro Asn Leu Met Gly Ser Phe Met  
165 170 175  
Gln Leu Asn Gly Leu Ser Ser Lys Tyr Ile Leu Ile Leu Ile Asp Gly  
180 185 190  
30 Lys Arg Val Tyr Gly Asp Val Gly Gly Gln Ala Asp Leu Ser Arg Ile  
195 200 205  
Ser Pro Asp Gln Ile Glu Arg Ile Glu Leu Val Lys Gly Ala Ser Ser  
210 215 220  
35 Ser Leu Tyr Gly Ser Asp Ala Ile Ala Gly Val Ile Asn Val Ile Thr  
225 230 235 240  
Lys Lys Asn Thr Asn Arg Leu Ser Ala Tyr Thr Ser His Arg Ile Ser  
245 250 255  
Lys Tyr Asn Asp Arg Gln Thr Asn Thr Ser Leu Asp Ile Asn Ile Gly  
260 265 270  
40 Lys Phe Ser Ser Asn Thr Asn Tyr Phe Phe Tyr His Thr Asp Gly Trp  
275 280 285  
Gln Asn Ser Pro Phe Glu Ile Lys Lys Lys Lys Gly Ser Gly Glu Pro  
290 295 300  
45 Val Leu Glu Glu Thr Tyr Lys Lys Thr Phe Arg Ala Gln Glu Asn Gln  
305 310 315 320  
Gly Val Ser Gln Ser Leu Ser Tyr Tyr Ala Thr Asn Asn Leu Ser Phe  
325 330 335  
Ser Gly Asn Val Gln Tyr Asn Lys Arg Gln Ile Phe Thr Pro Thr Phe  
340 345 350  
50 Ser Glu Lys Lys Ala Tyr Asp Met Asp Tyr Arg Ala Leu Thr Ala Ser  
355 360 365  
Leu Gly Thr Asn Tyr Leu Phe Pro Asn Gly Leu His Thr Leu Ser Phe  
370 375 380  
55 Asp Ala Val Tyr Asp Arg Phe Arg Phe Gly Tyr Leu Tyr His Asp Lys  
385 390 395 400  
Asp Ser Ser Glu Ser Leu Ile Asn Asn Gln Gly Gln Thr Glu Gln Pro  
405 410 415  
Thr Phe Phe Pro Gly Gln Leu Arg Asn Lys Asn Asp Gln Ile Arg Tyr  
420 425 430  
60 Thr Ala Glu Ala Arg Gly Val Phe Thr Leu Pro Tyr Ala Gln Lys Leu  
435 440 445  
Thr Gly Gly Leu Glu Tyr Phe Arg Glu Glu Leu Ile Ser Pro Tyr Asn  
450 455 460  
65 Leu Ile Thr Asp Lys Ala Asp Ala Ser Thr Leu Ser Ala Tyr Val Gln  
465 470 475 480  
Asp Glu Trp Lys Pro Leu Asp Trp Phe Asn Met Thr Ala Gly Phe Arg  
485 490 495  
Leu Val His His Gln Glu Phe Gly Thr Arg Met Thr Pro Lys Val Ser  
500 505 510  
70 Ile Leu Ala Lys Tyr Gly Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn  
515 520 525  
Gly Tyr Lys Thr Pro Thr Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu  
530 535 540  
75 Thr Thr Met Gly Ser His Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys  
545 550 555 560

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Pro Gln Met Ser Asp Tyr Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly  
 565 570 575  
 Pro Ile Ser Phe Ser Ala Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu  
 580 585 590  
 5 Ile Ser Phe Met Asp Ile Pro Thr Ser Pro Glu His Glu Ala Gln Gly  
 595 600 605  
 Ile Lys Lys Thr Lys Gln Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg  
 610 615 620  
 10 Gly Leu Asp Val Leu Cys Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu  
 625 630 635 640  
 Gly Ala Gly Tyr Ser Leu Val Glu Ala Lys Asn Leu Gln Thr Asp Glu  
 645 650 655  
 Trp Leu Glu Gly Ala Ala Arg His Arg Ala Asn Val His Ala Asp Trp  
 660 665 670  
 15 Val His Tyr Trp Gly Gln Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg  
 675 680 685  
 Ile Gln Ser Glu Arg Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr  
 690 695 700  
 20 Leu Trp Arg Leu Ala Thr Ser His Arg Phe Ala His Phe Arg His Ile  
 705 710 715 720  
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp  
 725 730 735  
 Asp Arg Pro Met Gly Val Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr  
 740 745 750  
 25 Phe Phe Ala Gln Ile Ala Ile Arg Phe Asn Asn  
 755 760

## (2) INFORMATION FOR SEQ ID NO:296

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...365
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg  
 1 5 10 15  
 50 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile  
 20 25 30  
 Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe  
 35 40 45  
 55 Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe  
 50 55 60  
 Met Leu Arg Pro Ala Glu Ile Ile Gln Gly Gln Ile Glu Val Thr  
 65 70 75 80  
 Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg  
 85 90 95  
 60 Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile  
 100 105 110  
 Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu  
 115 120 125  
 65 Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser  
 130 135 140  
 Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly  
 145 150 155 160  
 Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp  
 165 170 175  
 70 Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg  
 180 185 190  
 Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met  
 195 200 205  
 75 Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu  
 210 215 220

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Val Asp Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn  
 225 230 235 240  
 Glu Thr Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe  
 245 250 255  
 5 Pro Lys Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile  
 260 265 270  
 Ala Glu Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe  
 275 280 285  
 10 Leu Ser Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala  
 290 295 300  
 Leu Asn Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met  
 305 310 315 320  
 Gly Thr Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp  
 325 330 335  
 15 Leu Lys Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala  
 340 345 350  
 Gln Lys Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys  
 355 360 365  
 20 (i2) INFORMATION FOR SEQ ID NO:297  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...320  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297  
 40 Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys  
 1 5 10 15  
 Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile  
 20 25 30  
 45 Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu  
 35 40 45  
 Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser  
 50 55 60  
 Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val  
 65 70 75 80  
 50 Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys  
 85 90 95  
 Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val  
 100 105 110  
 55 Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr  
 115 120 125  
 Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly  
 130 135 140  
 Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln  
 145 150 155 160  
 60 Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln  
 165 170 175  
 Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val  
 180 185 190  
 65 Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro  
 195 200 205  
 Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile  
 210 215 220  
 Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe  
 225 230 235 240  
 70 Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu  
 245 250 255  
 Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn  
 260 265 270  
 75 Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu  
 275 280 285

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Ile Asn Gln Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr  
 290 295 300  
 Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 305 310 315 320

5

(2) INFORMATION FOR SEQ ID NO:298

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...502

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

Ser Lys Ile Val Leu Arg Lys Phe Cys Thr Leu Ala Arg Met Lys Lys  
 1 5 10 15  
 Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe  
 20 25 30  
 Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu Thr Glu Glu  
 35 40 45  
 Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val Leu Ser Asn  
 50 55 60  
 Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile Ser Ile Lys  
 65 70 75 80  
 His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly Leu Asp Pro  
 85 90 95  
 Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu Lys Leu Met  
 100 105 110  
 Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser Gln Arg Pro  
 115 120 125  
 Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met Pro Ala Asp  
 130 135 140  
 Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile Asp Gly Lys  
 145 150 155 160  
 Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala Leu Lys Gly  
 165 170 175  
 Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr Gly Glu Thr  
 180 185 190  
 Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile Met Asn Ser  
 195 200 205  
 Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr Ile Arg Leu  
 210 215 220  
 Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr Ala Leu Leu  
 225 230 235 240  
 Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu Asp Leu Arg  
 245 250 255  
 Gly Asn Gly Gly Leu Met Gln Ala Ala Ile Glu Ile Val Asn Leu  
 260 265 270  
 Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly Arg Ile Ala  
 275 280 285  
 Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile Asp Thr Lys  
 290 295 300  
 Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser Ser Ser Glu  
 305 310 315 320  
 Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val Leu Met Gly  
 325 330 335  
 Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg Gln Leu Pro  
 340 345 350  
 Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr Ile Pro Ser  
 355 360 365  
 Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn Arg Thr Gly  
 370 375 380  
 Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe Tyr Thr Ala  
 385 390 395 400

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Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro Asp Ile Glu  
 405 410 415  
 Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met Ala Ile Asn  
 420 425 430  
 5 Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys His Lys Thr  
 435 440 445  
 Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala  
 450 455 460  
 10 Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser  
 465 470 475 480  
 Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr  
 485 490 495  
 Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys  
 500 505 510  
 15 Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn  
 515 520 525  
 Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Glu Arg Gly Ser  
 530 535 540  
 20 Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys  
 545 550 555 560  
 Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro  
 565 570 575  
 Lys Ala Glu Asn Lys Gly  
 580  
 25  
 (2) INFORMATION FOR SEQ ID NO:299  
 (i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 985 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...985  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299  
 45 Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser  
 1 5 10 15  
 Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr  
 20 25 30  
 50 Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met  
 35 40 45  
 Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr  
 50 55 60  
 55 Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys  
 65 70 75 80  
 Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg  
 85 90 95  
 Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu  
 100 105 110  
 60 Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val  
 115 120 125  
 Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe  
 130 135 140  
 65 Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala  
 145 150 155 160  
 Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala  
 165 170 175  
 Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala  
 180 185 190  
 70 Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu  
 195 200 205  
 Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser  
 210 215 220  
 75 Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly  
 225 230 235 240

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Asp Leu Ile Ala Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn  
 Thr Asp Ala Thr Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala  
 245 250 255  
 5 Ala Thr Ala Asp Ser Ala Ala Val Gln Ala Val Ala Asp Ser Ala Thr  
 260 265 270  
 Val Ala Gln Lys Glu Ala Lys Asp Ala Thr Arg Lys Asp Ala Leu Phe  
 275 280 285  
 10 Ser Leu Leu Thr Pro Val Asn Arg Gly Gly Ala Val Val Gly Val Ala  
 290 295 300  
 Arg Arg Ala Asn Met Ala Gln Ile Ser Glu Met Leu Gln Gln Ala His  
 305 310 315 320  
 Asp Leu Lys Val Thr Arg Glu Asp Val Leu Phe Leu Trp Gly Ala Lys  
 325 330 335  
 15 Ala Ile Glu Asp Pro Glu Thr Lys Lys Glu Thr Asp Leu Tyr Glu Leu  
 340 345 350  
 Tyr Ala Ile Arg Thr Asn Arg Thr Gly Asp Pro Asp Leu Gly Gly Asp  
 355 360 365  
 20 Val Val Thr Ser Ala Lys Ser Asp Ile Gln Asn Asp Phe Gly Arg Ser  
 370 375 380  
 Glu Pro Ile Val Ser Met Thr Met Asn Glu Glu Gly Ala Arg Lys Trp  
 385 390 395 400  
 Ala Arg Ile Thr Lys Asp Asn Val Gly Arg Ala Ile Ala Ile Val Leu  
 405 410 415  
 25 Asp Gly Val Val Tyr Ser Ala Pro Asn Val Asn Asp Glu Ile Thr Gly  
 420 425 430  
 Gly Arg Ser Gln Ile Ser Gly His Phe Thr Val Glu Glu Ala Gly Asp  
 435 440 445  
 30 Leu Ala Asn Val Leu Asn Ser Gly Lys Met Asp Ala Thr Val Ser Ile  
 450 455 460  
 Glu Gln Glu Asn Val Ile Gly Pro Thr Leu Gly Ala Glu Ser Ile Lys  
 465 470 475 480  
 Ala Gly Phe Leu Ser Phe Leu Leu Ala Leu Val Ile Leu Met Cys Tyr  
 485 490 495  
 35 Met Cys Leu Ala Tyr Gly Phe Leu Pro Gly Leu Ile Ala Asn Gly Ala  
 500 505 510  
 Leu Ile Val Asn Ser Phe Phe Thr Leu Gly Val Leu Ala Ser Phe His  
 515 520 525  
 40 Ala Val Leu Thr Leu Ser Gly Ile Ala Gly Leu Val Leu Thr Leu Gly  
 530 535 540  
 Met Ala Val Asp Ala Asn Val Leu Ile Phe Glu Arg Ile Lys Glu Glu  
 545 550 555 560  
 Leu Arg Ala Gly Lys Thr Pro Ile Arg Ala Val Thr Asp Gly Tyr Gly  
 565 570 575  
 45 Asn Ala Phe Ser Ala Ile Phe Asp Ser Asn Val Thr Thr Ile Ile Thr  
 580 585 590  
 Gly Ile Ile Leu Phe Leu Tyr Gly Thr Gly Pro Ile Arg Gly Phe Ala  
 595 600 605  
 50 Thr Thr Leu Ile Ile Gly Leu Ile Ala Ser Phe Ile Thr Ala Val Phe  
 610 615 620  
 Leu Thr Arg Ile Val Phe Glu Lys Leu Ala Lys Lys Gly Arg Leu Asp  
 625 630 635 640  
 Lys Ile Thr Phe Thr Thr Ser Ile Thr Arg Asn Leu Leu Val Asn Pro  
 645 650 655  
 55 Ser Tyr Asn Ile Leu Gly Lys Arg Lys Thr Gly Phe Ile Ile Pro Val  
 660 665 670  
 Ile Ile Ile Val Leu Gly Leu Ile Ala Ser Phe Thr Ile Gly Leu Asn  
 675 680 685 690  
 60 Arg Gly Ile Glu Phe Ser Gly Gly Arg Asn Tyr Val Val Lys Phe Asp  
 695 700 705 710  
 Gln Pro Val Ser Ser Glu Ala Val Arg Ser Ala Leu Ser Ser Pro Leu  
 715 720 725 730  
 Gln Glu Lys Val Leu Val Thr Ser Ile Gly Thr Glu Gly Thr Glu Val  
 735 740 745 750  
 65 Arg Ile Ser Thr Asn Tyr Lys Ile Gln Glu Glu Ser Glu Glu Thr Glu  
 755 760 765  
 Ala Glu Ile Thr Asp Lys Leu Tyr Gln Ser Leu Lys Gly Phe Tyr Thr  
 770 775 780  
 70 Gln Gln Pro Thr Ala Asp Gln Phe Leu Asp Asn Ile Ile Ser Ser Gln  
 785 790 795 800  
 Lys Val Ser Pro Ser Met Ser Ser Asp Ile Thr Arg Gly Ala Ile Trp  
 805 810 815  
 Ala Val Leu Leu Ser Met Ile Phe Met Ala Ile Tyr Ile Leu Ile Arg  
 820 825 830  
 75 Phe Arg Asp Ile Ser Phe Ser Ala Gly Val Phe Val Ser Val Ala Ala

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5                   835                   840                   845  
 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu  
 850                   855                   860  
 Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala  
 865                   870                   875                   880  
 Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile  
 885                   890                   895  
 Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile  
 900                   905                   910  
 10 Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu  
 915                   920                   925  
 Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr  
 930                   935                   940  
 15 Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr  
 945                   950                   955                   960  
 Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys  
 965                   970                   975  
 Arg Lys Leu Asn Lys Ala Ala Lys Lys  
 980                   985  
 20  
 (2) INFORMATION FOR SEQ ID NO:300  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1046 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25  
 (ii) MOLECULE TYPE: protein  
 30  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1046  
 40  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300  
 Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His  
 1                   5                   10                   15  
 Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg  
 20                   25                   30  
 45 Met Thr Leu Phe Phe Leu Cys Leu Thr Ser Ile Gly Trp Ala Met  
 35                   40                   45  
 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
 50                   55                   60  
 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
 65                   70                   75                   80  
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
 85                   90                   95  
 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
 100                   105                   110  
 55 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
 115                   120                   125  
 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
 130                   135                   140  
 60 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
 145                   150                   155                   160  
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
 165                   170                   175  
 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
 180                   185                   190  
 65 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
 195                   200                   205  
 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
 210                   215                   220  
 70 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
 225                   230                   235                   240  
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
 245                   250                   255  
 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
 260                   265                   270  
 75 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met

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		275				280				285				
		Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp												
		290				295				300				
		Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly												
5		305				310				315				320
		Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly												
						325				330				335
		Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys												
						340				345				350
10		Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile Ser Phe Ser												
						355				360				365
		Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly Tyr Phe Asp												
						370				375				380
15		Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg Tyr Ser Gly												
						385				390				400
		Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys Val Gly Ala												
						405				410				415
		Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp Tyr Phe Gly												
						420				425				430
20		Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr Met Pro Arg												
						435				440				445
		Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp Val Tyr Tyr												
						450				455				460
25		Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr Phe Ala Lys												
						465				470				475
		Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val Asn Gly Phe												
						485				490				495
		Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala Gln Ala Gly												
						500				505				510
30		Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met Pro Asn Asn												
						515				520				525
		Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg Ala Tyr Arg												
						530				535				540
35		Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys Phe Ser Ile												
						545				550				555
		Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu Tyr Ile Glu												
						565				570				575
		Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe Glu Ser Asp												
						580				585				590
40		Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser Leu Ser Leu												
						595				600				605
		Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe Phe Ser Arg												
						610				615				620
45		Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe Ser Val Arg												
						625				630				635
		Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser Ala Trp Phe												
						645				650				655
		Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe Ile Gln Glu												
						660				665				670
50		Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr Gly Thr Thr												
						675				680				685
		Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu Val Thr Val												
						690				695				700
55		Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser Thr Ala Gly												
						705				710				715
		Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn Phe Gly Leu												
						725				730				735
		Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val Asp Phe Tyr												
						740				745				750
60		Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met Pro Tyr Ile												
						755				760				765
		Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met Lys Asn Thr												
						770				775				780
65		Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn Lys Asp Trp												
						785				790				795
		Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln Glu Ile Thr												
						805				810				815
		Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn Thr Gly Thr												
						820				825				830
70		Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala Glu Tyr Ala												
						835				840				845
		Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val Pro Gly Gln												
						850				855				860
75		Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr Ser Ala Asp												
						865				870				875
														880





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Lys Thr Glu Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr  
 260 265 270  
 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn  
 275 280 285  
 5 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His  
 290 295 300  
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu  
 305 310 315 320  
 10 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr  
 325 330 335  
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp  
 340 345 350  
 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Cys Gln  
 355 360 365  
 15 Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile  
 370 375 380  
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala  
 385 390 395 400  
 20 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr  
 405 410 415  
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys  
 420 425 430  
 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly  
 435 440 445  
 25 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu  
 450 455 460  
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr  
 465 470 475 480  
 30 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys  
 485 490 495  
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys  
 500 505 510  
 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro  
 515 520 525  
 35 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly  
 530 535 540  
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Pro Thr Asn Trp  
 545 550 555 560  
 40 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn  
 565 570 575  
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys  
 580 585 590  
 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile  
 595 600 605  
 45 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr  
 610 615 620  
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn  
 625 630 635 640  
 50 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser  
 645 650 655  
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp  
 660 665 670  
 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys  
 675 680 685  
 55 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala  
 690 695 700  
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr  
 705 710 715 720  
 60 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe  
 725 730 735  
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr  
 740 745 750  
 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu  
 755 760 765  
 65 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu  
 770 775 780  
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg  
 785 790 795 800  
 70 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile  
 805 810 815  
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr  
 820 825 830  
 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu  
 835 840 845  
 75 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu

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850  
Lys Ile His Ile Gly  
865

855

860

- 5 (2) INFORMATION FOR SEQ ID NO:302
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302
- 25 Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys  
1 5 10 15  
Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg  
20 25 30  
30 Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile Phe Phe  
35 40 45  
Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr  
50 55 60  
Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro  
65 70 75 80  
35 Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro  
85 90 95  
Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
100 105
- 40 (2) INFORMATION FOR SEQ ID NO:303
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 861 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303
- 60 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu  
1 5 10 15  
Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln  
20 25 30  
65 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile  
35 40 45  
Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu  
50 55 60  
Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly  
65 70 75 80  
70 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr  
85 90 95  
Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu  
100 105 110  
75 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile  
115 120 125

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Phe Met Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe  
 130 135 140  
 Gly Gln Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile  
 145 150 155  
 5 Leu Asp Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser  
 165 170 175  
 Ser Pro Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala  
 180 185 190  
 10 Pro Glu Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Arg Ser  
 195 200 205  
 Gly Gly Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala  
 210 215 220  
 Met Ala Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu  
 225 230 235  
 15 Ile Glu Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro  
 245 250 255  
 Val Leu Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly  
 260 265 270  
 20 Leu Ala Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp  
 275 280 285  
 Lys Arg Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys  
 290 295 300  
 Tyr Arg Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu  
 305 310 315 320  
 25 Lys Lys Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile  
 325 330 335  
 Val Gly Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu  
 340 345 350  
 30 Lys Pro Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr  
 355 360 365  
 Leu Asp Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg  
 370 375 380  
 Arg Phe Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu  
 385 390 395 400  
 35 Thr Ile Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val  
 405 410 415  
 Arg Tyr Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg  
 420 425 430  
 40 Tyr Val Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp  
 435 440 445  
 Glu Ala Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu  
 450 455 460  
 Ile Glu Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu  
 465 470 475 480  
 45 Ser Ala Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp  
 485 490 495  
 Gln Glu Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp  
 500 505 510  
 50 Glu Glu Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val  
 515 520 525  
 Ala His Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser  
 530 535 540  
 Thr Gly Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr  
 545 550 555 560  
 55 Lys Val Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile  
 565 570 575  
 Gln Arg Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser  
 580 585 590  
 60 Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys  
 595 600 605  
 Lys Leu Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val  
 610 615 620  
 Asp Met Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly  
 625 630 635 640  
 65 Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu  
 645 650 655  
 Arg Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu  
 660 665 670  
 70 Lys Ala His Ala Asp Val Phe Asn Leu Leu Gln Val Met Asp Glu  
 675 680 685  
 Gly Gln Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr  
 690 695 700  
 Val Ile Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe  
 705 710 715 720  
 75 Gly Gln Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys

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```

20      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 456 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

25      (ii) MOLECULE TYPE: protein

          (iii) HYPOTHETICAL: YES

30      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

          (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...456

35      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

```

[illegible]

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290 295 300  
 Trp Gln Lys Arg Ile Asn Thr Thr Val Phe Val Pro Glu Ser Met Tyr  
 305 310 315 320  
 Ala Asn Lys Leu Met Arg Leu Leu Met Gln Arg Lys Lys Ser Ile Ala  
 325 330 335  
 5 Ile Val Ile Asp Glu Leu Gly Gly Thr Ala Gly Met Val Thr Leu Glu  
 340 345 350  
 Asp Leu Val Glu Glu Ile Phe Gly Asp Ile Glu Asp Glu His Asp Thr  
 355 360 365  
 10 Arg Lys Ile Ile Ala Lys Gln Leu Gly Pro His Thr Tyr Leu Val Ser  
 370 375 380  
 Gly Arg Met Glu Ile Asp Asp Val Asn Glu Arg Phe Gly Leu Ser Leu  
 385 390 395 400  
 15 Pro Glu Ser Asp Asp Tyr Leu Thr Val Ala Gly Phe Ile Leu Asn Ser  
 405 410 415  
 His Gln Asn Ile Pro Gln Ala Asn Glu Val Val Glu Ile Ala Pro Tyr  
 420 425 430  
 Thr Phe Thr Ile Leu Arg Ser Ser Ser Thr Lys Ile Glu Leu Val Lys  
 435 440 445  
 20 Met Ser Ile Asp Asp Gln Ser Asn  
 450 455  
 (2) INFORMATION FOR SEQ ID NO:305  
 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...299  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305  
 Leu Lys Lys Glu Ile Thr Met Lys Gln Asn Tyr Phe Lys Arg Val Cys  
 1 5 10 15  
 45 Ser Leu Leu Trp Leu Val Leu Pro Met Leu Ile Met Pro Leu Glu Val  
 20 25 30  
 Ala Ala Gln Glu Ile Ile Pro Asn Glu Glu Val Leu Glu Ser Leu Thr  
 35 40 45  
 50 Phe Val Ala Pro Val Glu Glu Thr Asp Ala Ile Glu Ala Glu Val Glu  
 50 55 60  
 Ala Leu Gln Glu Ile Val Ala Thr Glu Glu Ile Ala Glu Gln Ala Val  
 65 70 75 80  
 Arg Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Val Lys Ile Ala Ser  
 85 90 95  
 55 Gly Leu Thr Glu Pro Thr Phe Leu Asp Glu Asp Val Pro Ala Gly Glu  
 100 105 110  
 His Thr Tyr Cys Val Glu Val Gln Tyr Gln Gly Val Ser Asp Lys  
 115 120 125  
 60 Val Cys Val Asp Val Glu Val Lys Asp Phe Lys Pro Val Thr Asn Leu  
 130 135 140  
 Thr Gly Thr Ala Ser Asn Asp Glu Val Ser Leu Asp Trp Asp Gly Val  
 145 150 155 160  
 Glu Glu Lys Ala Glu Glu Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn  
 165 170 175  
 65 Val Tyr Lys Asn Gly Thr Leu Ile Gly Asn Thr Ala Glu Thr His Tyr  
 180 185 190  
 Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val  
 195 200 205  
 70 Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val-Thr Val Thr Val  
 210 215 220  
 Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu  
 225 230 235 240  
 Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr  
 245 250 255  
 75 Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu

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260  
 Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly  
 275  
 280  
 290  
 Asn Lys His His Val Ser Lys Ile Gln Val Arg  
 295

(2) INFORMATION FOR SEQ ID NO:306

10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...377

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

1 Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu  
 5  
 10 Val Val Phe Arg Ser Gly Phe Ile Leu Cys Glu Asn Thr Leu Ala  
 20  
 30 Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu  
 35  
 40 Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn  
 50  
 55 Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile  
 65  
 70 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu  
 85  
 90 Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr  
 100  
 110 Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro  
 115  
 120 Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val  
 130  
 140 Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser  
 145  
 150 Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu  
 165  
 170 Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly  
 180  
 190 Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn  
 195  
 200 Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe  
 210  
 220 Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg  
 225  
 230 Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg  
 245  
 250 Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp  
 260  
 270 Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr  
 275  
 280 Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn  
 290  
 300 Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val  
 305  
 310 Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr  
 325  
 330 Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr  
 340  
 350 Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr  
 355  
 360 Val Tyr Thr Glu Lys Ile Gln Ile Gln  
 370  
 375

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(2) INFORMATION FOR SEQ ID NO:307

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

20 Phe Gly Ile Ser Pro Ser Met Lys Lys Ser Phe Leu Leu Ala Ile Val  
 1 5 10 15  
 Met Leu Phe Gly Ile Ala Met Gln Gly His Ser Ala Pro Val Thr Lys  
 20 25 30  
 25 Glu Arg Ala Leu Ser Leu Ala Arg Leu Ala Leu Arg Gln Val Ser Leu  
 35 40 45  
 Arg Met Gly Gln Thr Ala Val Ser Asp Lys Ile Ser Ile Asp Tyr Val  
 50 55 60  
 30 Tyr Arg Gln Gly Asp Ala Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly  
 65 70 75 80  
 Ser Pro Ala Tyr Phe Tyr Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr  
 85 90 95  
 Ala Leu Val Ala Ala Asp Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser  
 100 105 110  
 35 Pro Ile Gly Arg Phe Asp Met Asp Ser Met Pro Asp Asn Leu Arg Met  
 115 120 125  
 Trp Leu Gln Ile Tyr Asp Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys  
 130 135 140  
 40 Ala Gln Leu Asn Glu Glu Ile Leu Arg Thr Glu Gly Val Pro Ala Glu  
 145 150 155 160  
 Val His Ala Leu Met Asp Asn Gly His Phe Ala Asn Asp Pro Met Arg  
 165 170 175  
 Trp Asn Gln Gly Tyr Pro Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn  
 180 185 190  
 45 Gly Asn His Ala Tyr Thr Gly Cys Val Ala Thr Ala Ala Ala Gln Ile  
 195 200 205  
 Met Arg Tyr His Ser Trp Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr  
 210 215 220  
 50 His Ala Gly Ser Leu Val Gly Asn Trp Ser Gly Thr Phe Gly Glu Met  
 225 230 235 240  
 Tyr Asp Trp Ile Asn Met Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr  
 245 250 255  
 Gln Ser Gln Val Asp Ala Tyr Ala Thr Leu Met Arg Asp Val Ser Ala  
 260 265 270  
 55 Ser Val Ser Met Ser Phe Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val  
 275 280 285  
 Tyr Val Val Gly Ala Leu Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu  
 290 295 300  
 60 Gln Leu His Val Arg Ala Leu Tyr Thr Ser Gln Glu Trp His Asp Met  
 305 310 315 320  
 Ile Arg Gly Glu Leu Ala Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn  
 325 330 335  
 Asn Gln Ser Ile Gly His Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp  
 340 345 350  
 65 Gly Thr Phe His Phe Asn Trp Gly Trp Gly Gly Val Ser Asn Gly Phe  
 355 360 365  
 Tyr Lys Leu Thr Leu Leu Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu  
 370 375 380  
 70 Gly Ile Gly Phe Thr Ile Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro  
 385 390 395 400  
 Ala Lys Thr Pro Ala Glu Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala  
 405 410 415  
 Leu Lys Asp Ile Glu Ala Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val  
 420 425 430  
 75 Gly Tyr Ser Ile Tyr Asn Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu

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1      5      10      15
Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
20      25      30
5 Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
35      40      45
Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
50      55      60
Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
65      70      75      80
10 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
85      90      95
Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
100      105      110
15 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
115      120      125
Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
130      135      140
Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
145      150      155      160
20 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
165      170      175
Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
180      185      190
Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
195      200      205
25 Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
210      215      220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
225      230      235      240
30 Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
245      250      255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
260      265      270
35 Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
275      280      285
Asn Pro Gln Ser Asp Gly Lys
290      295

```

## (2) INFORMATION FOR SEQ ID NO:309

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

```

60 Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
1      5      10      15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
20      25      30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
35      40      45
65 Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
50      55      60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
65      70      75      80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
95      100      105      110
70 Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
100      105      110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
115      120      125
75 Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile

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130 135 140  
 Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp  
 145 150 155 160  
 5 Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser  
 165 170 175  
 Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His  
 180 185 190  
 Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg  
 195 200 205  
 10 Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala  
 210 215 220  
 Gln Gln Gly Thr Leu Lys  
 225 230  
 15 (2) INFORMATION FOR SEQ ID NO:310  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...342  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310  
 35 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys  
 1 5 10 15  
 Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn  
 20 25 30  
 40 Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys  
 35 40 45  
 Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu  
 50 55 60  
 Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu  
 65 70 75 80  
 45 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp  
 85 90 95  
 Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly  
 100 105 110  
 50 Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser  
 115 120 125  
 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly  
 130 135 140  
 Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val  
 145 150 155 160  
 55 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val  
 165 170 175  
 Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His  
 180 185 190  
 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val  
 195 200 205  
 60 Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly  
 210 215 220  
 Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe  
 225 230 235 240  
 65 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly  
 245 250 255  
 Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg  
 260 265 270  
 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys  
 275 280 285  
 70 Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly  
 290 295 300  
 Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys  
 305 310 315 320  
 75 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly

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325  
Lys Ala Leu Arg Ile Lys 330 335  
340

## 5 (2) INFORMATION FOR SEQ ID NO:311

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

25 Pro Ser Lys Thr Ile Ile Lys Thr Met Ala Lys Ile Asn Phe Tyr Ala  
1 5 10 15  
Glu Gly Val Ser Leu Pro Arg Ile Arg Arg Ile Val Gly Lys Trp  
20 25 30  
Ile Ala Glu Val Cys Ser Arg Tyr Gly Lys Ala Val Gly Glu Ile Ser  
35 40 45  
Tyr Leu Phe Cys Asp Asp Glu Tyr Ile Leu Lys Ala Asn Gln Glu Phe  
50 55 60  
Leu Asp His Asp Tyr Tyr Thr Asp Ile Ile Thr Phe Asp Ser Cys Glu  
65 70 75 80  
35 Ala Asp Thr Val Asn Gly Asp Leu Leu Ile Ser Leu Asp Thr Val Arg  
85 90 95  
Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg  
100 105 110  
40 Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser  
115 120 125  
Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val  
130 135 140  
Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr  
145 150 155

## 45 (2) INFORMATION FOR SEQ ID NO:312

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

65 Lys Ser Lys Thr Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly  
1 5 10 15  
Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr  
20 25 30  
70 Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly  
35 40 45  
Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu  
50 55 60  
Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly  
65 70 75 80

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Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu  
 85 90 95  
 Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu  
 100 105 110  
 5 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe  
 115 120 125  
 Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His  
 130 135 140  
 10 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser  
 145 150 155 160  
 Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val  
 165 170 175  
 Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala  
 180 185 190  
 15 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys  
 195 200 205  
 Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe  
 210 215 220  
 20 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly  
 225 230 235 240  
 Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn  
 245 250 255  
 Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg  
 260 265 270  
 25 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr  
 275 280 285  
 Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His  
 290 295 300  
 30 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe  
 305 310 315 320  
 Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro  
 325 330 335  
 Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys  
 340 345 350  
 35 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu  
 355 360 365  
 Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys  
 370 375 380  
 40 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:313

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...387  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala  
 1 5 10 15  
 65 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr  
 20 25 30  
 Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala  
 35 40 45  
 Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu  
 50 55 60  
 70 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val  
 65 70 75 80  
 Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg  
 85 90 95  
 75 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys  
 100 105 110

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Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe  
 115 120 125  
 Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His  
 130 135 140  
 5 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu  
 145 150 155 160  
 Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr  
 165 170 175  
 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp  
 180 185 190  
 10 Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly  
 195 200 205  
 Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu  
 210 215 220  
 15 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp  
 225 230 235 240  
 Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly  
 245 250 255  
 20 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro  
 260 265 270  
 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val  
 275 280 285  
 Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn  
 290 295 300  
 25 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys  
 305 310 315 320  
 Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met  
 325 330 335  
 30 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys  
 340 345 350  
 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser  
 355 360 365  
 Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr  
 370 375 380  
 35 Ala Ala Glu  
 385

(2) INFORMATION FOR SEQ ID NO:314

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...195  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val  
 1 5 10 15  
 60 Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe  
 20 25 30  
 Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala  
 35 40 45  
 65 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln  
 50 55 60  
 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala  
 65 70 75 80  
 Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu  
 85 90 95  
 70 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro  
 100 105 110  
 Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile  
 115 120 125  
 75 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr  
 130 135 140

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Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu  
 145 150 155 160  
 Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser  
 165 170 175  
 5. Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser  
 180 185 190  
 Gly Ile Ala  
 195

10 (2) INFORMATION FOR SEQ ID NO:315

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 876 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...876

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

30 Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu  
 1 5 10 15  
 Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr  
 20 25 30  
 Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn  
 35 40 45  
 Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser  
 50 55 60  
 Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser  
 65 70 75 80  
 40 Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr  
 85 90 95  
 Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile  
 100 105 110  
 Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr  
 115 120 125  
 45 Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp  
 130 135 140  
 Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser  
 145 150 155 160  
 50 Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr  
 165 170 175  
 Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn Ser Thr Asn Leu Ser  
 180 185 190  
 Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val Glu Asp Asn Cys Gln  
 195 200 205  
 55 Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly Leu Glu Gly Ala Tyr  
 210 215 220  
 Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe Ser Ser Leu Ala Gly  
 225 230 235 240  
 60 Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met Ile Glu Arg Val Glu  
 245 250 255  
 Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly Ser Asn Ala Val Gly  
 260 265 270  
 Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu Arg Asn Ser Ala Glu  
 275 280 285  
 65 Ile Ser His Ser Thr Met Thr Phe Asp His Ala Lys Gly Trp Gly Ser  
 290 295 300  
 Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met Leu Thr Glu Asp Arg  
 305 310 315 320  
 70 Lys Ala Gly Val Met Val Phe Gly Gln His Asn Tyr Arg Pro Gly Gln  
 325 330 335  
 Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro Asn Leu Arg Asn Arg  
 340 345 350  
 75 Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly Leu Tyr Ser Lys Ala  
 355 360 365

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Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg Arg Gly Gly Asp Arg  
 370 375 380  
 Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala Glu Tyr Leu Gln His  
 385 390 395 400  
 5 Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln Gly Phe Ser Gly Gly  
 405 410 415  
 Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln Asp Val Gln Arg Arg  
 420 425 430  
 10 Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn Leu Leu Asn Gly Ala  
 435 440 445  
 Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr Asn Asp Ala Phe Thr  
 450 455 460  
 Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe Asp Leu Gln Gly Gly  
 465 470 475 480  
 15 Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp Asp Phe Thr Gly Gly  
 485 490 495  
 Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg Ser Gly Tyr Arg Pro  
 500 505 510  
 20 Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser Gln Tyr Asp Gln Leu  
 515 520 525  
 Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile Gly Ala Arg Ile Asp  
 530 535 540  
 Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr Ile Asp Pro Leu Phe  
 545 550 555 560  
 25 Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn Pro Asn Lys Asn Leu  
 565 570 575  
 Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg Ala Pro Gln Tyr Phe  
 580 585 590  
 30 Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly Thr Pro Ile Ser Arg  
 595 600 605  
 Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser Arg Ser Ile Ser Ala  
 610 615 620  
 Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp Gln Phe Asn Ile Met  
 625 630 635 640  
 35 Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln Phe Lys Pro Ser Asp  
 645 650 655  
 Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp Ile Ile Arg Thr Ile  
 660 665 670  
 40 Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr Gly Val Asn Leu Glu  
 675 680 685  
 Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu Gln Leu Gly Gly Thr  
 690 695 700  
 Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr Thr Ala Val Glu Ala Asp  
 705 710 715 720  
 45 Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys Asp Tyr Val Arg Thr  
 725 730 735  
 Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val Arg Pro Thr Glu His  
 740 745 750  
 50 Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val  
 755 760 765  
 His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp  
 770 775 780  
 Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala  
 785 790 795 800  
 55 Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp  
 805 810 815  
 Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu  
 820 825 830  
 60 Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr  
 835 840 845  
 Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln  
 850 855 860  
 Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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## (VI) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

## (IX) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...899

## (XII) SEQUENCE DESCRIPTION: SEQ ID NO:316

10 Ile Leu Asn His Leu Arg Lys Thr Met Tyr Lys Lys Ile Ile Ala Val  
 1 5 10 15  
 Ala Ala Leu Phe Cys Ala Ser Ile Gly Ile Leu Lys Gly Gln Ser Ser  
 20 25 30  
 15 Asp Leu Thr Pro Gln Asp Thr Ile Tyr Ser Pro Glu Ile Ser Tyr Ala  
 35 40 45  
 Lys Pro Ile His Lys Thr Ile Ala Ser Ile Glu Ile Glu Gly Met Arg  
 50 55 60  
 20 Ser Phe Asp Asp Phe Val Leu Arg Asn Leu Ser Gly Leu Ala Val Gly  
 65 70 75 80  
 Asp Glu Val Leu Ile Pro Gly Asp Ala Met Ser Ala Ala Val Asn Arg  
 85 90 95  
 Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys  
 100 105 110  
 25 Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro  
 115 120 125  
 Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu  
 130 135 140  
 30 Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg  
 145 150 155 160  
 Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu  
 165 170 175  
 Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu  
 180 185 190  
 35 Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser  
 195 200 205  
 Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser  
 210 215 220  
 40 Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser  
 225 230 235 240  
 Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His  
 245 250 255  
 Lys Phe Val Glu Glu Ser Tyr Arg Glu Asp Leu Val Arg Leu Ile Glu  
 260 265 270  
 45 Lys Tyr Gln Glu Tyr Gly Tyr Arg Asp Ala Glu Ile Leu Thr Asp Ser  
 275 280 285  
 Val Val Lys Ala Pro Asp Gly Lys Arg Val Asp Ile Tyr Leu Asn Ile  
 290 295 300  
 50 Glu Glu Gly Gln Lys Tyr Ile Lys Asp Val Asn Phe Val Gly Asn  
 305 310 315 320  
 Ser Gln Tyr Pro Ser Glu Tyr Leu Glu Arg Val Leu Gly Ile Lys Ser  
 325 330 335  
 Gly Asp Val Tyr Asn Gln Arg Arg Leu Ala Lys Arg Leu Asn Glu Asp  
 340 345 350  
 55 Glu Asp Ala Val Gly Asn Leu Tyr Tyr Asn Asn Gly Tyr Ile Phe Ala  
 355 360 365  
 Trp Val Asp Pro Val Glu Thr Asn Val Val Gly Asp Ser Val Ser Leu  
 370 375 380  
 60 Asp Ile Arg Ile Ala Glu Gly Lys Gln Ala Asn Ile Asn Lys Val Ile  
 385 390 395 400  
 Ile Lys Gly Asn Thr Val Val Tyr Glu Asp Val Val Arg Arg Glu Leu  
 405 410 415  
 Tyr Thr Lys Pro Gly Gln Leu Phe Ser Arg Glu Asp Ile Ile Asn Ser  
 420 425 430  
 65 Ile Arg Leu Ile Asn Gln Leu Gly His Phe Asp Ala Glu Lys Ser Ile  
 435 440 445  
 Pro Arg Pro Ile Pro Asn Pro Glu Thr Gly Thr Val Asp Ile Glu Tyr  
 450 455 460  
 70 Asp Leu Val Pro Arg Ser Ser Asp Gln Leu Glu Leu Ser Val Gly Trp  
 465 470 475 480  
 Ser Gln Ser Gly Leu Leu Phe Arg Gly Ala Ile Lys Phe Thr Asn Phe  
 485 490 495  
 Ser Val Gly Asn Leu Leu His Pro Ser Met Tyr Lys Lys Gly Ile Ile  
 500 505 510  
 75 Pro Gln Gly Asp Gly Gln Thr Leu Ser Leu Ser Ala Gln Thr Asn Gly

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515 520 525  
 Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly  
 530 535 540  
 Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr  
 545 550 555 560  
 Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr  
 565 570 575  
 Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn  
 580 585 590  
 10 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro  
 595 600 605  
 Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg  
 610 615 620  
 15 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr  
 625 630 635 640  
 Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe  
 645 650 655  
 His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg  
 660 665 670  
 20 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Asp Phe Met  
 675 680 685  
 Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp  
 690 695 700  
 25 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu  
 705 710 715 720  
 Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn  
 725 730 735  
 Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly  
 740 745 750  
 30 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr  
 755 760 765  
 Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met  
 770 775 780  
 35 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly  
 785 790 795 800  
 Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu  
 805 810 815  
 Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala  
 820 825 830  
 40 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro  
 835 840 845  
 Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro  
 850 855 860  
 45 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro  
 865 870 875 880  
 Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly  
 885 890 895  
 Gln Glu Phe  
 50  
 (2) INFORMATION FOR SEQ ID NO:317  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 amino acids  
 55 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 60 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...177  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317  
 70  
 Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly  
 1 5 10 15  
 Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu  
 20 25 30  
 75 Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met

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35 40 45  
 Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu  
 50 55 60  
 5 Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp  
 65 70 75 80  
 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile  
 85 90 95  
 Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly  
 100 105 110  
 10 Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile  
 115 120 125  
 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn  
 130 135 140  
 15 Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser  
 145 150 155 160  
 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser  
 165 170 175  
 Lys

20

(2) INFORMATION FOR SEQ ID NO:318

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...170  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

40

Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu  
 1 5 10 15  
 Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn  
 20 25 30  
 45 Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys  
 35 40 45  
 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met  
 50 55 60  
 50 Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp  
 65 70 75 80  
 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp  
 85 90 95  
 Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu  
 100 105 110  
 55 Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala  
 115 120 125  
 Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met  
 130 135 140  
 60 Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr  
 145 150 155 160  
 Ala Lys Val Lys Ala Lys Leu Gly Ile Lys  
 165 170

65

(2) INFORMATION FOR SEQ ID NO:319

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:

70

75

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...828

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

10 Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn  
 1 5 10 15  
 Gly Ile Tyr Arg Leu Ser Phe Ile Leu Cys Cys Leu Leu Cys Ser  
 20 25 30  
 Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp  
 35 40 45  
 15 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr  
 50 55 60  
 Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met  
 65 70 75 80  
 20 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr  
 85 90 95  
 Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu  
 100 105 110  
 Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val  
 115 120 125  
 25 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg  
 130 135 140  
 Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile  
 145 150 155 160  
 30 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr  
 165 170 175  
 Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly  
 180 185 190  
 Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly  
 195 200 205  
 35 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala  
 210 215 220  
 Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp  
 225 230 235 240  
 40 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly  
 245 250 255  
 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser  
 260 265 270  
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr  
 275 280 285  
 45 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr  
 290 295 300  
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly  
 305 310 315 320  
 50 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr  
 325 330 335  
 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp  
 340 345 350  
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met  
 355 360 365  
 55 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala  
 370 375 380  
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe  
 385 390 395 400  
 60 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser  
 405 410 415  
 Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His  
 420 425 430  
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly  
 435 440 445  
 65 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala  
 450 455 460  
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp  
 465 470 475 480  
 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr  
 485 490 495  
 70 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala  
 500 505 510  
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser  
 515 520 525  
 75 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu

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530 535 540  
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro  
 545 550 555 560  
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe  
 565 570 575  
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val  
 580 585 590  
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu  
 595 600 605  
 10 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe  
 610 615 620  
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile  
 625 630 635 640  
 15 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly  
 645 650 655  
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly  
 660 665 670  
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu  
 675 680 685  
 20 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe  
 690 695 700  
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala  
 705 710 715 720  
 25 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser  
 725 730 735  
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val  
 740 745 750  
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala  
 755 760 765  
 30 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala  
 770 775 780  
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp  
 785 790 795 800  
 35 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr  
 805 810 815  
 Arg Arg Gln Phe Asn Leu Arg Leu Val Glu Phe  
 820 825  
  
 (2) INFORMATION FOR SEQ ID NO:320  
 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 55 (B) LOCATION 1...679  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320  
 60 Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His  
 1 5 10 15  
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys  
 20 25 30  
 Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr  
 35 40 45  
 65 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg  
 50 55 60  
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn  
 65 70 75 80  
 Tyr Arg Ala Ala Gly Arg Gln Ala Lys Ala Leu Arg Gly Tyr Leu Asn  
 70 85 90 95  
 Ala Arg Arg Tyr Gly Tyr Pro Asp Ser Val Val Leu Leu Arg Leu Ala  
 100 105 110  
 Gln Thr Tyr Gln Gln Gly Gly Asn Tyr Lys Glu Ala Glu Val Leu Phe  
 115 120 125  
 75 Arg Gly Tyr Leu Glu Ala Tyr Pro Lys Ser Tyr Phe Ala Ala Ile Gly

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130 135 140  
 Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg  
 145 150 155 160  
 Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe  
 165 170 175  
 Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser  
 180 185 190  
 Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys  
 195 200 205  
 Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly  
 210 215 220  
 Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Pro Trp Asp Glu Gly  
 225 230 235 240  
 Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala  
 245 250 255  
 Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala  
 260 265 270  
 Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met  
 275 280 285  
 Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly  
 290 295 300  
 Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys  
 305 310 315 320  
 Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu  
 325 330 335  
 Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe  
 340 345 350  
 Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly  
 355 360 365  
 Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln  
 370 375 380  
 Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp  
 385 390 395 400  
 Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu  
 405 410 415  
 Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala  
 420 425 430  
 Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr  
 435 440 445  
 Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly  
 450 455 460  
 Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe  
 465 470 475 480  
 Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp  
 485 490 495  
 Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr  
 500 505 510  
 Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val  
 515 520 525  
 Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile  
 530 535 540  
 Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser  
 545 550 555 560  
 Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile  
 565 570 575  
 Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu  
 580 585 590  
 Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser  
 595 600 605  
 Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser  
 610 615 620  
 Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu  
 625 630 635 640  
 Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu  
 645 650 655  
 Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg  
 660 665 670  
 Val Ile Glu Glu Glu Leu Arg  
 675

(2) INFORMATION FOR SEQ ID NO:321

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

15 Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val  
1 5 10 15  
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg  
20 20 25 30  
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu  
35 40 45  
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile  
50 55 60  
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln  
25 65 70 75 80  
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His  
85 90 95  
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu  
100 105 110  
30 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys  
115 120 125  
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser  
130 135 140  
35 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg  
145 150 155 160  
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile  
165 170 175  
40 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu  
180 185 190  
Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn  
195 200 205  
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys  
210 215 220  
45 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala  
225 230 235 240  
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp  
245 250 255  
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser  
260 265 270  
50 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val  
275 280 285  
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala  
290 295 300  
55 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu  
305 310 315 320  
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly  
325 330 335  
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser  
340 345 350  
60 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln  
355 360 365  
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala  
370 375 380  
65 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly  
385 390 395 400  
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu  
405 410 415  
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln  
420 425 430  
70 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn  
435 440 445  
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu  
450 455 460  
75 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys  
465 470 475 480

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Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val  
 485 490 495  
 Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr  
 500 505 510  
 5 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln  
 515 520 525  
 Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro  
 530 535 540  
 10 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr  
 545 550 555 560  
 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe  
 565 570 575  
 His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn  
 580 585 590  
 15 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile  
 595 600 605  
 Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe  
 610 615 620  
 20 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met  
 625 630 635 640  
 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg  
 645 650 655  
 Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu  
 660 665 670  
 25 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn  
 675 680 685  
 Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu  
 690 695 700  
 30 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro  
 705 710 715 720  
 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr  
 725 730 735  
 Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr  
 740 745 750  
 35 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val  
 755 760 765  
 Met Val Asn Phe  
 770

40 (2) INFORMATION FOR SEQ ID NO:322

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 484 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

60 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp  
 1 5 10 15  
 Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys  
 20 25 30  
 65 Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val  
 35 40 45  
 Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala  
 50 55 60  
 Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala  
 65 70 75 80  
 70 Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg  
 85 90 95  
 Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val  
 100 105 110  
 75 Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly  
 115 120 125



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Phe Ser Ser Ser Glu Gly Ile Glu Met Gly Arg Thr His Asn Thr Gln  
 130 135 140  
 Gly Gly Val Asn Val Ser Met Pro Leu Val Ser Ala Gln Leu Trp Lys  
 145 150 155 160  
 5 Ser Ile Ala Met Thr Gly Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala  
 165 170 175  
 Arg Ser Ser Arg Ile Asp Leu Val Ala Glu Val Lys Lys Ala Tyr Leu  
 180 185 190  
 10 Ser Val Leu Leu Ala Glu Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr  
 195 200 205  
 Asp Asn Ala Leu Ala Asn Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg  
 210 215 220  
 Gly Leu Val Ala Glu Tyr Asp Lys Ile Arg Ala Asn Val Gln Val Arg  
 225 230 235 240  
 15 Asn Ile Glu Pro Asn Leu Leu Gln Ala Gln Asn Ser Val Ala Leu Ala  
 245 250 255  
 Leu Trp Gln Leu Lys Val Leu Met Ser Met Glu Val Glu Thr Pro Ile  
 260 265 270  
 20 Arg Leu Ser Gly Ser Leu Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly  
 275 280 285  
 Tyr Phe Ala Ala Asp Thr Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln  
 290 295 300  
 Leu Asp Ile Gln Arg Arg Leu Ala Val Ser Ala Asp Lys Leu Asn Lys  
 305 310 315 320  
 25 Tyr Ser Phe Leu Pro Thr Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser  
 325 330 335  
 Leu Asn Ser Asn Asp Ile Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr  
 340 345 350  
 30 Pro Phe Ser Thr Ile Ser Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly  
 355 360 365  
 Gly Lys Arg Leu Tyr Asn Val Lys Gln Ser Ala Leu Ser Ile Arg Gln  
 370 375 380  
 Ile Asp Leu Gln Arg Arg His Ile Glu Gln Ser Ile Arg Met Gly Ile  
 385 390 395 400  
 35 Lys Asn Gln Asn Asp Arg Leu Arg Thr Cys Met Gln Arg Phe Val Ala  
 405 410 415  
 Ser Glu Glu Ala Val Arg Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu  
 420 425 430  
 40 Lys Arg Tyr Gln Thr Gly Glu Gly Thr Leu Val Glu Leu Asn Asp Ala  
 435 440 445  
 Asp Val Ala Leu Leu Gln Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe  
 450 455 460  
 45 Asp Phe Met Thr Ala Lys Ala Glu Leu Asp Lys Met Asn Gly Met Gly  
 465 470 475 480  
 Ile Pro Glu Gln

## (C) INFORMATION FOR SEQ ID NO:323

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...540  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

Phe His Asn Phe Asp Phe Leu Asn Gly Ile Lys Leu Phe Ser Met Ala  
 1 5 10 15  
 70 Asn Asn Thr Leu Leu Ala Lys Thr Arg Tyr Val Cys Leu Val Gly  
 20 25 30  
 Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu Val Thr  
 35 40 45  
 75 Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr  
 50 55 60

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Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln  
 65 70 75 80  
 Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr  
 85 90 95  
 5 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro  
 100 105 110  
 Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu  
 115 120 125  
 10 Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe  
 130 135 140  
 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser  
 145 150 155 160  
 Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro  
 165 170 175  
 15 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly  
 180 185 190  
 Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg  
 195 200 205  
 20 Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala  
 210 215 220  
 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile  
 225 230 235 240  
 Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg  
 245 250 255  
 25 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala  
 260 265 270  
 Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly  
 275 280 285  
 30 Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile  
 290 295 300  
 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile  
 305 310 315 320  
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg  
 325 330 335  
 35 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser  
 340 345 350  
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr  
 355 360 365  
 40 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp  
 370 375 380  
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser  
 385 390 395 400  
 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg  
 405 410 415  
 45 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu  
 420 425 430  
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys  
 435 440 445  
 50 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu  
 450 455 460  
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr  
 465 470 475 480  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
 485 490 495  
 55 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 500 505 510  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 515 520 525  
 60 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:324

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 75

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...293

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr  
 1 5 10 15  
 Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr  
 20 25 30  
 Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val  
 35 40 45  
 Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe  
 50 55 60  
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg  
 65 70 75 80  
 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys  
 85 90 95  
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp  
 100 105 110  
 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala  
 115 120 125  
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser  
 130 135 140  
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln  
 145 150 155 160  
 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val  
 165 170 175  
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp  
 180 185 190  
 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro  
 195 200 205  
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg  
 210 215 220  
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly  
 225 230 235 240  
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe  
 245 250 255  
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser  
 260 265 270  
 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala  
 275 280 285  
 Ser Phe Ala Leu Lys  
 290

## 45 (2) INFORMATION FOR SEQ ID NO:325

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## 50 (ii) MOLECULE TYPE: protein

## 55 (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## 60 (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...280

## 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu  
 1 5 10 15  
 Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala  
 20 25 30  
 Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly  
 35 40 45  
 Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro  
 50 55 60  
 Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr  
 65 70 75 80

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Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala  
 85 90 95  
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala  
 100 105 110  
 5 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro  
 115 120 125  
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg  
 130 135 140  
 10 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu  
 145 150 155 160  
 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr  
 165 170 175  
 Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser  
 180 185 190  
 15 Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly  
 195 200 205  
 Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly  
 210 215 220  
 20 Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln  
 225 230 235 240  
 Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly  
 245 250 255  
 Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu  
 260 265 270  
 25 Ile Gly Ile Lys Pro Gly Lys Lys  
 275 280

(2) INFORMATION FOR SEQ ID NO:326

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 803 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...803  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys  
 1 5 10 15  
 50 Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu  
 20 25 30  
 Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys  
 35 40 45  
 55 Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met  
 50 55 60  
 Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His Ala Gly Gln Gln  
 65 70 75 80  
 Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr Pro Asn Gly Ala  
 85 90 95  
 60 Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile Pro Phe Gly Leu  
 100 105 110  
 Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val Ile Ser Lys Trp  
 115 120 125  
 65 Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile Ser Gln Val Lys  
 130 135 140  
 Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu Arg Glu His Gly  
 145 150 155 160  
 Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr Leu Lys Lys Asp  
 165 170 175  
 70 Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met Ala Ser Pro Tyr  
 180 185 190  
 His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr Phe Pro Asp Ser  
 195 200 205  
 75 Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg Lys Gly Asp Gln  
 210 215 220

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Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr Ile Ser Ala Leu  
 235 230 235 240  
 Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln Asp Ile Ile Tyr  
 245 250 255  
 5 Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys Leu Arg Ala Lys  
 260 265 270  
 Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro Trp Arg Ile Gly  
 275 280 285  
 10 Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu Ser Pro Thr Asp  
 290 295 300  
 Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr Arg Lys Met Pro  
 305 310 315 320  
 Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe Ser Gly Asn  
 325 330 335  
 15 Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys Ser Leu Ala Arg  
 340 345 350  
 Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu Gln Arg Asp Ser  
 355 360 365  
 20 Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr Leu Asp Lys Pro  
 370 375 380  
 Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys Ser Asn Asp Phe  
 385 390 395 400  
 Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg Asn Val Phe Gly  
 405 410 415  
 25 Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser Tyr Glu Trp Glu  
 420 425 430  
 Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu Ile Asp Ile Asn  
 435 440 445  
 30 Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe Pro Ser Ile Val  
 450 455 460  
 Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Tyr Pro Thr Thr Thr Thr  
 465 470 475 480  
 Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His Tyr Phe Ser Met  
 485 490 495  
 35 Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln Pro Ser Lys Glu  
 500 505 510  
 His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr Asn Leu Leu Gly  
 515 520 525  
 40 His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn Asn Pro Pro Leu  
 530 535 540  
 Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met Gly Tyr Ile Tyr  
 545 550 555 560  
 Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His His Leu Trp Met  
 565 570 575  
 45 Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn Leu Ile Tyr Leu  
 580 585 590  
 Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe Val Gly Val Pro  
 595 600 605  
 50 Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg Phe Tyr Ser Tyr Thr  
 610 615 620  
 Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly Thr Gly Val Ile  
 625 630 635 640  
 Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser Glu Gln Phe Tyr  
 645 650 655  
 55 Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val Arg Ser Ile Gly  
 660 665 670  
 Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr Ser Tyr Leu Asp  
 675 680 685  
 60 Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu Tyr Arg Gly Lys  
 690 695 700  
 Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp Ala Gly Asn Val  
 705 710 715 720  
 Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly Ala Leu Ser Glu  
 725 730 735  
 65 Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala Leu Gly Thr Gly  
 740 745 750  
 Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val Arg Val Asp Val  
 755 760 765  
 70 Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys Lys Gly Tyr Tyr  
 770 775 780  
 Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His Leu Ala Val Gly  
 785 790 795 800  
 Tyr Pro Phe

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## (C) INFORMATION FOR SEQ ID NO:327

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 783 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

## (iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...783

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

20 Ser Leu Ser Pro Tyr Ile Arg Phe Pro Met Ser Ser His Ser Val Arg  
1 5 10 15  
Tyr Leu Ile Gly Ile Ala Gly Cys Leu Leu Met Leu Ala Ser Ser  
20 25 30  
25 Cys Ser Val Thr Arg Tyr Val Pro Asp Gly Ser Arg Leu Leu Asp Arg  
35 40 45  
Val Thr Ile Ala Ser Glu Thr Gly Ser Ile Ala Leu Pro Glu Asp Ile  
50 55 60  
30 Arg Asp Tyr Thr Leu Gln Gln Pro Asn Tyr Arg Leu Phe Gly Met Thr  
65 70 75 80  
Arg Trp Leu Leu Arg Val Tyr Ser Ser Ser Asn Pro Asn Ser Asn Ser  
85 90 95  
Trp Trp Asn Arg Ser Leu Arg Lys Met Gly Glu Pro Pro Val Leu Ile  
100 105 110  
35 Asp Ser Val Leu Thr Asp Arg Thr Ala Asn Arg Leu Ala Lys Ala Met  
115 120 125  
Ala Gly Asp Gly Phe Leu Asp Ala Thr Ala Arg Ala Val Val Asp Thr  
130 135 140  
40 Gly Leu Tyr Lys Lys Ala Arg Ile Thr Tyr Leu Ile Gln Pro Gly Ser  
145 150 155 160  
Arg Tyr Tyr Ile Arg Asn Met Ala Leu Asp Val Lys Asn Pro Leu Leu  
165 170 175  
Pro Pro Val Ala Leu Gly Asn Ser Leu Pro Ser Ala Tyr Lys Val Gly  
180 185 190  
45 Ile Ser Glu Gly Ser Pro Leu Ser Pro Ile Val Leu Asp Glu Glu Arg  
195 200 205  
Lys Ala Ile Ala Arg His Met Arg Asn Asn Gly Phe Trp Lys Phe Ser  
210 215 220  
Ala Glu Asp Val Tyr Tyr Glu Ala Asp Thr Thr Val Ser Gly Gly Ser  
225 230 235 240  
50 Gly Thr Lys Ser Ala Asp Leu Lys Leu Val Val Asn Gly Ile Gly Arg  
245 250 255  
Tyr Pro Tyr Arg Ile Gly Arg Val Phe Phe His Ala Asp Tyr Asp Pro  
260 265 270  
55 Leu Glu Ser Asp Phe Arg Val Gln Glu Leu Pro Arg Ile Asp Ser Ile  
275 280 285  
Ser Arg Gly Asp Tyr Thr Val Tyr Tyr Gly Ser Arg Gly Arg Tyr Ile  
290 295 300  
60 Arg Ala Ser Ala Leu Thr Arg Ser Val Ser Val Thr Pro Gly Ala Phe  
305 310 315 320  
Phe Cys Glu Asp Asp Val Glu Arg Ser Tyr Ile Lys Leu Asn Ala Leu  
325 330 335  
Pro Ile Val Arg Asn Val Asn Ile Arg Phe Val Glu His Asn Gly Lys  
340 345 350  
65 Asp Glu Ile Ala Leu Ala Asp Ser Ser Arg Leu Val Asp Cys Tyr Ile  
355 360 365  
Leu Thr Val Pro Ala Lys Ser Lys Ser Phe Glu Ala Glu Val Leu Gly  
370 375 380  
70 Thr Asn Ser Ala Gly Asp Phe Gly Ala Ala Leu Ser Leu Gly Phe Thr  
385 390 395 400  
Asp Arg Asn Leu Phe Arg Gly Ala Glu Met Phe Asn Ile Lys Leu Lys  
405 410 415  
Gly Ala Tyr Glu Ala Ile Arg Lys Gly Ser His Ser Phe Met Glu Tyr  
420 425 430  
75 Gly Val Glu Ser Ser Leu Arg Phe Pro Arg Leu Leu Phe Pro Phe Ile

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435 440 445  
 Ser Asp Glu Thr Arg Arg Arg Leu Arg Ala Ser Thr Glu Trp Lys Ile  
 150 455 460  
 5 Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser  
 465 470 475 480  
 10 Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg  
 485 490 495  
 His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile  
 500 505 510  
 15 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn  
 515 520 525  
 Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr  
 530 535 540  
 20 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg  
 545 550 555 560  
 Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu  
 565 570 575  
 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu  
 580 585 590  
 25 His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val  
 595 600 605  
 Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu  
 610 615 620  
 30 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr  
 625 630 635 640  
 Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu  
 645 650 655  
 Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln  
 660 665 670  
 35 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu  
 675 680 685  
 Phe Trp Lys Phe Arg Ala Ala Phe Val Asp Ala Gly Asn Val Trp  
 690 695 700  
 40 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp  
 705 710 715 720  
 Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu  
 725 730 735  
 Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr  
 740 745 750  
 45 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn  
 755 760 765  
 Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe  
 770 775 780  
 45 (2) INFORMATION FOR SEQ ID NO:328  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50  
 (ii) MOLECULE TYPE: protein  
 55 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...875  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328  
 65 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu  
 1 5 10 15  
 Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala  
 20 25 30  
 70 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro  
 35 40 45  
 Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly  
 50 55 60  
 Val Thr Thr Asp Met Asp Gly Gly Phe Arg Phe Glu Val Pro Ala Lys  
 65 70 75 80  
 75 Ser Val Leu Thr Phe Arg Cys Val Gly Tyr Ala Thr Val Thr Arg Ser





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His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile  
 690 695 700  
 Asp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn  
 705 710 715 720  
 5 Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp  
 725 730 735  
 Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr  
 740 745 750  
 10 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile  
 755 760 765  
 Gly Lys Tyr Asn Phe Leu Gly Lys Asn Tyr Ala Gly Phe Asn Pro Ala  
 770 775 780  
 Thr Arg Asn Ala Gln Gln Tyr Glu Ala Asp Gly Lys Glu Ile Val Glu  
 785 790 795 800  
 15 Ser Trp Lys Leu Pro Asp Val Gly Leu Phe Asp Leu Ser Ala Ser Tyr  
 805 810 815  
 Asn Phe Lys Leu Gly Ser Leu Ser Thr Phe Tyr Phe Asn Met Asp  
 820 825 830  
 20 Asn Val Ala Asp Lys Arg Tyr Val Ser Asp Ala Asp Asn Ile Ile  
 835 840 845  
 Gly Lys Lys His Asp Glu Ala Ser Ala Leu Val Trp Tyr Gly Phe Gly  
 850 855 860  
 Arg Thr Trp Ser Thr Gly Ile Arg Val Asn Phe  
 865 870 875  
 25 (2) INFORMATION FOR SEQ ID NO:329  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 460 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...460  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329  
 Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp  
 1 5 10 15  
 Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe  
 20 25 30  
 50 Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile  
 35 40 45  
 Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys  
 50 55 60  
 Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu  
 65 70 75 80  
 Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu  
 85 90 95  
 Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp  
 100 105 110  
 60 Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val  
 115 120 125  
 Cys His Gln Leu Ser Val Glu Lys Ala Arg Ser Asp Glu Tyr Ala  
 130 135 140  
 Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile  
 145 150 155 160  
 65 Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met  
 165 170 175  
 Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg  
 180 185 190  
 70 Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu  
 195 200 205  
 Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu  
 210 215 220  
 75 Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln  
 225 230 235 240

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Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe  
 210 215 220  
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu  
 225 230 235 240  
 5 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val  
 245 250 255  
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly  
 260 265 270  
 10 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr  
 275 280 285  
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu  
 290 295 300  
 Pro Arg Val Asp Asp Gly Thr Leu Pro Pro Glu Phe Gly Pro Glu  
 305 310 315 320  
 15 Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr  
 325 330 335  
 Lys Tyr Glu Val Glu Ile  
 340

20 (2) INFORMATION FOR SEQ ID NO:331  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25  
 (ii) MOLECULE TYPE: protein  
 30 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...329  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

40 Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile  
 1 5 10 15  
 Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly  
 20 25 30  
 45 Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr  
 35 40 45  
 Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr  
 50 55 60  
 Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala  
 65 70 75 80  
 50 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro  
 85 90 95  
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala  
 100 105 110  
 55 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu  
 115 120 125  
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly  
 130 135 140  
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr  
 145 150 155 160  
 60 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser  
 165 170 175  
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu  
 180 185 190  
 65 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp  
 195 200 205  
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met  
 210 215 220  
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser  
 225 230 235 240  
 70 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu  
 245 250 255  
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp  
 260 265 270  
 75 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe  
 275 280 285

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Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala Arg Pro  
 290 295 300  
 Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Ile Leu His  
 305 310 315 320  
 5 Ile Ala Arg Ala Leu Ala His Glu Arg  
 325

(2) INFORMATION FOR SEQ ID NO:332

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 878 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

Ala Asp Ser Ile Arg Tyr Pro Leu Tyr Phe Phe Gly Arg Asn Arg Lys  
 1 5 10 15  
 30 Lys Cys Phe Arg Glu Pro Ile Pro Thr Leu Tyr Asn Lys Asn Met Ile  
 20 25 30  
 Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe Ser Gly  
 35 35 40 45  
 Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp Ala Asn  
 50 55 60  
 Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu Val Gly  
 65 70 75 80  
 Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr Asp Ala  
 85 90 95  
 40 Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile Thr Leu  
 100 105 110  
 Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val Arg Val  
 115 120 125  
 45 Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu Asp Ala  
 130 135 140  
 Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu Thr Leu  
 145 150 155 160  
 Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys Val Phe  
 165 170 175  
 50 Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe Gln Pro  
 180 185 190  
 Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn Gln Val  
 195 200 205  
 55 Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile Asp Ser  
 210 215 220  
 Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu Gln Ile  
 225 230 235 240  
 Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly Ser  
 245 250 255  
 60 Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile Ile Thr  
 260 265 270  
 Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu Ser Phe  
 275 280 285  
 65 Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala Ser Ile  
 290 295 300  
 Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln Ala Arg  
 305 310 315 320  
 Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu Leu Gly  
 325 330 335  
 70 Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg Leu Ser  
 340 345 350  
 Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu Phe Arg  
 355 360 365  
 75 Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly Val Ala  
 370 375 380

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Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr Asp Leu  
 385 390 395 400  
 Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser Gly Gln  
 405 410 415  
 5 Ile Val Asn Arg Lys Ser Tyr Tyr Gly Ile Gly Glu Ile Asp Val  
 420 425 430  
 Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln Asp Gln  
 435 440 445  
 10 Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met Gly Gly  
 450 455 460  
 Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro Ser Gln  
 465 470 475 480  
 Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp Val Met  
 485 490 495  
 15 Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn Thr Ile  
 500 505 510  
 Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser Leu Phe  
 515 520 525  
 20 Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val Gly Ala  
 530 535 540  
 Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser Pro Arg  
 545 550 555 560  
 Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg Ala Thr  
 565 570 575  
 25 Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp Leu His  
 580 585 590  
 Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp Pro Asn  
 595 600 605  
 30 Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp Met Tyr  
 610 615 620  
 His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly Phe Tyr  
 625 630 635 640  
 Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp Gln His  
 645 650 655  
 35 Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala Lys Val  
 660 665 670  
 Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe Gln Leu  
 675 680 685  
 40 Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala Gln Glu  
 690 695 700  
 Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val Thr Glu  
 705 710 715 720  
 Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met Thr Asp  
 725 730 735  
 45 Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr Leu Ala  
 740 745 750  
 Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala Tyr Thr  
 755 760 765  
 50 Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys Ser Ala  
 770 775 780  
 Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu Thr Gly  
 785 790 795 800  
 Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe Phe Asp  
 805 810 815  
 55 Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala Thr Glu  
 820 825 830  
 Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe Gln Lys  
 835 840 845  
 60 Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr Gly Pro  
 850 855 860  
 Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:333

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...206

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

10 Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu  
1 5 10 15  
Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln  
20 25 30  
Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu  
35 40 45  
15 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu  
50 55 60  
Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe  
65 70 75 80  
Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp  
85 90 95  
20 Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu  
100 105 110  
Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg  
115 120 125  
25 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala  
130 135 140  
Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu  
145 150 155 160  
30 Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile  
165 170 175  
Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr  
180 185 190  
Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser  
195 200 205

35

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

50

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

55

Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr  
1 5 10 15  
Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg  
20 25 30  
60 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser  
35 40 45  
Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg  
50 55 60  
65 Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala  
65 70 75 80  
Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr  
85 90 95  
Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser  
100 105 110  
70 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser  
115 120 125  
Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu  
130 135 140  
75 Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln  
145 150 155 160

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5 Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg  
 165 170 175  
 Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr  
 180 185 190  
 Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp  
 195 200 205  
 10 Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg  
 210 215 220  
 Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu  
 225 230 235 240  
 Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu  
 245 250 255  
 Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg  
 260 265 270  
 15 Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile  
 275 280 285  
 Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Tyr Phe Pro  
 290 295 300  
 20 Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu  
 305 310 315 320  
 Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys  
 325 330 335  
 Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe  
 340 345 350  
 25 Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile  
 355 360 365  
 Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys  
 370 375 380  
 30 Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile  
 385 390 395 400  
 Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr  
 405 410 415  
 Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala  
 420 425 430  
 35 Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala  
 435 440 445  
 Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly  
 450 455 460  
 40 Lys Asp Phe  
 465

## (2) INFORMATION FOR SEQ ID NO:335

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...451  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

65 Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys  
 1 5 10 15  
 Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser  
 20 25 30  
 Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser  
 35 40 45  
 Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr  
 50 55 60  
 70 Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly  
 65 70 75 80  
 Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr  
 85 90 95  
 75 Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met  
 100 105 110

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Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His  
 115 120 125  
 Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Leu  
 130 135 140  
 5 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg  
 145 150 155 160  
 Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu  
 165 170 175  
 10 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro  
 180 185 190  
 Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu  
 195 200 205  
 Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu  
 210 215 220  
 15 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro  
 225 230 235 240  
 Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ala Gly  
 245 250 255  
 20 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys  
 260 265 270  
 Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala  
 275 280 285  
 Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser  
 290 295 300  
 25 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg  
 305 310 315 320  
 Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe  
 325 330 335  
 30 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg  
 340 345 350  
 Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser  
 355 360 365  
 Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Leu Ala Ser Tyr  
 370 375 380  
 35 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala  
 385 390 395 400  
 Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr  
 405 410 415  
 40 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala  
 420 425 430  
 Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys  
 435 440 445  
 Leu Ser Asp  
 450

(2) INFORMATION FOR SEQ ID NO:336

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

65 Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys  
 1 5 10 15  
 Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln  
 20 25 30  
 70 Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser  
 35 40 45  
 Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser  
 50 55 60  
 75 Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro  
 65 70 75 80

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Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln  
85 90 95  
Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val  
100 105 110  
5 Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp  
115 120 125  
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu  
130 135 140  
10 Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr  
145 150 155  
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His  
165 170 175  
15 Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu  
180 185 190  
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys  
195 200 205  
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val  
210 215 220  
20 Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys  
225 230 235  
Glu Ile Asn Ile Asn Cys Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys  
245 250 255  
Asn Gly Val Val Gln Met Ile Met Val Lys Gly Gln Tyr Ile Ser Met  
260 265 270  
25 Cys Ser Gly Asn Leu Leu Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu  
275 280 285  
Ile Ile Ser Ala Gly His Cys Ala Ser Ile Thr Thr Asn Phe Gly Val  
290 295 300  
30 Thr Gln Ser Glu Leu Asp Lys Trp Ile Phe Thr Phe His Tyr Glu Lys  
305 310 315  
Arg Gly Cys Ser Asn Gly Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile  
325 330 335  
Ile Gly Ala Ser Met Lys Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp  
340 345 350  
35 Gly Leu Leu Leu Gln Leu Asn Asp Glu Val Pro Leu Arg Tyr Arg Val  
355 360 365  
Tyr Tyr Asn Gly Trp Asp Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala  
370 375 380  
40 Gly Ile His His Pro Ala Gly Asp Ala Met Lys Ile Ser Ile Leu Lys  
385 390 395  
Lys Thr Pro Ala Leu Asn Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly  
405 410 415  
Thr Asp Asp His Phe Tyr Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly  
420 425 430  
45 Gly Ser Ser Gly Ser Ser Leu Phe Asn Gln Asn Lys His Val Val Gly  
435 440 445  
Thr Leu Thr Gly Gly Ala Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly  
450 455 460  
50 Arg Leu Asn Ser His Trp Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser  
465 470 475  
Arg Met Asp Ile Tyr Leu Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile  
485 490 495  
Leu Asn Gly Thr Tyr Arg Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro  
500 505 510  
55 Arg Leu Leu Leu Gln Ser Thr Gly Asp Gln Val Glu Leu Asn Trp Thr  
515 520 525  
Ala Val Pro Ala Asp Gln Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His  
530 535 540  
60 Ile Phe Arg Asn Gly Lys Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr  
545 550 555  
Ser Asp Ala Ile Asp Glu Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr  
565 570 575  
Glu Val Ser Ala Arg Phe Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu  
580 585 590  
65 Ser Tyr Lys Asp Thr Asp Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp  
595 600 605  
Ile Gln Thr Lys Leu Lys Pro Asp Val Thr Pro Leu Pro Gly Gly Gly  
610 615 620  
70 Val Ser Leu Ser Trp Lys Val Pro Phe Leu Ser Gln Leu Val Ser Arg  
625 630 635  
Phe Gly Glu Ser Pro Asn Pro Val Phe Lys Thr Phe Glu Val Pro Tyr  
645 650 655  
Val Ser Ala Ala Ala Gln Thr Pro Asn Pro Pro Val Gly Val Val  
660 665 670  
75 Ile Ala Asp Lys Phe Met Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile

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5                   675                   680                   685  
 Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu  
 690                   695                   700  
 Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro  
 705                   710                   715                   720  
 Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro  
 725                   730                   735  
 Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro  
 740                   745                   750  
 10   Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp  
 755                   760                   765  
 Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val  
 770                   775                   780  
 15   Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile  
 785                   790                   795                   800  
 Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu  
 805                   810                   815  
 Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu  
 820                   825                   830  
 20   Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln  
 835                   840                   845  
 Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp  
 850                   855                   860  
 25   Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly  
 865                   870                   875                   880  
 Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val  
 885                   890                   895  
 Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala  
 900                   905                   910  
 30   Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu  
 915                   920                   925  
 Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr  
 930                   935                   940  
 35   Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val  
 945                   950                   955                   960  
 Lys Gln

(2) INFORMATION FOR SEQ ID NO:337

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

60   Trp Lys Lys Ser Asn Pro Gln Tyr Arg Gly Arg Thr Ala Asn Tyr Arg  
 1                   5                   10                   15  
 Asp His Tyr Asn Thr Glu Ser Tyr Leu Ser Leu Arg Arg Asn Gln Thr  
 20                   25                   30  
 Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu  
 35                   40                   45  
 65   Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn  
 50                   55                   60  
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala  
 65                   70                   75                   80  
 70   Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile  
 85                   90                   95  
 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser  
 100                   105                   110  
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu  
 115                   120                   125  
 75   Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val

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130 135 140  
 Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser  
 145 150 155 160  
 Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro  
 165 170 175  
 Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala  
 180 185 190  
 Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala  
 195 200 205  
 10 Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu  
 210 215 220  
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly  
 225 230 235 240  
 15 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys  
 245 250 255  
 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile  
 260 265 270  
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys  
 275 280 285  
 20 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro  
 290 295 300  
 Asp Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln  
 305 310 315 320  
 25 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile  
 325 330 335  
 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly  
 340 345 350  
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu  
 355 360 365  
 30 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn  
 370 375 380  
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile  
 385 390 395 400  
 35 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly  
 405 410 415  
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr  
 420 425 430  
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val  
 435 440 445  
 40 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala  
 450 455 460  
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile  
 465 470 475 480  
 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu  
 485 490 495  
 45 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val  
 500 505 510  
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr  
 515 520 525  
 50 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr  
 530 535 540  
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr  
 545 550 555 560  
 55 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala  
 565 570 575  
 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu  
 580 585 590  
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn  
 595 600 605  
 60 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys  
 610 615 620  
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp  
 625 630 635 640  
 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly  
 645 650 655  
 65 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln  
 660 665 670  
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val  
 675 680 685  
 70 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys  
 690 695 700

(2) INFORMATION FOR SEQ ID NO:338

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(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1312 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1312  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

20 Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala  
 1 5 10 15  
 Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg  
 20 25 30  
 Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln  
 35 40 45  
 25 Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser  
 50 55 60  
 Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val  
 65 70 75 80  
 Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe  
 85 90 95  
 30 Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu  
 100 105 110  
 Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser  
 115 120 125  
 35 Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn  
 130 135 140  
 Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu  
 145 150 155 160  
 Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr  
 165 170 175  
 40 Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp  
 180 185 190  
 Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe  
 195 200 205  
 45 Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu  
 210 215 220  
 Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr  
 225 230 235 240  
 Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala  
 245 250 255  
 50 Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr  
 260 265 270  
 Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys  
 275 280 285  
 55 Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro  
 290 295 300  
 His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly  
 305 310 315 320  
 Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro  
 325 330 335  
 60 Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile  
 340 345 350  
 Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys  
 355 360 365  
 65 Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala  
 370 375 380  
 Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser  
 385 390 395 400  
 Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr  
 405 410 415  
 70 Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile  
 420 425 430  
 Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu  
 435 440 445  
 75 Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn  
 450 455 460

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Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu Arg Leu  
 465 470 475 480  
 Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile Leu Lys  
 485 490 495  
 5 Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu Asn Asn  
 500 505 510  
 Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr Val Trp  
 515 520 525  
 10 Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg Leu Asn  
 530 535 540  
 Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser Ser Ala  
 545 550 555 560  
 Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr Thr Tyr  
 565 570 575  
 15 Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg Ala Thr  
 580 585 590  
 Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu Phe Tyr  
 595 600 605  
 20 Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val Val Gly  
 610 615 620  
 Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp Thr Tyr  
 625 630 635 640  
 Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn Ile Met  
 645 650 655  
 25 Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn Asn Thr  
 660 665 670  
 Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu Lys Ile  
 675 680 685  
 30 Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile Gln Val  
 690 695 700  
 Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile Ser Gly  
 705 710 715 720  
 Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp Gly Leu  
 725 730 735  
 35 Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu Asn Leu  
 740 745 750  
 Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser Val Lys  
 755 760 765  
 40 Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu Ile Ser  
 770 775 780  
 Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn Cys Asp  
 785 790 795 800  
 Leu Ser Val Glu Asn Ser Met Phe Ser Ser Gly Ile Thr Val Phe  
 805 810 815  
 45 Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys Ala Lys  
 820 825 830  
 Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr His Ile  
 835 840 845  
 50 Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile Lys Leu  
 850 855 860  
 Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val Asn Cys  
 865 870 875 880  
 Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu  
 885 890 895  
 55 His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly Ser Thr  
 900 905 910  
 Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn  
 915 920 925  
 60 His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn  
 930 935 940  
 Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg  
 945 950 955 960  
 Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn Phe His  
 965 970 975  
 65 Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp  
 980 985 990  
 Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp Gly Asn  
 995 1000 1005  
 70 Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp Leu Phe  
 1010 1015 1020  
 Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn  
 1025 1030 1035 1040  
 Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly  
 1045 1050 1055  
 75 Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met Val Glu

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1060 1065 1070  
 Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Leu Lys Glu Leu Phe  
 1075 1080 1085  
 5 Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr  
 1090 1095 1100  
 Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr  
 1105 1110 1115 1120  
 Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln  
 1125 1130 1135  
 10 Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr  
 1140 1145 1150  
 Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn  
 1155 1160 1165  
 15 Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu  
 1170 1175 1180  
 Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn  
 1185 1190 1195 1200  
 Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro  
 1205 1210 1215  
 20 Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile  
 1220 1225 1230  
 Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp  
 1235 1240 1245  
 25 Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser  
 1250 1255 1260  
 Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser  
 1265 1270 1275 1280  
 Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr  
 1285 1290 1295  
 30 Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys  
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:339

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 938 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...938  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile  
 1 5 10 15  
 55 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser  
 20 25 30  
 Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn  
 35 40 45  
 60 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu  
 50 55 60  
 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala  
 65 70 75 80  
 Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val  
 85 90 95  
 65 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly  
 100 105 110  
 Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala  
 115 120 125  
 70 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu  
 130 135 140  
 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe  
 145 150 155 160  
 Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val  
 165 170 175  
 75 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala

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180 185 190  
 Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu  
 195 200 205  
 5 Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr  
 210 215 220  
 Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp  
 225 230 235 240  
 Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu  
 245 250 255  
 10 Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln  
 260 265 270  
 Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu  
 275 280 285  
 15 Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp  
 290 295 300  
 Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr  
 305 310 315 320  
 Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly  
 325 330 335  
 20 Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr  
 340 345 350  
 Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser  
 355 360 365  
 25 Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn  
 370 375 380  
 Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp  
 385 390 395 400  
 Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met  
 405 410 415  
 30 Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu  
 420 425 430  
 Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile  
 435 440 445  
 35 Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys  
 450 455 460  
 Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr  
 465 470 475 480  
 Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile  
 485 490 495  
 40 Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu  
 500 505 510  
 Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn  
 515 520 525  
 45 Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val  
 530 535 540  
 Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu  
 545 550 555 560  
 Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln  
 565 570 575  
 50 Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu  
 580 585 590  
 Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile  
 595 600 605  
 55 Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met  
 610 615 620  
 Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro  
 625 630 635 640  
 Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu  
 645 650 655  
 60 Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val  
 660 665 670  
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala  
 675 680 685  
 65 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala  
 690 695 700  
 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys  
 705 710 715 720  
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu  
 725 730 735  
 70 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro  
 740 745 750  
 Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu  
 755 760 765  
 75 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys  
 770 775 780

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Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 785 790 795 800  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 805 810 815  
 5 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 820 825 830  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 835 840 845  
 10 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 850 855 860  
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 865 870 875 880  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 885 890 895  
 15 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 900 905 910  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 915 920 925  
 20 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 930 935

## (2) INFORMATION FOR SEQ ID NO:340

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 30 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...606  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser  
 1 5 10 15  
 45 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val  
 20 25 30  
 Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro  
 35 40 45  
 Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu  
 50 55 60  
 Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro  
 65 70 75 80  
 Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe  
 85 90 95  
 55 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu  
 100 105 110  
 Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile  
 115 120 125  
 Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp  
 130 135 140  
 60 Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys  
 145 150 155 160  
 Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg  
 165 170 175  
 65 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu  
 180 185 190  
 Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg  
 195 200 205  
 Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val  
 210 215 220  
 70 Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly  
 225 230 235 240  
 Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg  
 245 250 255  
 75 Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His  
 260 265 270



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Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile  
 275 280 285  
 Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn  
 290 295 300  
 5 Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu  
 305 310 315 320  
 Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp  
 325 330 335  
 10 Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe  
 340 345 350  
 Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu  
 355 360 365  
 Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val  
 370 375 380  
 15 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu  
 385 390 395 400  
 Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln  
 405 410 415  
 20 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr  
 420 425 430  
 Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu  
 435 440 445  
 Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu  
 450 455 460  
 25 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu  
 465 470 475 480  
 Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly  
 485 490 495  
 30 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu  
 500 505 510  
 Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val  
 515 520 525  
 Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly  
 530 535 540  
 35 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser  
 545 550 555 560  
 Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys  
 565 570 575  
 40 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro  
 580 585 590  
 Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe  
 595 600 605  
 (2) INFORMATION FOR SEQ ID NO:341  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...357  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341  
 Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys  
 1 5 10 15  
 Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His  
 20 25 30  
 Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala  
 35 40 45  
 70 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala  
 50 55 60  
 Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn  
 65 70 75 80  
 75 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly  
 85 90 95

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Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met  
 100 105 110  
 Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly  
 115 120 125  
 5 Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln  
 130 135 140  
 Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln  
 145 150 155 160  
 10 Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser  
 165 170 175  
 Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu  
 180 185 190  
 Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser  
 195 200 205  
 15 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn  
 210 215 220  
 Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg  
 225 230 235 240  
 20 Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu  
 245 250 255  
 Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met  
 260 265 270  
 Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser  
 275 280 285  
 25 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp  
 290 295 300  
 Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val  
 305 310 315 320  
 30 Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr  
 325 330 335  
 His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp  
 340 345 350  
 Asp Lys Ser Ile Phe  
 355

35 (2) INFORMATION FOR SEQ ID NO:342  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 amino acids  
 40 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 45 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...337  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

55 Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu  
 1 5 10 15  
 Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu  
 20 25 30  
 60 Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile  
 35 40 45  
 Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly  
 50 55 60  
 65 Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Thr Gly Lys  
 65 70 75 80  
 Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln  
 85 90 95  
 Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg  
 100 105 110  
 70 Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu  
 115 120 125  
 Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp  
 130 135 140  
 75 Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln  
 145 150 155 160

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Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn  
 165 170 175  
 Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu  
 180 185 190  
 5 Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala  
 195 200 205  
 Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu  
 210 215 220  
 10 Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu  
 225 230 235 240  
 Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr  
 245 250 255  
 Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val  
 260 265 270  
 15 Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala  
 275 280 285  
 Val Asn Glu Ser Phe Gly Glu Val Glu Thr Gly Ile Phe Ile Ala  
 290 295 300  
 20 Val Gly Lys Ile Leu Glu Lys Lys Gln Arg His Ile Glu Ser Phe  
 305 310 315 320  
 Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg  
 325 330 335  
 Ser

25 (2) INFORMATION FOR SEQ ID NO:343  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 566 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...566  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343  
 Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp  
 1 5 10 15  
 Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala  
 20 25 30  
 50 Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln  
 35 40 45  
 Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro  
 50 55 60  
 55 Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg  
 65 70 75 80  
 Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr  
 85 90 95  
 Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro  
 100 105 110  
 60 Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg  
 115 120 125  
 Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser  
 130 135 140  
 65 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu  
 145 150 155 160  
 Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His  
 165 170 175  
 Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg  
 180 185 190  
 70 Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg  
 195 200 205  
 Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser  
 210 215 220  
 75 Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser  
 225 230 235 240

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Ala Ala Tyr Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg  
 245 250 255  
 Pro Gly Gln Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val  
 260 265 270  
 5 Asp Val Ser Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr  
 275 280 285  
 Val Asn Gly Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp  
 290 295 300  
 10 Ala Ile Gly Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg  
 305 310 315 320  
 Ser Ser Ile Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr  
 325 330 335  
 Gly Ser Trp His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr  
 340 345 350  
 15 Ala Leu Arg Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp  
 355 360 365  
 Asp Asn Tyr His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp  
 370 375 380  
 20 Tyr Met Leu Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile  
 385 390 395 400  
 Arg Thr Asp Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe  
 405 410 415  
 Tyr Gly Tyr Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser  
 420 425 430  
 25 Gly Met Leu Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser  
 435 440 445  
 Lys Leu Asp Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu  
 450 455 460  
 30 Thr His Ser Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr  
 465 470 475 480  
 Gln Leu Ala Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu  
 485 490 495  
 Val Arg Ser Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg  
 500 505 510  
 35 Leu Met Thr Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp  
 515 520 525  
 Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser  
 530 535 540  
 40 Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys  
 545 550 555 560  
 Asn Ile Ser Tyr Leu Phe  
 565

45 (2) INFORMATION FOR SEQ ID NO:344  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 60 (B) LOCATION 1...819  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344  
 65 Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly  
 1 5 10 15  
 Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser  
 20 25 30  
 Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr  
 35 40 45  
 70 Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe  
 50 55 60  
 Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala  
 65 70 75 80  
 75 Val Leu Pro Phe Cys Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu  
 85 90 95

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Ile Asp Ser Leu Ser Asn Val Gln Leu Gln Thr Val Gln Val Val Ala  
 100 105 110  
 Thr Arg Ala Thr Ala Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys  
 115 120 125  
 5 Ala Glu Leu Ser Lys Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu  
 130 135 140  
 Met Leu Thr Pro Ser Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile  
 145 150 155 160  
 10 Gly Tyr Ser Gly Phe Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn  
 165 170 175  
 Ile Thr Thr Asn Gly Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val  
 180 185 190  
 Phe Trp Val Asn Met Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln  
 195 200 205  
 15 Val Gln Arg Gly Val Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly  
 210 215 220  
 Ala Ser Val Asn Met Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly  
 225 230 235 240  
 20 Arg Val Asp Leu Ser Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val  
 245 250 255  
 Lys Leu Gly Ser Gly Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg  
 260 265 270  
 Leu Ser Lys Ile Gly Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp  
 275 280 285  
 25 Leu Lys Ser Tyr Phe Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala  
 290 295 300  
 Leu Arg Phe Ile Thr Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp  
 305 310 315 320  
 30 Asn Gly Leu Ser Lys Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn  
 325 330 335  
 Ser Ala Gly Leu Met Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr  
 340 345 350  
 His Asn Thr Asp Asn Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr  
 355 360 365  
 35 His Ser Phe Ser Pro Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr  
 370 375 380  
 Ala Gly Tyr Gly Tyr Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys  
 385 390 395 400  
 40 Glu Tyr Ala Leu Gln Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys  
 405 410 415  
 Thr Asp Leu Ile Arg Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu  
 420 425 430  
 Ile Gly Ser Leu Asn Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly  
 435 440 445  
 45 Ala Ser Gly Asn Ile Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr  
 450 455 460  
 Ile Lys Lys Tyr Asn Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg  
 465 470 475 480  
 50 Asn Arg Ala Asp Lys Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp  
 485 490 495  
 Gln Ile Thr Pro Glu Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr  
 500 505 510  
 Ile Gly Tyr Thr Ile Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln  
 515 520 525  
 55 Gly Ser Met Gln His Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn  
 530 535 540  
 Pro Lys Ala Gly Leu Thr Tyr Ser Phe Asp Asp Ala His Thr Ala Tyr  
 545 550 555 560  
 60 Ala Ser Val Ala Val Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr  
 565 570 575  
 Glu Ala Gly Ile Gly Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr  
 580 585 590  
 Glu Leu Gly Tyr Arg Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly  
 595 600 605  
 65 Leu Tyr Tyr Met Gln Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu  
 610 615 620  
 Ser Asp Val Gly Gln Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg  
 625 630 635 640  
 70 Met Gly Leu Glu Leu Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu  
 645 650 655  
 Arg Trp Asp Ala Ser Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr  
 660 665 670  
 Val Gln Tyr Thr Ser Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu  
 675 680 685  
 75 Lys Glu Glu Thr Leu Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val

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690 695 700  
 Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala  
 705 710 715 720  
 Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg  
 5 725 730 735  
 Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly  
 740 745 750  
 Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln  
 755 760 765  
 10 Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr  
 770 775 780  
 Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp  
 785 790 795 800  
 15 Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr  
 805 810 815  
 Ile Asp Phe

## (2) INFORMATION FOR SEQ ID NO:345

20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 532 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

35

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...532

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

40

Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg  
 1 5 10 15  
 Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg  
 20 25 30  
 Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu Leu  
 35 40 45  
 45 Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met  
 50 55 60  
 Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys  
 65 70 75 80  
 50 Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val  
 85 90 95  
 Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser  
 100 105 110  
 Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn  
 115 120 125  
 55 Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu  
 130 135 140  
 Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala  
 145 150 155 160  
 60 Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn  
 165 170 175  
 Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile  
 180 185 190  
 Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn  
 195 200 205  
 65 Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu  
 210 215 220  
 Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr  
 225 230 235 240  
 70 Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn  
 245 250 255  
 Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala  
 260 265 270  
 Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly  
 275 280 285  
 75 Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe

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290  
 Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile  
 305  
 Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg  
 325  
 Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser  
 340  
 Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr  
 355  
 Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His  
 370  
 His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr  
 385  
 Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val  
 405  
 Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr  
 420  
 Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu  
 435  
 Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys  
 450  
 Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala  
 465  
 Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp  
 485  
 His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln  
 500  
 Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val  
 515  
 Gly Phe His Phe  
 530

295  
 Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile  
 310  
 Ser Gly Cys Gln Leu Leu Ala His Glu Arg  
 330  
 Phe Asp Tyr Tyr Asn Ser  
 345  
 Glu Glu Val Leu Val Thr Pro Tyr  
 360  
 Ala Leu Gly Gly Gly Leu Ile Phe Gln His  
 375  
 Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr  
 390  
 Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val  
 410  
 Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr  
 425  
 Leu Trp Ser Trp Leu Leu Gly Val Glu  
 440  
 Ile Gly Tyr Glu Glu Pro His Gln Lys  
 455  
 Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala  
 470  
 Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp  
 490  
 Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln  
 505  
 Phe Asp Thr Gly Asp Ile Gln Leu Arg Val  
 520  
 Phe

300  
 Leu Leu Ser Gln Ile  
 315  
 Leu Leu Ala His Glu Arg  
 335  
 Tyr Tyr Asn Ser  
 350  
 Thr Pro Tyr  
 365  
 Ile Phe Gln His  
 380  
 Tyr Ala Glu Thr Tyr  
 395  
 Ser Asp His Tyr Asn Val  
 415  
 Ser Gly Lys Leu Tyr  
 430  
 Val Glu  
 445  
 His Gln Lys  
 460  
 Ser Lys Ala  
 475  
 Pro Gly Pro Trp  
 495  
 Tyr Gln  
 510  
 Arg Val  
 525

(2) INFORMATION FOR SEQ ID NO:346

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met  
 1 5 10 15  
 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala  
 20 25 30  
 Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu  
 35 40 45  
 Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn  
 50 55 60  
 Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys  
 65 70 75 80  
 Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr  
 85 90 95  
 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu  
 100 105 110  
 Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala  
 115 120 125  
 Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser  
 130 135 140  
 Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala  
 145 150 155 160  
 Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe  
 165 170 175  
 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp

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180 185 190  
 Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys  
 195 200 205  
 Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn  
 210 215 220  
 Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala  
 225 230 235 240  
 Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu  
 245 250 255  
 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu  
 260 265 270  
 Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe  
 275 280 285  
 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO:347

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...221  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg  
 1 5 10 15  
 Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile  
 20 25 30  
 Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn  
 35 40 45  
 Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn  
 50 55 60  
 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Glu Phe Ala  
 65 70 75 80  
 Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met  
 85 90 95  
 Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His  
 100 105 110  
 Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp  
 115 120 125  
 Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val  
 130 135 140  
 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp  
 145 150 155 160  
 Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu  
 165 170 175  
 Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu  
 180 185 190  
 His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu  
 195 200 205  
 Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:348

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...240

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

```

1   Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
    1       5       10       15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
    20       25       30
15 Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
    35       40       45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
    50       55       60
20 Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
    65       70       75       80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
    85       90       95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
    100      105      110
25 Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
    115      120      125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
    130      135      140
30 Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
    145      150      155      160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
    165      170      175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
    180      185      190
35 Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
    195      200      205
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
    210      215      220
40 Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
    225      230      235      240
Phe Val Gly Ile Gly Tyr Arg Phe
    245

```

45 (2) INFORMATION FOR SEQ ID NO:349

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...211

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

```

65 Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Val Val Leu Leu
    1       5       10       15
Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
    20       25       30
Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
    35       40       45
70 Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
    50       55       60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
    65       70       75       80
75 Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
    85       90       95

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Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala  
 100 105 110  
 Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp  
 115 120 125  
 5 Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser  
 130 135 140  
 Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val  
 145 150 155 160  
 10 Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val  
 165 170 175  
 Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val  
 180 185 190  
 Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser  
 195 200 205  
 15 Thr His Phe  
 210

(2) INFORMATION FOR SEQ ID NO:350

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 953 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...953
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu  
 1 5 10 15  
 40 Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu  
 20 25 30  
 Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala  
 35 40 45  
 45 Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile  
 50 55 60  
 Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser  
 65 70 75 80  
 Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile  
 85 90 95  
 50 Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg  
 100 105 110  
 Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu  
 115 120 125  
 55 Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr  
 130 135 140  
 Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe  
 145 150 155 160  
 Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe  
 165 170 175  
 60 Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu  
 180 185 190  
 Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met  
 195 200 205  
 65 Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro  
 210 215 220  
 His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp  
 225 230 235 240  
 Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro  
 245 250 255  
 70 Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser  
 260 265 270  
 Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr  
 275 280 285  
 75 Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu  
 290 295 300

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Ala Leu Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala  
 305 310 315 320  
 Gln Ser Lys Tyr Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala  
 325 330 335  
 5 Asn Tyr Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr  
 340 345 350  
 Ser Lys Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro  
 355 360 365  
 10 Lys Ala Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr  
 370 375 380  
 Gly Ser Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala  
 385 390 395 400  
 Arg Thr Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe  
 405 410 415  
 15 Pro Gly Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn  
 420 425 430  
 Met Arg Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn  
 435 440 445  
 20 Met Ser Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu  
 450 455 460  
 Arg Trp Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn  
 465 470 475 480  
 Ser Ile Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg  
 485 490 495  
 25 Asp Trp Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val  
 500 505 510  
 Pro Leu Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu  
 515 520 525  
 30 Trp Trp Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys  
 530 535 540  
 Thr Phe Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp  
 545 550 555 560  
 Tyr Ser Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys  
 565 570 575  
 35 Pro Trp Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His  
 580 585 590  
 Arg Phe Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys  
 595 600 605  
 40 Arg Arg Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly  
 610 615 620  
 Lys Leu His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly  
 625 630 635 640  
 Ala Pro Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn  
 645 650 655  
 45 Asn Leu Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys  
 660 665 670  
 Lys Ile Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met  
 675 680 685  
 50 Phe Ala Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu  
 690 695 700  
 Arg Leu Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro  
 705 710 715 720  
 Tyr Leu Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr  
 725 730 735  
 55 Lys Ser Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu  
 740 745 750  
 Ile Ser Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu  
 755 760 765  
 60 Ser Gly Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu  
 770 775 780  
 Lys Lys Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp  
 785 790 795 800  
 Ile Leu Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu  
 805 810 815  
 65 Glu Arg Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala  
 820 825 830  
 Tyr Ser Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala  
 835 840 845  
 70 Thr Asp Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg  
 850 855 860  
 Val Thr Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn  
 865 870 875 880  
 Trp Ser Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile  
 885 890 895  
 75 Thr Ser Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile

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5 Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val  
 Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser  
 Asn Arg Pro Ile Thr Asn Thr Trp Tyr  
 10 (2) INFORMATION FOR SEQ ID NO:351  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1251  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351  
 30 Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro  
 1 5 10 15  
 Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile  
 20 25 30  
 Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile  
 35 35 40 45  
 Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile  
 50 55 60  
 Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn  
 65 70 75 80  
 Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp  
 40 85 90 95  
 Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro  
 100 105 110  
 Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro  
 115 120 125  
 45 Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro  
 130 135 140  
 Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr  
 145 150 155 160  
 Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln  
 165 170 175  
 50 Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile  
 180 185 190  
 Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala  
 195 200 205  
 55 Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His  
 210 215 220  
 Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile  
 225 230 235 240  
 Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys  
 245 250 255  
 60 Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile  
 260 265 270  
 Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn  
 275 280 285  
 65 Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro  
 290 295 300  
 Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val  
 305 310 315 320  
 Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser  
 325 330 335  
 70 Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser  
 340 345 350  
 Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val  
 355 360 365  
 75 Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn

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370 375 380  
 Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys Asn Ser Gly Tyr Thr Ile  
 385 390 395 400  
 His Thr Ile Gly Tyr Asp Leu Gly Asp Phe Ala Leu Ala Asn Asn Ser  
 405 410 415  
 Leu Lys Leu Thr Ala Thr Asp Glu Asn His Phe Phe Thr Ala Thr Pro  
 420 425 430  
 Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile Ala Gln Thr Ile Asn Ile  
 435 440 445  
 Gly Ile Gln Arg Gly Glu Val Thr Asp Phe Val Ala Pro Gly Phe Ile  
 450 455 460  
 Val Lys Asn Leu Thr Gln Ser Gly Asp Val Thr His Leu Leu Asn Val  
 465 470 475 480  
 Ser Asn Gly Thr Val His Tyr Asp Val Ser Thr Lys Lys Leu Thr Trp  
 485 490 495  
 Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu Ala Thr Ile Thr Tyr Arg  
 500 505 510  
 Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn Asn Asp Ile Pro Val Asn  
 515 520 525  
 Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly Gly Phe Asp Thr Asn Thr  
 530 535 540  
 Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn Gly Glu Pro Asn Gln Gln  
 545 550 555 560  
 Leu Ile Phe Pro Arg Pro Thr Val Lys Leu Gly Tyr Gly Val Ile Lys  
 565 570 575  
 Arg His Tyr Val Leu Val Asn Lys Asp Gly Gln Pro Ile Gln Ala Asn  
 580 585 590  
 Gly Thr Val Val Ser Ser Leu Ser Glu Ala His Val Leu Gln Ser Gln  
 595 600 605  
 Asp Phe Phe Leu Pro Ser Gly Gly Gly His Ile Val Pro Lys Trp Ile  
 610 615 620  
 Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln Tyr Tyr Ser Val Pro Pro  
 625 630 635 640  
 Thr Asn Thr Val Ile Thr Thr Ala Asp Gly Lys Arg Tyr Arg Phe Val  
 645 650 655  
 Glu Val Pro Gly Ser Thr Pro Asn Pro Gly Gln Ile Gly Ile Ser Trp  
 660 665 670  
 Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala Tyr Lys Leu Leu Asn Tyr  
 675 680 685  
 Trp Met Gly Gly Thr Thr Asp Gln Gln Ser Glu Trp Asp Val Thr Ser  
 690 695 700  
 Asn Trp Thr Gly Ala Gln Val Pro Leu Thr Gly Glu Asp Val Glu Phe  
 705 710 715 720  
 Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala Val Ala Asp Leu His Val  
 725 730 735  
 Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn Leu Ile Asn Asn Ser Asp  
 740 745 750  
 Lys Asp Leu Val Val Thr Thr Ser Ser Gln Leu Thr Ile Asn Gly Val  
 755 760 765  
 Val Glu Asp Asn Asn Pro Asn Val Gly Thr Ile Val Val Lys Ser Ser  
 770 775 780  
 Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe Ala Asn Pro Gly Tyr Asn  
 785 790 795 800  
 Gln Asn Val Gly Gly Thr Val Glu Phe Tyr Asn Gln Gly Tyr Asp Cys  
 805 810 815  
 Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp Gln Tyr Phe Gly Ile Pro  
 820 825 830  
 Val Asn Glu Ser Gly Phe Pro Ile Asn Asp Val Gly Gly Asn Glu Thr  
 835 840 845  
 Val Asn Gln Trp Val Glu Pro Phe Asn Gly Asp Lys Trp Arg Pro Ala  
 850 855 860  
 Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys Phe Lys Gly Tyr Gln Ile  
 865 870 875 880  
 Thr Asn Asp Val Gln Ala Gln Pro Thr Gly Val Tyr Ser Phe Lys Gly  
 885 890 895  
 Met Ile Cys Val Cys Asp Ala Phe Leu Asn Leu Thr Arg Thr Ser Gly  
 900 905 910  
 Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly Asn Ser Tyr Thr Gly Ala  
 915 920 925  
 Ile Asp Ile Lys Gln Gly Ile Val Phe Pro Pro Glu Val Glu Gln Thr  
 930 935 940  
 Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp Gln Trp Arg Lys Leu Asn  
 945 950 955 960  
 Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly Gln Tyr Leu Ser Val Pro  
 965 970 975

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Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met  
 980 985 990  
 His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk  
 995 1000 1005  
 5 Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn  
 1010 1015 1020  
 Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met  
 1025 1030 1035 1040  
 10 Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu  
 1045 1050 1055  
 Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp  
 1060 1065 1070  
 Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr, Ala Met  
 1075 1080 1085  
 15 Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu  
 1090 1095 1100  
 Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr  
 1105 1110 1115 1120  
 20 Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu  
 1125 1130 1135  
 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser  
 1140 1145 1150  
 Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu  
 1155 1160 1165  
 25 Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr  
 1170 1175 1180  
 Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr  
 1185 1190 1195 1200  
 30 Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val  
 1205 1210 1215  
 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr  
 1220 1225 1230  
 Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu  
 1235 1240 1245  
 35 Val Glu Tyr  
 1250

## (2) INFORMATION FOR SEQ ID NO:352

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp  
 1 5 10 15  
 60 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu  
 20 25 30  
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr  
 35 40 45  
 65 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr  
 50 55 60  
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala  
 65 70 75 80  
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly  
 85 90 95  
 70 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly  
 100 105 110  
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val  
 115 120 125  
 75 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala  
 130 135 140

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Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser  
 145 150 155 160  
 Val Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe  
 165 170 175  
 5 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe  
 180 185 190  
 Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu  
 195 200 205  
 10 Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg  
 210 215 220  
 Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His  
 225 230 235 240  
 Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr  
 245 250 255  
 15 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly  
 260 265 270  
 Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala  
 275 280 285  
 20 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu  
 290 295 300  
 Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro  
 305 310 315 320  
 Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg  
 325 330 335  
 25 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu  
 340 345 350  
 Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe  
 355 360 365  
 30 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala  
 370 375 380  
 Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp  
 385 390 395 400  
 Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser  
 405 410 415  
 35 Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe  
 420 425

(2) INFORMATION FOR SEQ ID NO:353

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 464 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...464  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

Tyr Gly Lys Arg Arg Lys Leu Gly Thr Ser Val Arg Pro Ser Val Leu  
 1 5 10 15  
 60 Thr Gln Ile Arg Phe Ile Leu Asp Leu His Leu Ile Thr Asp Phe Phe  
 20 25 30  
 Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe  
 35 40 45  
 65 Ile Ile Asp Leu Leu Leu Leu Cys Cys Ser Ala Phe Met Ser Ser Cys  
 50 55 60  
 Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg  
 65 70 75 80  
 Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn  
 85 90 95  
 70 Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn  
 100 105 110  
 Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val  
 115 120 125  
 75 Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr  
 130 135 140

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    Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
    145      150      155      160
    Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Met Ser Val
    165      170      175
5   Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
    180      185      190
    Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr Asp Met Ser Val
    195      200      205
10  Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
    210      215      220
    Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
    225      230      235      240
    Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
    245      250      255
15  Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
    260      265      270
    Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
    275      280      285
20  Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
    290      295      300
    Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
    305      310      315      320
    Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
    325      330      335
25  Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
    340      345      350
    Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp
    355      360      365
30  Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe
    370      375      380
    Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro
    385      390      395      400
    Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly
    405      410      415
35  Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala
    420      425      430
    Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg
    435      440      445
40  Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu
    450      455      460

```

(2) INFORMATION FOR SEQ ID NO:354

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

```

    Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
    1      5      10      15
    Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
    20      25      30
65  Leu Thr Met Asn Ile Asp Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu
    35      40      45
    Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
    50      55      60
70  Asn Thr Ala Asn Leu Asn Leu Leu Ile Lys His Gly Gln Val Ile Asn
    65      70      75      80
    Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val
    85      90      95
75  Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
    100      105      110

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Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly  
 115 120 125  
 Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val  
 130 135 140  
 5 Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu  
 145 150 155 160  
 Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr  
 165 170 175  
 10 Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His  
 180 185 190  
 Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly  
 195 200 205  
 Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp  
 210 215 220  
 15 Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg  
 225 230 235 240  
 Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn  
 245 250 255  
 20 Thr Val Asp Val Gly Ile Asp Ile Ser Phe  
 260 265

(2) INFORMATION FOR SEQ ID NO:355

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 907 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...907  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu  
 1 5 10 15  
 45 Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu  
 20 25 30  
 Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe  
 35 40 45  
 Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile  
 50 55 60  
 His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser  
 65 70 75 80  
 Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn  
 85 90 95  
 55 Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly  
 100 105 110  
 Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp  
 115 120 125  
 Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val  
 130 135 140  
 60 Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val  
 145 150 155 160  
 Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His  
 165 170 175  
 65 Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu  
 180 185 190  
 Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile  
 195 200 205  
 Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn  
 210 215 220  
 70 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly  
 225 230 235 240  
 Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu  
 245 250 255  
 75 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe  
 260 265 270

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Arg Ser Ile Pro Ala His Thr Ile Lys Arg Val Glu Val Ile Thr Asp  
 275 280 285  
 Pro Gly Val Lys Tyr Asp Ala Glu Gly Thr Ser Ala Ile Leu Asp Ile  
 290 295 300  
 5 Val Thr Glu Glu Gly Lys Lys Leu Glu Gly Tyr Ser Gly Ser Ile Thr  
 305 310 315 320  
 Ala Ser Val Ser Asn Asn Pro Thr Ala Asn Gly Ser Ile Phe Leu Thr  
 325 330 335  
 10 Ala Lys Ser Gly Lys Val Gly Leu Thr Thr Asn Tyr Asn Tyr Tyr Gly  
 340 345 350  
 Gly Lys Asn Lys Gly Ser Arg Tyr Phe Thr Glu Arg Thr Thr Ser Met  
 355 360 365  
 Leu Gln Thr Ile Glu Glu Gly Lys Gly Gln Glu Thr Phe Gly Gly His  
 370 375 380  
 15 Phe Gly Asn Ala Leu Leu Ser Phe Glu Ile Asp Ser Leu Asn Leu Phe  
 385 390 395 400  
 Thr Val Gly Gly Asn Val Arg Leu Trp Glu Met Thr Thr Asp Arg Asn  
 405 410 415  
 20 Ser Val Glu Lys Ser Phe Ala Gly Ser Asn Leu Met Ser Tyr Ile Asp  
 420 425 430  
 Arg Lys Leu Lys Thr Gln Met Asp Ala Gly Ser Tyr Glu Leu Asn Ala  
 435 440 445  
 Asp Tyr Gln His Ser Thr Arg Leu Pro Gly Glu Leu Leu Thr Val Ser  
 450 455 460  
 25 Tyr Arg Phe Thr His Asn Pro Asn Asn Ser Glu Thr Phe Ile Asp Gln  
 465 470 475 480  
 Trp Lys Arg Asp Pro Leu Asn Thr Ala Asn Thr Ile Gln Tyr Ala Gly  
 485 490 495  
 30 Gln His Ser Lys Ser Asp Ala Gly Met Asp Glu His Thr Ala Gln Val  
 500 505 510  
 Asp Tyr Thr Arg Pro Leu Gly Gln Ala His Ser Leu Glu Ala Gly Leu  
 515 520 525  
 Lys Tyr Ile Tyr Arg His Ala Thr Ser Asp Pro Leu Tyr Glu Ile Arg  
 530 535 540  
 35 Pro Ser Glu Asp Ala Pro Trp Gln Pro Gly Ser Leu Tyr Ala Gln Asn  
 545 550 555 560  
 Pro Ser Asn Gly Lys Phe Arg His Asp Gln Tyr Ile Gly Ala Ala Tyr  
 565 570 575  
 40 Ala Gly Tyr Asn Tyr Arg Lys Asp Gln Tyr Ser Leu Gln Thr Gly Leu  
 580 585 590  
 Arg Val Glu Ser Ser Arg Leu Lys Ala Leu Phe Pro Glu Asn Ala Ala  
 595 600 605  
 Ala Asp Phe Ser His Asn Ser Phe Asp Trp Val Pro Gln Leu Thr Leu  
 610 615 620  
 45 Gly Tyr Thr Pro Ser Pro Met Lys Gln Leu Lys Leu Ala Tyr Asn Phe  
 625 630 635 640  
 Arg Ile Gln Arg Pro Ala Ile Gly Gln Leu Asn Pro Tyr Arg Leu Gln  
 645 650 655  
 50 Thr Asn Asp Tyr Gln Val Gln Tyr Gly Asn Pro Asp Leu Lys Ser Glu  
 660 665 670  
 Lys Arg His His Val Gly Leu Ser Tyr Asn Gln Tyr Gly Ala Lys Val  
 675 680 685  
 Met Leu Thr Ala Ser Leu Asp Tyr Asp Phe Cys Asn Asn Ala Ile Gln  
 690 695 700  
 55 Asn Tyr Thr Phe Ser Asp Pro Ala Asn Pro Asn Leu Phe His Gln Thr  
 705 710 715 720  
 Tyr Gly Asn Ile Gly Arg Glu His Ser Phe Ser Leu Asn Thr Tyr Ala  
 725 730 735  
 60 Met Tyr Thr Pro Ala Val Trp Val Arg Ile Met Leu Asn Gly Asn Ile  
 740 745 750  
 Asp Arg Thr Phe Gln Lys Ser Glu Ala Leu Gly Ile Asp Val Asn Ser  
 755 760 765  
 Trp Ser Gly Met Val Tyr Ser Gly Leu Met Phe Thr Leu Pro Lys Asp  
 770 775 780  
 65 Trp Thr Val Asn Leu Phe Gly Gly Tyr Tyr His Gly Gly Arg Ser Tyr  
 785 790 795 800  
 Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys  
 805 810 815  
 70 Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Asn Ile  
 820 825 830  
 His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe  
 835 840 845  
 Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser  
 850 855 860  
 75 Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu

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865 870 875 880  
 Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln  
 885 890 895  
 Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn  
 900 905

5 (2) INFORMATION FOR SEQ ID NO:356

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 450 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...450

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn  
 1 5 10 15  
 30 Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro  
 20 25 30  
 Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe  
 35 40 45  
 Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met  
 50 55 60  
 35 Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu  
 65 70 75 80  
 Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile  
 85 90 95  
 40 Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val  
 100 105 110  
 Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr  
 115 120 125  
 Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr  
 130 135 140  
 45 Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser  
 145 150 155 160  
 Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile  
 165 170 175  
 50 Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu  
 180 185 190  
 Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro  
 195 200 205  
 Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val  
 210 215 220  
 55 Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn  
 225 230 235 240  
 Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val  
 245 250 255  
 60 Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp  
 260 265 270  
 Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu  
 275 280 285  
 Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala  
 290 295 300  
 65 Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln  
 305 310 315 320  
 Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr  
 325 330 335  
 70 Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp  
 340 345 350  
 Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr  
 355 360 365  
 Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys  
 370 375 380  
 75 Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp

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385 390 395 400  
 Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg  
 405 410 415  
 Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu  
 420 425 430  
 Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly  
 435 440 445  
 Asn His  
 450

10 (2) INFORMATION FOR SEQ ID NO:357  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...447  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

1 5 10 15  
 Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg  
 20 25 30  
 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro  
 35 40 45  
 Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln  
 50 55 60  
 Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly  
 65 70 75 80  
 Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu  
 85 90 95  
 Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys  
 100 105 110  
 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val  
 115 120 125  
 Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met  
 130 135 140  
 Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln  
 145 150 155 160  
 Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser  
 165 170 175  
 Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val  
 180 185 190  
 Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr  
 195 200 205  
 Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr  
 210 215 220  
 Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro  
 225 230 235 240  
 Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe  
 245 250 255  
 Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr  
 260 265 270  
 Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala  
 275 280 285  
 Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg  
 290 295 300  
 Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg  
 305 310 315 320  
 Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp  
 325 330 335  
 Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp  
 340 345 350  
 Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...406

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

10 Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met  
 1 5 10 15  
 Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu  
 20 25 30  
 Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val  
 35 40 45  
 15 Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala  
 50 55 60  
 Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser  
 65 70 75 80  
 20 Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly  
 85 90 95  
 Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile  
 100 105 110  
 Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn  
 115 120 125  
 25 Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu  
 130 135 140  
 Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu  
 145 150 155 160  
 Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser  
 165 170 175  
 30 Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn  
 180 185 190  
 Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly  
 195 200 205  
 35 Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser  
 210 215 220  
 Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly  
 225 230 235 240  
 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly  
 245 250 255  
 40 Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu  
 260 265 270  
 Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp  
 275 280 285  
 45 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser  
 290 295 300  
 Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys  
 305 310 315 320  
 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr  
 325 330 335  
 50 Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr  
 340 345 350  
 Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn  
 355 360 365  
 55 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn  
 370 375 380  
 Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly  
 385 390 395 400  
 60 Leu Arg Asn Leu Phe His  
 405

(2) INFORMATION FOR SEQ ID NO:360

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 452 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...452

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

```

Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu
1      5      10      15
Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser
10     20     25     30
Phe Trp Glu Glu Ile Ala Pro Phe Ile Ser Asn Glu Pro Asn Val
35     40     45
Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr
50     55     60
Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu
15     65     70     75     80
Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp
85     90     95
Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr
20     100    105    110
Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln
115    120    125
Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe
25     130    135    140
Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser
145    150    155    160
Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser
165    170    175
Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro
30     180    185    190
Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
195    200    205
Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
35     210    215    220
Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
225    230    235    240
Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
245    250    255
Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
40     260    265    270
Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
275    280    285
Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
45     290    295    300
Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
305    310    315    320
Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
325    330    335
Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
50     340    345    350
Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
355    360    365
Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
370    375    380
Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
55     385    390    395    400
Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
405    410    415
Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
60     420    425    430
Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
435    440    445
Lys Val Gln Val
450

```

65

## (2) INFORMATION FOR SEQ ID NO:361

## (i) SEQUENCE CHARACTERISTICS:

```

70     (A) LENGTH: 331 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

```

## (ii) MOLECULE TYPE: protein

```

75     (iii) HYPOTHETICAL: YES

```

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...331

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly  
1 5 10 15  
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg  
20 25 30  
15 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser  
35 40 45  
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val  
50 55 60  
20 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His  
65 70 75 80  
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe  
85 90 95  
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His  
100 105 110  
25 Arg Ser Ser Leu Gln Leu Asn Glu Leu Asn Phe Ala Ala Glu Arg  
115 120 125  
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val  
130 135 140  
30 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn  
145 150 155 160  
Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly  
165 170 175  
Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His  
180 185 190  
35 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala  
195 200 205  
Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr  
210 215 220  
40 Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg  
225 230 235 240  
Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val  
245 250 255  
Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser  
260 265 270  
45 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly  
275 280 285  
Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly  
290 295 300  
50 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr  
305 310 315 320  
Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys  
325 330

55 (2) INFORMATION FOR SEQ ID NO:362

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 329 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

75 Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys  
1 5 10 15



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Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly  
 20 25 30  
 Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe  
 35 40 45  
 5 Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr  
 50 55 60  
 Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Ser Ile Thr Arg  
 65 70 75 80  
 10 Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu  
 85 90 95  
 Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met  
 100 105 110  
 Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala  
 115 120 125  
 15 Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala  
 130 135 140  
 Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn  
 145 150 155 160  
 20 Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile  
 165 170 175  
 Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr  
 180 185 190  
 Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr  
 195 200 205  
 25 Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile  
 210 215 220  
 Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu  
 225 230 235 240  
 30 Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe  
 245 250 255  
 Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe  
 260 265 270  
 Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu  
 275 280 285  
 35 Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe  
 290 295 300  
 Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly  
 305 310 315 320  
 40 Arg Arg Thr Ser Leu Tyr Tyr His Asp  
 325

(2) INFORMATION FOR SEQ ID NO:363

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...319  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val  
 1 5 10 15  
 65 Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His  
 20 25 30  
 Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val  
 35 40 45  
 Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val  
 50 55 60  
 70 Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys  
 65 70 75 80  
 Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg  
 85 90 95  
 75 Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His  
 100 105 110

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Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly  
 115 120 125  
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg  
 130 135 140  
 5 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile  
 145 150 155 160  
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys  
 165 170 175  
 10 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys  
 180 185 190  
 Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly  
 195 200 205  
 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp  
 210 215 220  
 15 Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr  
 225 230 235 240  
 Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln  
 245 250 255  
 20 Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala  
 260 265 270  
 Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr  
 275 280 285  
 Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala  
 290 295 300  
 25 Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:364

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 614 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...614
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met  
 1 5 10 15  
 50 Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu  
 20 25 30  
 Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu  
 35 40 45  
 55 Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val  
 50 55 60  
 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 65 70 75 80  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 85 90 95  
 60 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 100 105 110  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 115 120 125  
 65 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 130 135 140  
 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 145 150 155 160  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 165 170 175  
 70 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 180 185 190  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 195 200 205  
 75 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 210 215 220

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Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 225 230 235 240  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 245 250 255  
 5 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val  
 260 265 270  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 275 280 285  
 10 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 290 295 300  
 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 305 310 315 320  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 325 330 335  
 15 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 340 345 350  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 355 360 365  
 20 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys  
 370 375 380  
 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 385 390 395 400  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 405 410 415  
 25 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 420 425 430  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 435 440 445  
 30 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 450 455 460  
 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 465 470 475 480  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 485 490 495  
 35 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 500 505 510  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 515 520 525  
 40 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 530 535 540  
 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 545 550 555 560  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 565 570 575  
 45 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 580 585 590  
 Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 595 600 605  
 50 Glu Lys Leu Ser Glu Asn  
 610

## (2) INFORMATION FOR SEQ ID NO:365

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...243  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu  
 1 5 10 15  
 Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly  
 20 25 30

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His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr  
 35 40 45  
 Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile  
 50 55 60  
 5 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile  
 65 70 75 80  
 Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu  
 85 90 95  
 10 Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu  
 100 105 110  
 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe  
 115 120 125  
 Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr  
 130 135 140  
 15 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu  
 145 150 155 160  
 Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro  
 165 170 175  
 20 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser  
 180 185 190  
 Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys  
 195 200 205  
 Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe  
 210 215 220  
 25 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp  
 225 230 235 240  
 Thr Phe Asn

30 (2) INFORMATION FOR SEQ ID NO:366  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35  
 (ii) MOLECULE TYPE: protein  
 40 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...235  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

50 Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile  
 1 5 10 15  
 Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu  
 20 25 30  
 55 Tyr Glu Ile Gly Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala  
 35 40 45  
 Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly  
 50 55 60  
 Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp  
 65 70 75 80  
 60 Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp  
 85 90 95  
 Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg  
 100 105 110  
 65 Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly  
 115 120 125  
 Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe  
 130 135 140  
 Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly  
 145 150 155 160  
 70 Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu  
 165 170 175  
 Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp  
 180 185 190  
 75 Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val  
 195 200 205

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Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp  
 210 215 220  
 Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln  
 225 230 235

5 (2) INFORMATION FOR SEQ ID NO:367

10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 436 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...436

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367  
 Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp  
 1 5 10 15  
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala  
 20 25 30  
 35 Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly  
 35 40 45  
 Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu  
 50 55 60  
 Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala  
 65 70 75 80  
 Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala  
 85 90 95  
 Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg  
 100 105 110  
 40 Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys  
 115 120 125  
 Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr  
 130 135 140  
 45 Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr  
 145 150 155 160  
 Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile  
 165 170 175  
 Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser  
 180 185 190  
 50 Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu  
 195 200 205  
 Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala  
 210 215 220  
 55 Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Lys Ser Asp Arg  
 225 230 235 240  
 Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser  
 245 250 255  
 Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu  
 260 265 270  
 60 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro  
 275 280 285  
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu  
 290 295 300  
 65 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr  
 305 310 315 320  
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly  
 325 330 335  
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg  
 340 345 350  
 70 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr  
 355 360 365  
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly  
 370 375 380  
 75 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu  
 385 390 395 400

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Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala  
 405 410 415  
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys  
 420 425 430  
 5 Leu Lys Leu Asn  
 435

(2) INFORMATION FOR SEQ ID NO:368

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln  
 1 5 10 15  
 30 Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu  
 20 25 30  
 Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala  
 35 40 45  
 35 Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val  
 50 55 60  
 Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr  
 65 70 75 80  
 Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr  
 85 90 95  
 40 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile  
 100 105 110  
 Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn  
 115 120 125  
 45 Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala  
 130 135 140  
 Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr  
 145 150 155 160  
 Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro  
 165 170 175  
 50 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp  
 180 185 190  
 Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro  
 195 200 205  
 55 Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln  
 210 215 220  
 Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp  
 225 230 235 240  
 Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys  
 245 250 255  
 60 Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg  
 260 265 270  
 Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp  
 275 280 285  
 65 Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu  
 290 295 300  
 Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly  
 305 310 315 320  
 Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met  
 325 330 335  
 70 Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly  
 340 345 350  
 Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys  
 355 360 365  
 75 Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn  
 370 375 380

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 412 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...412

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

20 Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys  
 1 5 10 15  
 Leu Ile Lys Arg Ser Leu Leu Leu Gly Ala Val Leu Leu Ile Thr  
 20 25 30  
 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr  
 35 40 45  
 25 Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln  
 50 55 60  
 Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser  
 65 70 75 80  
 30 Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp  
 85 90 95  
 Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser  
 100 105 110  
 Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn  
 115 120 125  
 35 Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly  
 130 135 140  
 Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val  
 145 150 155 160  
 40 Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser  
 165 170 175  
 Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro  
 180 185 190  
 Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly  
 195 200 205  
 45 Tyr Asn Trp Tyr Trp Ser Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr  
 210 215 220  
 Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr  
 225 230 235 240  
 Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His Tyr Pro  
 245 250 255  
 50 Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr  
 260 265 270  
 Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly  
 275 280 285  
 55 Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys  
 290 295 300  
 Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys  
 305 310 315 320  
 Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val  
 325 330 335  
 60 Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn  
 340 345 350  
 Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg  
 355 360 365  
 65 Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn  
 370 375 380  
 Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met  
 385 390 395 400  
 70 Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 405 410

(2) INFORMATION FOR SEQ ID NO:370

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 amino acids



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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys  
1 5 10 15  
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Ala Leu Met  
20 25 30  
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser  
35 40 45  
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg  
50 55 60  
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile  
65 70 75 80  
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp  
85 90 95  
Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu  
100 105 110  
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu  
115 120 125  
Pro Glu Met Gly Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr  
130 135 140  
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser  
145 150 155 160  
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn  
165 170 175  
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg  
180 185 190  
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly  
195 200 205  
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu  
210 215 220  
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His  
225 230 235 240  
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp  
245 250 255  
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu  
260 265 270  
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu  
275 280 285  
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp  
290 295 300  
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser  
305 310 315 320  
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu  
325 330 335  
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met  
340 345 350  
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala  
355 360 365  
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln  
370 375 380  
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg  
385 390 395 400  
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp  
405 410 415  
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly  
420 425 430  
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile  
435 440 445  
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu  
450 455 460  
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

```

Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
1      5      10      15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20     20     25     30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35     40     45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50     55     60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
65     70     75     80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85     90     95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
100    105    110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115    120    125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
130    135    140
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
145    150    155    160
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
165    170    175
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
180    185    190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
195    200    205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
210    215    220
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
225    230    235    240
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
245    250    255
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
260    265    270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
275    280    285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly
290    295    300
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
305    310    315    320
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
325    330    335
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
340    345    350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
355    360    365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
370    375    380
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
385    390    395    400
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
405    410    415
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
420    425    430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
435    440    445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
450    455    460
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp

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100 105 110  
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
 115 120 125  
 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
 130 135 140  
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
 145 150 155 160  
 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
 165 170 175  
 10 Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile  
 180 185 190  
 Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln  
 195 200 205  
 15 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile  
 210 215 220  
 Gly Phe Phe Asn Ala Glu Ile Gln Pro Asn Gly Asn Phe Met Ile  
 225 230 235 240  
 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala  
 245 250 255  
 20 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala  
 260 265 270  
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 275 280 285  
 25 (2) INFORMATION FOR SEQ ID NO:374  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...378  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374  
 45 Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly  
 1 5 10 15  
 Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His  
 20 25 30  
 50 Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala  
 35 40 45  
 Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser  
 50 55 60  
 Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu  
 65 70 75 80  
 55 Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu  
 85 90 95  
 Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp  
 100 105 110  
 60 Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser  
 115 120 125  
 Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser  
 130 135 140  
 Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala  
 145 150 155 160  
 65 Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser  
 165 170 175  
 Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe  
 180 185 190  
 70 Ser Val Gly Ile His Glu Arg Ala His Trp Glu Glu Ala Gly Ser  
 195 200 205  
 Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu  
 210 215 220  
 Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala  
 225 230 235 240  
 75 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu

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245 250 255  
 Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro  
 260 265 270  
 5 Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser  
 275 280 285  
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe  
 290 295 300  
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile  
 305 310 315 320  
 10 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr  
 325 330 335  
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys  
 340 345 350  
 15 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly  
 355 360 365  
 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn  
 370 375  
 (2) INFORMATION FOR SEQ ID NO:375  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1269 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1269  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375  
 Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu  
 1 5 10 15  
 Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu  
 20 25 30  
 Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp  
 35 40 45  
 45 Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu  
 50 55 60  
 Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly  
 65 70 75 80  
 50 Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr  
 85 90 95  
 55 Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn  
 100 105 110  
 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys  
 115 120 125  
 55 Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser  
 130 135 140  
 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys  
 145 150 155 160  
 60 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu  
 165 170 175  
 Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 180 185 190  
 Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 195 200 205  
 65 Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile  
 210 215 220  
 Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg  
 225 230 235 240  
 70 Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 245 250 255  
 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 260 265 270  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 275 280 285  
 75 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys

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290 295 300  
 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg  
 305 310 315 320  
 5 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys  
 325 330 335  
 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu  
 340 345 350  
 Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 355 360 365  
 10 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu  
 370 375 380  
 Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 385 390 395 400  
 15 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 405 410 415  
 Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala  
 420 425 430  
 Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu  
 435 440 445  
 20 Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn  
 450 455 460  
 Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu  
 465 470 475 480  
 25 Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser  
 485 490 495  
 Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys  
 500 505 510  
 Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu  
 515 520 525  
 30 Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly  
 530 535 540  
 Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys  
 545 550 555 560  
 35 Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile  
 565 570 575  
 Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala  
 580 585 590  
 Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys  
 595 600 605  
 40 Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn  
 610 615 620  
 Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg  
 625 630 635 640  
 45 Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr  
 645 650 655  
 Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala  
 660 665 670  
 Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu  
 675 680 685  
 50 Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu  
 690 695 700  
 Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys  
 705 710 715 720  
 55 Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro  
 725 730 735  
 Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu  
 740 745 750  
 Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile  
 755 760 765  
 60 Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val  
 770 775 780  
 Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp  
 785 790 795 800  
 65 Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp  
 805 810 815  
 Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu  
 820 825 830  
 His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly  
 835 840 845  
 70 Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp  
 850 855 860  
 Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp  
 865 870 875 880  
 75 Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val  
 885 890 895

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Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile  
 900 905 910  
 Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp  
 915 920 925  
 5 Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu  
 930 935 940  
 Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr  
 945 950 955 960  
 10 Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe  
 965 970 975  
 Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu  
 980 985 990  
 Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro  
 995 1000 1005  
 15 Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr  
 1010 1015 1020  
 Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu  
 1025 1030 1035 1040  
 20 Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His  
 1045 1050 1055  
 Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala  
 1060 1065 1070  
 Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val  
 1075 1080 1085  
 25 Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr  
 1090 1095 1100  
 Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu  
 1105 1110 1115 1120  
 30 Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile  
 1125 1130 1135  
 Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro  
 1140 1145 1150  
 Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile  
 1155 1160 1165  
 35 Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro  
 1170 1175 1180  
 Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro  
 1185 1190 1195 1200  
 40 Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln  
 1205 1210 1215  
 Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala  
 1220 1225 1230  
 Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala  
 1235 1240 1245  
 45 Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu  
 1250 1255 1260  
 Val Asn Thr Asp Glu  
 1265  
 50 (2) INFORMATION FOR SEQ ID NO:376  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 amino acids  
 55 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 65 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...231  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376  
 70 Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu  
 1 5 10 15  
 Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg  
 20 25 30  
 75 Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val  
 35 40 45

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Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly  
 50 55 60  
 Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly  
 65 70 75 80  
 5 Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn  
 85 90 95  
 Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly  
 100 105 110  
 10 Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys  
 115 120 125  
 Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu  
 130 135 140  
 Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro  
 145 150 155 160  
 15 Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp  
 165 170 175  
 Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys  
 180 185 190  
 20 Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln  
 195 200 205  
 Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala  
 210 215 220  
 Gln Thr Val Ser Gln Gln Lys  
 225 230  
 25 (2) INFORMATION FOR SEQ ID NO:377  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 563 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...563  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377  
 45 Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser  
 1 5 10 15  
 Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe  
 20 25 30  
 50 Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala  
 35 40 45  
 Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu  
 50 55 60  
 55 Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr  
 65 70 75 80  
 Val Met Thr His Ser Gly Tyr Asp Thr Gly Asn Ser Asn Val Lys Ile  
 85 90 95  
 Phe Arg Ser Lys Asp Gln Gly Ala Thr Tyr Gln Lys Leu Arg Asp Trp  
 100 105 110  
 60 Asp Pro Ser Asp Asp Tyr Gln Phe Gln Asp Phe Asp Ile Val Val Thr  
 115 120 125  
 Gly Lys Asn Glu Ser Asp Ile Lys Ile Trp Ser Val Glu Leu Met Asn  
 130 135 140  
 65 Lys Pro Gly Gly Tyr Lys Ser Arg Val Ala Val Phe Ser Arg Asp Ala  
 145 150 155 160  
 Asn Ala Gln Asn Ala Lys Leu Val Tyr Lys Glu Asp Phe Ser Asn Val  
 165 170 175  
 Gln Leu Tyr Asp Val Asp Ile Ala Ser Asn Tyr Arg Ser Pro Ser Ser  
 180 185 190  
 70 Leu Asn Asn Gly Gly Asn Pro Phe Ala Leu Ala Phe Ala Tyr Thr Gly  
 195 200 205  
 Phe Asn Asn Thr His Lys Ile Ser Phe Val Asp Tyr Val Phe Ser Leu  
 210 215 220  
 75 Asn Gly Gly Gln Asn Phe Asn Lys Asn Leu Leu Phe Ser Gln Asp Gly  
 225 230 235 240

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Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu  
 245 250 255  
 Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met  
 260 265 270  
 5 Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val  
 275 280 285  
 Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu  
 290 295 300  
 10 Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp  
 305 310 315 320  
 Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr  
 325 330 335  
 Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr  
 340 345 350  
 15 Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp  
 355 360 365  
 Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn  
 370 375 380  
 20 Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr  
 385 390 395 400  
 Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala  
 405 410 415  
 Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr  
 420 425 430  
 25 Tyr Thr Ser Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn  
 435 440 445  
 Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly  
 450 455 460  
 30 Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val  
 465 470 475 480  
 Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro  
 485 490 495  
 Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys  
 500 505 510  
 35 Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe  
 515 520 525  
 Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr  
 530 535 540  
 40 Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu  
 545 550 555 560  
 Ile Val Glu

- 45 (2) INFORMATION FOR SEQ ID NO:378  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 60 (B) LOCATION 1...786  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

65 Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met  
 1 5 10 15  
 Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala  
 20 25 30  
 Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr  
 35 40 45  
 70 Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn  
 50 55 60  
 Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn  
 65 70 75 80  
 75 Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp  
 85 90 95

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Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His  
 100 105 110  
 Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu  
 115 120 125  
 5 Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly Ser  
 130 135 140  
 Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu  
 145 150 155 160  
 10 Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala  
 165 170 175  
 Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn  
 180 185 190  
 Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu  
 195 200 205  
 15 Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr  
 210 215 220  
 Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg  
 225 230 235 240  
 20 Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val  
 245 250 255  
 Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly  
 260 265 270  
 Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe  
 275 280 285  
 25 Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe  
 290 295 300  
 Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu  
 305 310 315 320  
 30 Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile  
 325 330 335  
 Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu  
 340 345 350  
 Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu  
 355 360 365  
 35 Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu  
 370 375 380  
 Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg  
 385 390 395 400  
 40 Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu  
 405 410 415  
 Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu  
 420 425 430  
 Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr  
 435 440 445  
 45 Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile  
 450 455 460  
 Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala  
 465 470 475 480  
 50 Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro  
 485 490 495  
 Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu  
 500 505 510  
 Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu  
 515 520 525  
 55 Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu  
 530 535 540  
 Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr  
 545 550 555 560  
 60 Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe  
 565 570 575  
 Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro  
 580 585 590  
 Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His  
 595 600 605  
 65 Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser  
 610 615 620  
 Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr Asn  
 625 630 635 640  
 70 Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu  
 645 650 655  
 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe  
 660 665 670  
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met  
 675 680 685  
 75 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro

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690 695 700  
 Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg  
 705 710 715 720  
 5 Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr  
 725 730 735  
 Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val  
 740 745 750  
 Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His  
 755 760 765  
 10 Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg  
 770 775 780  
 Pro Arg  
 785  
 15 (2) INFORMATION FOR SEQ ID NO:379  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 814 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 30 (B) LOCATION 1...814  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379  
 35 Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly  
 1 5 10 15  
 Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Gly Thr  
 20 25 30  
 40 Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln  
 35 40 45  
 Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln  
 50 55 60  
 Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys  
 65 70 75 80  
 45 Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu  
 85 90 95  
 Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg  
 100 105 110  
 50 Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu  
 115 120 125  
 Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile  
 130 135 140  
 Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn  
 145 150 155 160  
 55 Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn  
 165 170 175  
 Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala  
 180 185 190  
 Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp  
 195 200 205  
 60 Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln  
 210 215 220  
 Leu Phe Ile Gly Lys Glu Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp  
 225 230 235 240  
 65 Thr Ala Leu Ser Leu Asn Leu Pro Met Gly Ser Val Thr Gly Leu Gly  
 245 250 255  
 Ile Val Gly Glu Asp Ile Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr  
 260 265 270  
 Val Ala Ala Asn Gln Ser Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser  
 275 280 285  
 70 Ala Asp Ser Arg Leu Tyr Val Thr Asp Arg Gly Leu Phe Ile Cys Ala  
 290 295 300  
 Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe  
 305 310 315 320  
 75 Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr

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325 330 335  
 Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala  
 340 345 350  
 Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly  
 355 360 365  
 5 Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala  
 370 375 380  
 Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val  
 385 390 395 400  
 10 Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val  
 405 410 415  
 Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile  
 420 425 430  
 15 Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly  
 435 440 445  
 Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser  
 450 455 460  
 Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val  
 465 470 475 480  
 20 Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly  
 485 490 495  
 Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp  
 500 505 510  
 25 His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn  
 515 520 525  
 Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg  
 530 535 540  
 Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly  
 545 550 555 560  
 30 Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe  
 565 570 575  
 Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met  
 580 585 590  
 Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile  
 595 600 605  
 35 Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro  
 610 615 620  
 Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val  
 625 630 635 640  
 40 Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His  
 645 650 655  
 Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp  
 660 665 670  
 45 Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu  
 675 680 685  
 Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu  
 690 695 700  
 Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly  
 705 710 715 720  
 50 Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro  
 725 730 735  
 Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala  
 740 745 750  
 55 Gly Cys Ser Val Lys Ile Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln  
 755 760 765  
 Thr Glu Ser Val Thr Thr Glu Val Lys Trp Asn Ala Arg Gly Ala Asp  
 770 775 780  
 Gly Asn Arg Val Ala Ser Gly Val Tyr Ala Val Ala Val Tyr Asp Pro  
 785 790 795 800  
 60 Val Ser Lys Lys Ser Lys Leu Ile Arg Phe Ala Val Ile Arg  
 805 810

(2) INFORMATION FOR SEQ ID NO:380

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1162 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 75

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1162

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser	
	1				5					10					15		
10	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly	
				20				25						30			
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile	
				35				40					45				
15	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg	
				50			55					60					
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly	
	65					70				75					80		
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu	
					85					90				95			
20	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala	
				100					105					110			
	Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu	
				115				120					125				
25	His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp	
				130				135					140				
	Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala	
	145					150					155				160		
	Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu	
					165					170					175		
30	Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu	
				180					185					190			
	Ser	Phe	Ser	Ala	Val	Asn	Thr	Arg	Thr	Val	Lys	Phe	Pro	Leu	Arg	Gly	
				195				200					205				
35	Asn	Thr	Arg	Ser	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala	
				210				215					220				
	Lys	Ala	Arg	Ser	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn	
	225					230					235				240		
	Gly	Ile	Leu	Ile	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val	
					245					250					255		
40	Ser	Asn	Ser	Tyr	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr	
				260					265					270			
	Pro	Met	Asn	Ser	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser	
				275				280					285				
45	Met	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln	
				290				295				300					
	Asn	Asp	Leu	Arg	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser	
					310					315					320		
	Asn	Leu	Pro	Val	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu	
					325					330					335		
50	Val	Pro	Glu	Ser	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala	
				340					345					350			
	Ser	Leu	Val	Pro	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val	
				355				360					365				
55	Ala	Pro	Pro	Lys	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala	
				370				375					380				
	Val	Asp	Leu	Ser	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro	
				385				390				395			400		
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser	
					405					410					415		
60	Thr	Gln	Ala	Leu	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	
				420					425					430			
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe	
				435				440					445				
	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe	
				450				455					460				
65	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu	
				465				470				475			480		
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn	
					485				490					495			
70	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu	
				500					505					510			
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr	
				515				520					525				
75	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val	
				530			535					540					

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Asn Ile Gly Trp Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val  
 545 550 555 560  
 Arg Thr Pro Ala Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr  
 565 570 575  
 5 Glu Glu Asp Arg Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala  
 580 585 590  
 Ala Asp Asn Gly Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp  
 595 600 605  
 10 Thr Val Lys Arg Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln  
 610 615 620  
 Asp Val Tyr Pro His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly  
 625 630 635 640  
 Ala Lys Lys Lys Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu  
 645 650 655  
 15 Asn Tyr Ala Gly His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu  
 660 665 670  
 Leu Thr Leu Asn Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile  
 675 680 685  
 20 Trp Ile Thr Ala Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr  
 690 695 700  
 Ser Ala Gly Glu Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile  
 705 710 715 720  
 Met Phe Ser Thr Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile  
 725 730 735  
 25 Asn Gly Phe Met Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg  
 740 745 750  
 Tyr Arg Thr Met Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu  
 755 760 765  
 30 Ser Thr Val Phe Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met  
 770 775 780  
 Gly Asp Pro Ser Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu  
 785 790 795 800  
 Thr Ala Ile Asn Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met  
 805 810 815  
 35 Leu Lys Ser Leu Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu  
 820 825 830  
 Lys Gly Thr Phe Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val  
 835 840 845  
 40 Phe Asp Gly Arg Lys Lys Met Thr Ala Leu Glu Glu Glu Gly Asn Asp  
 850 855 860  
 Leu Ser Leu Val Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile  
 865 870 875 880  
 Ala Glu Val Lys Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys  
 885 890 895  
 45 Asp Val Asn Tyr Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr  
 900 905 910  
 Asn Glu Ser Thr Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg  
 915 920 925  
 50 Val Gln Pro Gly Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro  
 930 935 940  
 Glu Ile Ile Ser Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp  
 945 950 955 960  
 Glu Val Asn Pro Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn  
 965 970 975  
 55 Gly Ile Asn Ile Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys  
 980 985 990  
 Ile Asp Gly Arg Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr  
 995 1000 1005  
 60 Ser Ser Ala Thr Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro  
 1010 1015 1020  
 Ala Leu Ala Glu Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile  
 1025 1030 1035 1040  
 Phe Asn Asn Ala Val His His Asp Phe Ser Phe Arg Val Val Asp Gly  
 1045 1050 1055  
 65 Ile Ala Pro Asp Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg  
 1060 1065 1070  
 Glu Ser Ala Thr Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu  
 1075 1080 1085  
 70 Asn Val Ala Val Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser  
 1090 1095 1100  
 Leu Pro Val Lys Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile  
 1105 1110 1115 1120  
 Lys Trp Asp Leu Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe  
 1125 1130 1135  
 75 Tyr Leu Tyr Arg Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser

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Met Ala Lys Lys Met Ile Val Val Gly Gln  
 1140 1145 1150  
 1155 1160

5 (2) INFORMATION FOR SEQ ID NO:381

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 973 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (E) LOCATION 1...973

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

25 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu  
 1 5 10 15  
 Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys  
 20 25 30  
 Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile  
 30 35 40 45  
 Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln  
 50 55 60  
 Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu  
 65 70 75 80  
 35 Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr  
 85 90 95  
 Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu  
 100 105 110  
 Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp  
 40 115 120 125  
 Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys  
 130 135 140  
 Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala  
 145 150 155 160  
 45 Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu  
 165 170 175  
 Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu  
 180 185 190  
 Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr  
 50 195 200 205  
 Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala  
 210 215 220  
 Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn  
 225 230 235 240  
 55 Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu  
 245 250 255  
 Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr  
 260 265 270  
 Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys  
 60 275 280 285  
 Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr  
 290 295 300  
 Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser  
 305 310 315 320  
 65 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu  
 325 330 335  
 Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys  
 340 345 350  
 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln  
 70 355 360 365  
 Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu  
 370 375 380  
 Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile  
 385 390 395 400  
 75 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser

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405 410 415  
 Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His Asn Lys Leu Ile  
 420 425 430  
 5 Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr Gly Ile Thr His  
 435 440 445  
 Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu Asn Glu Lys Met  
 450 455 460  
 Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr Glu Leu His Lys  
 465 470 475 480  
 10 Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu Val Asn Gln Leu  
 485 490 495  
 Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr Pro Glu Trp Arg  
 500 505 510  
 15 Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile Asp Ser Phe Ala  
 515 520 525  
 Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu Gln Pro Glu Ser  
 530 535 540  
 Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu Gln Lys Ile Ile  
 545 550 555 560  
 20 Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu Ala Gly Gly Arg  
 565 570 575  
 Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys Asn Leu Ile Ile  
 580 585 590  
 25 Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr Asp Gln Ala His  
 595 600 605  
 Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr Glu Lys His Gly  
 610 615 620  
 Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val Glu Asn Leu Arg  
 625 630 635 640  
 30 Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly Ser Ala Phe Thr  
 645 650 655  
 Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro  
 660 665 670  
 35 Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro  
 675 680 685  
 Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe  
 690 695 700  
 Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile  
 705 710 715 720  
 40 Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser  
 725 730 735  
 Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro  
 740 745 750  
 45 Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu  
 755 760 765  
 Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile  
 770 775 780  
 Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile  
 785 790 795 800  
 50 Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu  
 805 810 815  
 Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys  
 820 825 830  
 55 Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu  
 835 840 845  
 Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys  
 850 855 860  
 Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln  
 865 870 875 880  
 60 Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys  
 885 890 895  
 Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr Ile Gln Gln Ile  
 900 905 910  
 65 Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu Ser Lys Asn Ile  
 915 920 925  
 Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro Ala Tyr Phe Ser  
 930 935 940  
 Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser Gln Tyr Arg Gln  
 945 950 955 960  
 70 Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr Val  
 965 970

(2) INFORMATION FOR SEQ ID NO:382

75

(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 563 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...563  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

His His Lys Thr Tyr Gln Thr Met Lys Lys Leu Leu Gln Ala Lys Ala  
 1 5 10 15  
 20 Leu Ile Leu Ala Leu Gly Leu Phe Gln Leu Pro Ala Ile Ala Gln Thr  
 20 25 30  
 Gln Met Gln Ala Asp Arg Thr Asn Gly Gln Phe Ala Thr Glu Glu Met  
 35 40 45  
 25 Gln Arg Ala Phe Gln Glu Thr Asn Pro Pro Ala Gly Pro Val Arg Ala  
 50 55 60  
 Ile Ala Glu Tyr Glu Arg Ser Ala Ala Val Leu Val Arg Tyr Pro Phe  
 65 70 75 80  
 Gly Ile Pro Met Glu Leu Ile Lys Glu Leu Ala Lys Asn Asp Lys Val  
 85 90 95  
 30 Ile Thr Ile Val Ala Ser Glu Ser Gln Lys Asn Thr Val Ile Thr Gln  
 100 105 110  
 Tyr Thr Gln Ser Gly Val Asn Leu Ser Asn Cys Asp Phe Ile Ile Ala  
 115 120 125  
 35 Lys Thr Asp Ser Tyr Trp Thr Arg Asp Tyr Thr Gly Trp Phe Ala Met  
 130 135 140  
 Tyr Asp Thr Asn Lys Val Gly Leu Val Asp Phe Ile Tyr Asn Arg Pro  
 145 150 155 160  
 Arg Pro Asn Asp Asp Glu Phe Pro Lys Tyr Glu Ala Gln Tyr Leu Gly  
 165 170 175  
 40 Ile Glu Met Phe Gly Met Lys Leu Lys Gln Thr Gly Gly Asn Tyr Met  
 180 185 190  
 Thr Asp Gly Tyr Gly Ser Ala Val Gln Ser His Ile Ala Tyr Thr Glu  
 195 200 205  
 45 Asn Ser Ser Leu Ser Gln Ala Gln Val Asn Gln Lys Met Lys Asp Tyr  
 210 215 220  
 Leu Gly Ile Thr His His Asp Val Val Gln Asp Pro Asn Gly Glu Tyr  
 225 230 235 240  
 Ile Asn His Val Asp Cys Trp Gly Lys Tyr Leu Ala Pro Asn Lys Ile  
 245 250 255  
 50 Leu Ile Arg Lys Val Pro Asp Asn His Pro Gln His Gln Ala Leu Glu  
 260 265 270  
 Asp Met Ala Ala Tyr Phe Ala Ala Gln Thr Cys Ala Trp Gly Thr Lys  
 275 280 285  
 55 Tyr Glu Val Tyr Arg Ala Leu Ala Thr Asn Glu Gln Pro Tyr Thr Asn  
 290 295 300  
 Ser Leu Ile Leu Asn Asn Arg Val Phe Val Pro Val Asn Gly Pro Ala  
 305 310 315 320  
 Ser Val Asp Asn Asp Ala Leu Asn Val Tyr Lys Thr Ala Met Pro Gly  
 325 330 335  
 60 Tyr Glu Ile Ile Gly Val Lys Gly Ala Ser Gly Thr Pro Trp Leu Gly  
 340 345 350  
 Thr Asp Ala Leu His Cys Arg Thr His Glu Val Ala Asp Lys Gly Tyr  
 355 360 365  
 65 Leu Tyr Ile Lys His Tyr Pro Ile Leu Gly Glu Gln Ala Gly Pro Asp  
 370 375 380  
 Tyr Lys Ile Glu Ala Asp Val Val Ser Cys Ala Asn Ala Thr Ile Ser  
 385 390 395 400  
 Pro Val Gln Cys Tyr Arg Ile Asn Gly Ser Gly Ser Phe Lys Ala  
 405 410 415  
 70 Ala Asp Met Thr Met Glu Ser Thr Gly His Tyr Thr Tyr Ser Phe Thr  
 420 425 430  
 Gly Leu Asn Lys Asn Asp Lys Val Glu Tyr Tyr Ile Ser Ala Ala Asp  
 435 440 445  
 75 Asn Ser Gly Arg Lys Glu Thr Tyr Pro Phe Ile Gly Glu Pro Asp Pro  
 450 455 460

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Phe Lys Phe Thr Cys Met Asn Glu Thr Asn Thr Cys Thr Val Thr Gly  
 465 470 475 480  
 Ala Ala Lys Ala Leu Arg Ala Trp Phe Asn Ala Gly Arg Ser Glu Leu  
 485 490 495  
 5 Ala Val Ser Val Ser Leu Asn Ile Ala Gly Thr Tyr Arg Ile Lys Leu  
 500 505 510  
 Tyr Asn Thr Ala Gly Glu Glu Val Ala Ala Met Thr Lys Glu Leu Val  
 515 520 525  
 10 Ala Gly Thr Ser Val Phe Ser Met Asp Val Tyr Ser Gln Ala Pro Gly  
 530 535 540  
 Thr Tyr Val Leu Val Val Glu Gly Asn Gly Ile Arg Glu Thr Met Lys  
 545 550 555 560  
 Ile Leu Lys

15 (2) INFORMATION FOR SEQ ID NO:383  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 20 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...437  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383  
 35 Thr Thr Asn Arg Lys Pro Asn Thr Asn Met Lys Leu Ser Ser Lys Lys  
 1 5 10 15  
 Ile Leu Ala Ile Ile Ala Leu Leu Thr Met Gly His Ala Val Gln Ala  
 20 25 30  
 40 Gln Phe Val Pro Ala Pro Thr Thr Gly Ile Arg Met Ser Val Thr Thr  
 35 40 45  
 Thr Lys Ala Val Gly Glu Lys Ile Glu Leu Leu Val His Ser Ile Glu  
 50 55 60  
 Lys Lys Gly Ile Trp Ile Asp Leu Asn Gly Asp Ala Thr Tyr Gln Gln  
 45 65 70 75 80  
 Gly Glu Glu Ile Thr Val Phe Asp Glu Ala Tyr His Glu Tyr Thr Ile  
 85 90 95  
 Gly Thr Gln Thr Leu Thr Ile Tyr Gly Asn Thr Thr Arg Leu Gly Cys  
 100 105 110  
 50 Arg Ser Thr Gly Ala Thr Ala Val Asp Val Thr Lys Asn Pro Asn Leu  
 115 120 125  
 Thr Tyr Leu Ala Cys Pro Lys Asn Asn Leu Lys Ser Leu Asp Leu Thr  
 130 135 140  
 Gln Asn Pro Lys Leu Leu Arg Val Trp Cys Asp Ser Asn Glu Ile Glu  
 55 145 150 155 160  
 Ser Leu Asp Leu Ser Gly Asn Pro Ala Leu Ile Ile Leu Gly Cys Asp  
 165 170 175  
 Arg Asn Lys Leu Thr Glu Leu Lys Thr Asp Asn Asn Pro Lys Leu Ala  
 180 185 190  
 60 Ser Leu Trp Cys Ser Asp Asn Asn Leu Thr Glu Leu Glu Ser Ala  
 195 200 205  
 Asn Pro Arg Leu Asn Asp Leu Trp Cys Phe Gly Asn Arg Ile Thr Lys  
 210 215 220  
 65 Leu Asp Leu Ser Ala Asn Pro Leu Leu Val Thr Leu Trp Cys Ser Asp  
 225 230 235 240  
 Asn Glu Leu Ser Thr Leu Asp Leu Ser Lys Asn Ser Asp Val Ala Tyr  
 245 250 255  
 Leu Trp Cys Ser Ser Asn Lys Leu Thr Ser Leu Asn Leu Ser Gly Val  
 260 265 270  
 70 Lys Gly Leu Ser Val Leu Val Cys His Ser Asn Gln Ile Ala Gly Glu  
 275 280 285  
 Glu Met Thr Lys Val Val Asn Ala Leu Pro Thr Leu Ser Pro Gly Ala  
 290 295 300  
 75 Gly Ala Gln Ser Lys Phe Val Val Val Asp Leu Lys Asp Thr Asp Glu  
 305 310 315 320

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Lys Asn Ile Cys Thr Val Lys Asp Val Glu Lys Ala Lys Ser Lys Asn  
 325 330 335  
 Trp Arg Val Phe Asp Phe Asn Gly Asp Ser Asp Asn Met Leu Pro Tyr  
 340 345 350  
 5 Glu Gly Ser Pro Thr Ser Asn Leu Ala Val Asp Ala Pro Thr Val Arg  
 355 360 365  
 Ile Tyr Pro Asn Pro Val Gly Arg Tyr Ala Leu Val Glu Ile Pro Glu  
 370 375 380  
 10 Ser Leu Leu Gly Gln Glu Ala Ala Leu Tyr Asp Met Asn Gly Val Lys  
 385 390 395 400  
 Val Tyr Ser Phe Ala Val Glu Ser Leu Arg Gln Asn Ile Asp Leu Thr  
 405 410 415  
 His Leu Pro Asp Gly Thr Tyr Phe Phe Arg Leu Asp Asn Tyr Thr Thr  
 420 425 430  
 15 Lys Leu Ile Lys Gln  
 435

(2) INFORMATION FOR SEQ ID NO:384

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 amino acids  
 (R) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...318  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Asn His Leu Lys Thr Asn Ile Lys Met Arg Lys Thr Ile Ile Phe Cys  
 1 5 10 15  
 40 Leu Leu Leu Ala Leu Phe Gly Cys Ser Trp Ala Gln Glu Arg Val Asp  
 20 25 30  
 Glu Lys Val Phe Ser Ala Gly Thr Ser Ile Phe Arg Gly Ile Leu Glu  
 35 40 45  
 45 Lys Val Lys Ala Pro Leu Met Tyr Gly Asp Arg Glu Val Trp Gly Met  
 50 55 60  
 Ala Arg Ala Ser Glu Asp Phe Phe Phe Ile Leu Pro Val Thr Asp Asp  
 65 70 75 80  
 Leu Thr Pro Val Leu Phe Tyr Asn Arg Leu Thr Asn Glu Pro Cys Phe  
 85 90 95  
 50 Val Ser Asp Gln Gly Ile Thr Glu Tyr Phe Lys Phe Ala Gln Glu Gly  
 100 105 110  
 Asp Tyr Ile Glu Val Glu Gly Ser Ser Val Phe Met Ala Asn Leu Leu  
 115 120 125  
 55 Tyr Tyr Arg Phe Phe Pro Thr Arg Ile Thr Ser Tyr Asn Ala Pro Ile  
 130 135 140  
 Glu Gly Val Val Ser Lys Thr Gly Asn Pro Ala Phe Thr Ile Pro Met  
 145 150 155 160  
 Leu Pro Gly Val Ser Asp Cys Ile Glu Ile Ser Asn Asn Arg Lys Val  
 165 170 175  
 60 Phe Leu Thr Asn Gln Leu Gly Val Val Asn Ile Thr Asp Gly Met Glu  
 180 185 190  
 Pro Pro Ile Ile Ala Gly Val Ser Ala Ser Tyr Gly Ser Ser Val Arg  
 195 200 205  
 65 Val Tyr Gly His Val Ser Gln Arg Trp Asp Ile Ile Gly His Cys Tyr  
 210 215 220  
 Leu Asp Ile Tyr Pro Thr Asn Cys Tyr Pro Leu Ser Thr Lys Pro Val  
 225 230 235 240  
 Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gly Arg Gln Ile Glu  
 245 250 255  
 70 Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu  
 260 265 270  
 Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu  
 275 280 285  
 75 Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr  
 290 295 300

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Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu  
305 310 315

5 (2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 461 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

25 Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe  
1 5 10 15  
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg  
20 25 30  
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser  
35 40 45  
30 Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser  
50 55 60  
Leu Ile Val Phe Gly Ala Phe Phe Ala Ala Val Gly Gln Thr Lys Asp  
65 70 75 80  
35 Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val  
85 90 95  
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp  
100 105 110  
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe  
115 120 125  
40 Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn  
130 135 140  
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg  
145 150 155 160  
45 Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala  
165 170 175  
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr  
180 185 190  
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser  
195 200 205  
50 Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile  
210 215 220  
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn  
225 230 235 240  
55 Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr  
245 250 255  
Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp  
260 265 270  
Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp  
275 280 285  
60 Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile  
290 295 300  
Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp  
305 310 315 320  
65 Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser  
325 330 335  
Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg  
340 345 350  
Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile  
355 360 365  
70 Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro  
370 375 380  
Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg  
385 390 395 400  
75 Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu  
405 410 415

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Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu  
 420 425 430  
 Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn  
 435 440 445  
 5 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:386

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...451
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys  
 1 5 10 15  
 30 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr  
 20 25 30  
 Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr  
 35 40 45  
 Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His  
 50 55 60  
 Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val  
 65 70 75 80  
 Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val  
 85 90 95  
 40 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro  
 100 105 110  
 Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Ser Ser Gly  
 115 120 125  
 45 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro  
 130 135 140  
 Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro  
 145 150 155 160  
 Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu  
 165 170 175  
 50 Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr  
 180 185 190  
 Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile  
 195 200 205  
 55 Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile  
 210 215 220  
 Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys  
 225 230 235 240  
 Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala  
 245 250 255  
 60 Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His  
 260 265 270  
 Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro  
 275 280 285  
 65 Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn  
 290 295 300  
 Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala  
 305 310 315 320  
 Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu  
 325 330 335  
 70 Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg  
 340 345 350  
 Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp  
 355 360 365  
 75 Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr  
 370 375 380

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Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala  
 305 390 395 400  
 Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu  
 405 410 415  
 5 Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp Thr Ser Lys  
 420 425 430  
 Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met Leu Tyr Lys  
 435 440 445  
 10 Glu Met Asn  
 450

## (2) INFORMATION FOR SEQ ID NO:387

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 25 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...195
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

Met Asp Lys Val Ser Tyr Ala Leu Gly Leu Ser Ile Gly Asn Asn Phe  
 1 5 10 15  
 35 Lys Ser Ser Gly Ile Asp Ser Val Val Met Asp Asp Phe Met Gln Gly  
 20 25 30  
 Leu Ser Asp Val Leu Glu Glu Lys Ala Pro Gln Leu Ser Tyr Asp Glu  
 35 40 45  
 Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met Asp Leu Gln Gln Lys Ala  
 50 55 60  
 40 Val Lys Leu Asn Lys Glu Ala Glu Glu Phe Leu Lys Ile Asn Ala  
 65 70 75 80  
 His Lys Glu Gly Val Thr Thr Leu Pro Ser Gly Leu Gln Tyr Glu Val  
 85 90 95  
 45 Ile Lys Met Gly Glu Gly Pro Lys Pro Thr Leu Ser Asp Thr Val Thr  
 100 105 110  
 Cys His Tyr His Gly Thr Leu Ile Asn Gly Ile Val Phe Asp Ser Ser  
 115 120 125  
 Met Asp Arg Gly Glu Pro Ala Ser Phe Pro Leu Arg Gly Val Ile Ala  
 130 135 140  
 50 Gly Trp Thr Glu Ile Leu Gln Leu Met Pro Val Gly Ser Lys Trp Lys  
 145 150 155 160  
 Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly Asp Arg Gly Ala Gly Glu  
 165 170 175  
 55 His Ile Lys Pro Gly Ser Thr Leu Ile Phe Ile Ile Glu Leu Leu Ser  
 180 185 190  
 Ile Asn Lys  
 195

- 60 (2) INFORMATION FOR SEQ ID NO:388
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...273
- 75

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115 120 125  
 Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu  
 130 135 140  
 Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys  
 145 150 155 160  
 Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn  
 165 170 175  
 Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu  
 180 185 190  
 10 Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr  
 195 200 205  
 Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr  
 210 215 220  
 Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly  
 225 230 235 240  
 Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val  
 245 250 255  
 Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile  
 260 265 270  
 20 Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile  
 275 280 285  
 Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala  
 290 295 300  
 Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr  
 305 310 315 320  
 Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His  
 325 330 335  
 Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro  
 340 345 350  
 30 Thr Lys Lys Asp Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu  
 355 360 365  
 Ala Tyr Asp Lys Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His  
 370 375 380  
 Asn Leu Met Arg Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe  
 385 390 395 400  
 35 Tyr Gly Trp Ser Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys  
 405 410 415  
 Lys Arg Arg Arg Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala  
 420 425 430  
 40 Cys Trp Val Trp His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro  
 435 440 445  
 His Pro Thr Pro Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu  
 450 455 460  
 45 Trp Val His Ala Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser  
 465 470 475 480  
 Met Lys Leu Tyr Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu  
 485 490 495  
 Pro Lys Glu Gly Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg  
 500 505 510  
 50 Ile Val Glu Lys Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val  
 515 520 525  
 Gln Tyr Leu Ser Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr  
 530 535 540  
 Glu Tyr Phe Val Glu Lys Ile Ile Val Glu  
 545 550

## (2) INFORMATION FOR SEQ ID NO:390

- 60 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...550  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

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Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile  
 1 5 10 15  
 Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp  
 20 25 30  
 Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp  
 35 40 45  
 Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met  
 50 55 60  
 Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser  
 65 70 75 80  
 Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu  
 85 90 95  
 Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly  
 100 105 110  
 Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu  
 115 120 125  
 Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His  
 130 135 140  
 Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro  
 145 150 155 160  
 Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro  
 165 170 175  
 Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val  
 180 185 190  
 Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu  
 195 200 205  
 Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln  
 210 215 220  
 Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro  
 225 230 235 240  
 Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met  
 245 250 255  
 Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val  
 260 265 270  
 Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Glu Glu  
 275 280 285  
 Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu  
 290 295 300  
 Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu  
 305 310 315 320  
 Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro  
 325 330 335  
 Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp  
 340 345 350  
 Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys  
 355 360 365  
 Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg  
 370 375 380  
 Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser  
 385 390 395 400  
 Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg  
 405 410 415  
 Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp  
 420 425 430  
 His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro  
 435 440 445  
 Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala  
 450 455 460  
 Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr  
 465 470 475 480  
 Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly  
 485 490 495  
 Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys  
 500 505 510  
 Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser  
 515 520 525  
 Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val  
 530 535 540  
 Glu Lys Ile Ile Val Glu  
 545 550

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(2) INFORMATION FOR SEQ ID NO:391

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Leu | Leu | Pro | Phe | Leu | Leu | Leu | Ala | Gly | Leu | Val | Ala | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Asn | Val | Ser | Ala | Gln | Ser | Pro | Arg | Ile | Pro | Gln | Val | Asp | Val | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Arg | Ile | Ala | Arg | Asn | Ala | Arg | Tyr | Arg | Leu | Asp | Lys | Ile | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Asp | Ser | Arg | Gln | Ile | Phe | Asp | Tyr | Phe | Tyr | Lys | Glu | Glu | Thr | Ile |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Pro | Thr | Lys | Ile | Gln | Thr | Thr | Thr | Gly | Gly | Ala | Ile | Thr | Ser | Ile | Asp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Phe | Tyr | Glu | Asp | Asp | Arg | Leu | Val | Gln | Val | Arg | Tyr | Phe | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asn | Asn | Leu | Glu | Leu | Lys | Gln | Ala | Glu | Lys | Tyr | Val | Tyr | Asp | Gly | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Val | Leu | Arg | Glu | Ile | Arg | Lys | Ser | Pro | Thr | Asp | Glu | Thr | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Lys | Val | Ser | Tyr | His | Tyr | Leu | Cys | Gly | Ser | Asp | Met | Pro | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Ile | Thr | Thr | Glu | Met | Ser | Asp | Gly | Tyr | Phe | Glu | Ser | His | Thr | Leu |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | Tyr | Leu | Asn | Gly | Lys | Ile | Ala | Arg | Ile | Asp | Ile | Met | Thr | Gln | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Pro | Ser | Ala | Glu | Leu | Ile | Glu | Thr | Gly | Arg | Met | Val | Tyr | Glu | Phe |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Asp | Ala | Asn | Asn | Asp | Ala | Val | Leu | Leu | Arg | Asp | Ser | Val | Phe | Leu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gln | Asn | Lys | Trp | Val | Glu | Met | Phe | Thr | His | Arg | Tyr | Thr | Tyr | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Lys | His | Asn | Cys | Ile | Arg | Trp | Glu | Gln | Asp | Glu | Phe | Gly | Thr | Leu |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |     |
| Thr | Leu | Ala | Asn | Asn | Phe | Glu | Tyr | Asp | Thr | Thr | Ile | Pro | Leu | Ser | Ser |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Leu | Phe | Pro | Thr | His | Glu | Glu | Phe | Phe | Arg | Pro | Leu | Leu | Pro | Asn |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Phe | Met | Lys | His | Met | Arg | Thr | Lys | Gln | Thr | Tyr | Phe | Asn | Asn | Ser | Gly |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Glu | Gly | Leu | Ser | Glu | Val | Cys | Asp | Tyr | Asn | Tyr | Phe | Tyr | Thr | Asp | Met |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Gln | Gly | Asn | Ala | Leu | Thr | Asp | Val | Ala | Val | Asn | Glu | Ser | Ile | Lys | Ile |
|     | 305 |     |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |     |
| Tyr | Pro | Arg | Pro | Ala | Thr | Asp | Phe | Leu | Arg | Ile | Glu | Gly | Ser | Gln | Leu |
|     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Arg | Leu | Ser | Leu | Phe | Asp | Met | Asn | Gly | Lys | Leu | Ile | Arg | Ala | Thr |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Glu | Leu | Thr | Gly | Asp | Leu | Ala | Ile | Ile | Gly | Val | Ala | Ser | Leu | Pro | Arg |
|     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |     |
| Gly | Thr | Tyr | Ile | Ala | Glu | Ile | Thr | Ala | Ala | Asn | Ser | Lys | Thr | Ile | Arg |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Ala | Lys | Val | Ser | Leu | Arg |     |     |     |     |     |     |     |     |     |     |
|     | 385 |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |
- (2) INFORMATION FOR SEQ ID NO:392
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu Leu  
1 5 10 15  
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln  
20 25 30  
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp  
35 40 45  
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu  
50 55 60  
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro  
65 70 75 80  
Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile  
85 90 95  
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser  
100 105 110  
Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val  
115 120 125  
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp  
130 135 140  
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys  
145 150 155 160  
Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile  
165 170 175  
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp  
180 185 190  
Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser  
195 200 205  
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr  
210 215 220  
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe  
225 230 235 240  
Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys  
245 250 255  
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala  
260 265 270  
Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg  
275 280 285 290  
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys  
295 300 305  
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly  
310 315 320  
Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile  
325 330 335  
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala  
340 345 350  
Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro  
355 360 365  
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile  
370 375 380  
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr  
385 390 395 400  
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
405 410

(2) INFORMATION FOR SEQ ID NO:393

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...246

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn Ala Val Tyr Pro  
 1 5 10 15  
 15 Glu Val Gly Ile Ala Thr Tyr Lys Leu Lys Ser Leu Asp Ile Asp  
 20 25 30  
 Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln Pro Met Ala Asn  
 35 40 45  
 20 Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu Arg Phe Glu Glu  
 50 55 60  
 Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser Ala Ser Cys Val  
 65 70 75 80  
 Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg Pro Thr Gly His  
 85 90 95  
 25 Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys Glu Phe Leu His  
 100 105 110  
 Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe Ala His Lys Val  
 115 120 125  
 30 Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu His Leu Ser Thr  
 130 135 140  
 Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val Arg Arg Leu Leu  
 145 150 155 160  
 Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys Arg Ile Asp Glu  
 165 170 175  
 35 Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu Pro Glu Val Ser  
 180 185 190  
 Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile Ser Thr Gly Ala  
 195 200 205  
 40 Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met His Met Gln Gly  
 210 215 220  
 Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile His Ala Val Glu  
 225 230 235 240  
 Ile Leu Ala Ala Asn Leu  
 245

45

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...246

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu Val Val Glu Met Arg  
 1 5 10 15  
 Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn  
 20 25 30  
 70 Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly  
 35 40 45  
 Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile  
 50 55 60  
 75 Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys  
 65 70 75 80

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Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln  
 85 90 95  
 Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe  
 100 105 110  
 5 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg  
 115 120 125  
 Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys  
 130 135 140  
 10 Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala  
 145 150 155 160  
 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr  
 165 170 175  
 Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr  
 180 185 190  
 15 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser  
 195 200 205  
 Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn  
 210 215 220  
 20 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg  
 225 230 235 240  
 Lys Asn Thr Glu Ile Asp

25 (2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...241

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

45 Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys  
 1 5 10 15  
 Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala  
 20 25 30  
 Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr  
 35 40 45  
 50 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala  
 50 55 60  
 Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro  
 65 70 75 80  
 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu  
 85 90 95  
 55 Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr  
 100 105 110  
 Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu  
 115 120 125  
 60 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu  
 130 135 140  
 Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala  
 145 150 155 160  
 65 Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser  
 165 170 175  
 Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln  
 180 185 190  
 Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His  
 195 200 205  
 70 Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser  
 210 215 220  
 Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile  
 225 230 235  
 75 Asp



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20 25 30  
 Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu  
 35 40 45  
 Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu  
 50 55 60  
 Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val  
 65 70 75 80  
 Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu  
 85 90 95  
 10 Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly  
 100 105 110  
 Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys  
 115 120 125  
 15 Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln Leu Ser Gly  
 130 135 140  
 Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val Ala Asn Pro  
 145 150 155 160  
 Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Lys Asn  
 165 170 175  
 20 Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg Glu Gly Ala  
 180 185 190  
 Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg Ser Ala Gly  
 195 200 205  
 25 Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg  
 210 215

(2) INFORMATION FOR SEQ ID NO:398

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 595 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...595  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

Met Lys Glu Phe Phe Lys Met Phe Phe Ala Ser Ile Leu Gly Val Ile  
 1 5 10 15  
 Thr Ala Gly Ile Ile Leu Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly  
 20 25 30  
 50 Ile Val Ala Gly Ile Ala Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys  
 35 40 45  
 Ile Glu Ala Asn Ser Ile Leu His Ile Unk Asn Ser Ser Phe Pro Glu  
 50 55 60  
 55 Ile Val Ser Ala Asn Pro Trp Ser Met Leu Thr Gly Lys Asp Glu Ser  
 65 70 75 80  
 Val Ser Leu Ser Gln Ala Val Glu Ala Ile Gly Gln Ala Lys Asn Asn  
 85 90 95  
 60 Pro Asn Ile Thr Gly Ile Phe Leu Asp Leu Asp Asn Leu Ser Val Gly  
 100 105 110  
 Met Ala Ser Ala Glu Glu Leu Arg Arg Ala Leu Gln Asp Phe Lys Met  
 115 120 125  
 Ser Gly Lys Phe Val Val Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly  
 130 135 140  
 65 Tyr Tyr Leu Ser Ser Ile Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly  
 145 150 155 160  
 Met Leu Gly Leu Ile Gly Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp  
 165 170 175  
 70 Ala Leu Asp Lys Phe Gly Val Lys Met Glu Ile Phe Lys Val Gly Thr  
 180 185 190  
 Tyr Lys Ala Ala Val Glu Pro Phe Met Leu Asn Arg Met Ser Asp Ala  
 195 200 205  
 Asn Arg Glu Gln Ile Thr Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile  
 210 215 220  
 75 Thr Ser Asp Ile Ala Glu Ser Arg Lys Thr Ala Met Asp Ser Val Lys

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225 230 235 240  
 Met Phe Ala Asp Lys Gly Glu Met Phe Gly Leu Ala Glu Lys Ala Val  
 245 250 255  
 Glu Met Lys Leu Val Asp Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys  
 260 265 270  
 Glu Leu Lys Lys Met Ser Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe  
 275 280 285  
 Val Ser Leu Ser Gln Val Leu Ala Asn Gly Pro Met Asn Lys Thr Lys  
 290 295 300  
 10 Gly Ser Arg Ile Ala Val Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu  
 305 310 315 320  
 Ile Ile Lys Lys Pro Phe Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu  
 325 330 335  
 15 Leu Ala Lys Glu Ile Lys Ala Ala Ala Asp Asp Asp Ile Lys Ala  
 340 345 350  
 Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu  
 355 360 365  
 Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val  
 370 375 380  
 20 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys  
 385 390 395 400  
 Ala Ala Asn Ser Ile Val Ala Glu His Thr Thr Leu Thr Gly Ser Ile  
 405 410 415  
 25 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile  
 420 425 430  
 Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly  
 435 440 445  
 Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg  
 450 455 460  
 30 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly  
 465 470 475 480  
 Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val  
 485 490 495  
 35 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly  
 500 505 510  
 Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly  
 515 520 525  
 Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu  
 530 535 540  
 40 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser  
 545 550 555 560  
 Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser  
 565 570 575  
 45 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe  
 580 585 590  
 Met Pro Tyr  
 595  
 (2) INFORMATION FOR SEQ ID NO:399  
 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 65 (B) LOCATION 1...589  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399  
 70 Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu  
 1 5 10 15  
 Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala  
 20 25 30  
 Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile  
 35 40 45  
 75 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro

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50 55 60  
 Trp Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala  
 65 70 75 80  
 Val Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile  
 85 90 95  
 Phe Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu  
 100 105 110  
 Leu Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val  
 115 120 125  
 Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile  
 130 135 140  
 Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly  
 145 150 155 160  
 Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly  
 165 170 175  
 Val Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu  
 180 185 190  
 Pro Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr  
 195 200 205  
 Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu  
 210 215 220  
 Ser Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly  
 225 230 235 240  
 Glu Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp  
 245 250 255  
 Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser  
 260 265 270  
 Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val  
 275 280 285  
 Leu Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val  
 290 295 300  
 Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe  
 305 310 315 320  
 Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys  
 325 330 335  
 Ala Ala Ala Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn  
 340 345 350  
 Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val  
 355 360 365  
 Ala Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val  
 370 375 380  
 Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val  
 385 390 395 400  
 Ala Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe  
 405 410 415  
 Pro Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val  
 420 425 430  
 Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met  
 435 440 445  
 Thr Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr  
 450 455 460  
 Asp Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala  
 465 470 475 480  
 Gln Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala  
 485 490 495  
 Leu Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile  
 500 505 510  
 Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu  
 515 520 525  
 Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser  
 530 535 540  
 Ala Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro  
 545 550 555 560  
 Glu Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser  
 565 570 575  
 Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr  
 580 585

(2) INFORMATION FOR SEQ ID NO: 400

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

15 Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe  
1 5 10 15  
Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu  
20 20 25 30  
Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg  
35 40 45  
20 Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr  
50 55 60  
Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn Asn His Phe Gly  
65 70 75 80  
Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp  
25 85 90 95  
Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser  
100 105 110  
Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu  
115 120 125  
30 Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln  
130 135 140  
Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys  
145 150 155 160  
35 Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro  
165 170 175  
Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln  
180 185 190  
Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser  
195 200 205  
40 Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser  
210 215 220  
Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn  
225 230 235 240  
45 Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu  
245 250 255  
Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val  
260 265 270  
Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg  
275 280 285  
50 Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro  
290 295 300  
Gln Glu Gly Asp Ile Leu Arg Leu Arg  
305 310

55 (2) INFORMATION FOR SEQ ID NO:401

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 523 amino acids  
60 (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
70 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

75 Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala

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1 Lys Glu His Val Lys Val Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile  
 20 25 30  
 5 Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr  
 35 40 45  
 Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu  
 50 55 60  
 Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met  
 65 70 75 80  
 10 Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile  
 85 90 95  
 Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly  
 100 105 110  
 15 Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu  
 115 120 125  
 Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu  
 130 135 140  
 Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala  
 145 150 155 160  
 20 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val  
 165 170 175  
 Lys Lys Ala Gly Gly Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser  
 180 185 190  
 25 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp  
 195 200 205  
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg  
 210 215 220  
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe  
 225 230 235 240  
 30 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu  
 245 250 255  
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His  
 260 265 270  
 35 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr  
 275 280 285  
 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val  
 290 295 300  
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala  
 305 310 315 320  
 40 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu  
 325 330 335  
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala  
 340 345 350  
 45 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln  
 355 360 365  
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln  
 370 375 380  
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile  
 385 390 395 400  
 50 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala  
 405 410 415  
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile  
 420 425 430  
 55 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met  
 435 440 445  
 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp  
 450 455 460  
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met  
 465 470 475 480  
 60 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg  
 485 490 495  
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg  
 500 505 510  
 65 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg  
 515 520

(2) INFORMATION FOR SEQ ID NO:402

70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...375

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

Met Asn Phe Leu Lys Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr  
 1 5 10 15  
 Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val  
 20 25 30  
 Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg Val Ser Leu  
 35 40 45  
 Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys  
 50 55 60  
 Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu  
 65 70 75 80  
 Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu  
 85 90 95  
 Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile  
 100 105 110  
 Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile  
 115 120 125  
 Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg  
 130 135 140  
 Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr  
 145 150 155 160  
 Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys  
 165 170 175  
 Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp  
 180 185 190  
 Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln  
 195 200 205  
 Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu  
 210 215 220  
 Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser  
 225 230 235 240  
 Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu  
 245 250 255  
 Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala  
 260 265 270  
 Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu  
 275 280 285  
 Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr  
 290 295 300  
 Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro  
 305 310 315 320  
 Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp  
 325 330 335  
 Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val  
 340 345 350  
 Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe  
 355 360 365  
 Val Glu Ile Gly Tyr Met Asn  
 370 375

(2) INFORMATION FOR SEQ ID NO:403

(1) SEQUENCE CHARACTERISTICS:

65 (A) LENGTH: 362 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

70 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

5 Met Ile Tyr Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu  
1 5 10 15  
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg  
20 25 30  
10 Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln  
35 40 45  
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly  
50 55 60  
15 Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile  
65 70 75 80  
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn  
85 90 95  
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile  
100 105 110  
20 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile  
115 120 125  
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val  
130 135 140  
25 Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly  
145 150 155 160  
Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val  
165 170 175  
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu  
180 185 190  
30 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val  
195 200 205  
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu  
210 215 220  
35 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser  
225 230 235 240  
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu  
245 250 255  
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met  
260 265 270  
40 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp  
275 280 285  
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe  
290 295 300  
45 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu  
305 310 315 320  
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu  
325 330 335  
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys  
340 345 350  
50 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:404

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 640 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
60 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
(vi) ORIGINAL SOURCE:  
65 (A) ORGANISM: Porphyromonas gingivalis  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...640  
70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val  
1 5 10 15  
75 Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly

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20 25 30  
 Lys Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg  
 35 40 45  
 5 Lys Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys  
 50 55 60  
 Thr Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val  
 65 70 75 80  
 Ser Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn  
 85 90 95  
 10 Asn Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu  
 100 105 110  
 Ile Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr  
 115 120 125  
 15 Leu Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe  
 130 135 140  
 Asn Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly  
 145 150 155 160  
 Leu Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala  
 165 170 175  
 20 Tyr Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp  
 180 185 190  
 Leu Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly  
 195 200 205  
 25 Val Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp  
 210 215 220  
 Asp Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser  
 225 230 235 240  
 Gln Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu  
 245 250 255  
 30 Lys Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser  
 260 265 270  
 Thr Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys  
 275 280 285  
 35 His Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp  
 290 295 300  
 Arg Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp  
 305 310 315 320  
 Ala Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly  
 325 330 335  
 40 Ser Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly  
 340 345 350  
 Lys Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly  
 355 360 365  
 45 Ala Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu  
 370 375 380  
 Leu Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly  
 385 390 395 400  
 Val Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys  
 405 410 415  
 50 Ser Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile  
 420 425 430  
 His Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile  
 435 440 445  
 55 Gly Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro  
 450 455 460  
 Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val  
 465 470 475 480  
 Thr Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu  
 485 490 495  
 60 Ala Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu  
 500 505 510  
 Ala Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp  
 515 520 525  
 65 Lys Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu  
 530 535 540  
 Lys Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp  
 545 550 555 560  
 Thr Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala  
 565 570 575  
 70 Ala Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala  
 580 585 590  
 Gly Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln  
 595 600 605  
 75 Pro Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln  
 610 615 620

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Pro Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
 625 630 635 640

## (2) INFORMATION FOR SEQ ID NO:405

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 449 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...449
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405
- Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr  
 1 5 10 15  
 Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu  
 20 25 30  
 Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr  
 35 40 45  
 Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala  
 50 55 60  
 Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys  
 65 70 75 80  
 Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile  
 85 90 95  
 Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala  
 100 105 110  
 Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly  
 115 120 125  
 Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu  
 130 135 140  
 Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr  
 145 150 155 160  
 Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile  
 165 170 175  
 Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly  
 180 185 190  
 Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn  
 195 200 205  
 Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys  
 210 215 220  
 Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn  
 225 230 235 240  
 Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly  
 245 250 255  
 Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe  
 260 265 270  
 Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu  
 275 280 285  
 Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr  
 290 295 300  
 Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala  
 305 310 315 320  
 Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala  
 325 330 335  
 Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu  
 340 345 350  
 Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg  
 355 360 365  
 Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly  
 370 375 380  
 Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly  
 385 390 395 400  
 Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala  
 405 410 415



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Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg Ile Ile  
 420 425 430  
 Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu Ala Gly  
 435 440 445  
 5 Gly

(2) INFORMATION FOR SEQ ID NO:406

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 941 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...941

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu Leu Val Gly Phe  
 1 5 10 15  
 30 Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro Leu Pro Thr Asp  
 20 25 30  
 Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu Thr Tyr Phe Ile  
 35 35 40 45  
 Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe Ile Ala Gln  
 50 55 60  
 35 Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser Gly Leu Ala His  
 65 70 75 80  
 Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn Phe Pro Gly Lys  
 85 90 95  
 40 Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg Phe Gly Gln Asn  
 100 105 110  
 Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr Thr Ile Met Asp  
 115 120 125  
 45 Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys Leu Leu Ile Leu  
 130 135 140  
 His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His Glu Ile Asp Glu  
 145 150 155 160  
 Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg Arg Asp Ala Asn  
 165 170 175  
 50 Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met Pro Gly Asn Lys  
 180 185 190  
 Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val Val Leu Asn Phe  
 195 200 205  
 55 Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp Tyr Arg Pro Asp  
 210 215 220  
 Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val Asp Tyr Val Glu  
 225 230 235 240  
 Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala Pro Val Asn Pro  
 245 250 255  
 60 Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp Glu Pro Ile Val  
 260 265 270  
 Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln Leu Ser Ile Ser  
 275 280 285  
 65 Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly Ser Ile Phe Gly  
 290 295 300  
 Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr Ala Val Asn Glu  
 305 310 315 320  
 Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro Phe Leu Ser Ala  
 325 330 335  
 70 Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln Thr Lys Asp Ala  
 340 345 350  
 Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala Glu Lys Ala Met  
 355 360 365  
 75 Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln Phe Gly Ile Thr  
 370 375 380

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Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu Lys Arg Tyr Glu  
 385 390 395 400  
 Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn Ala Tyr Ala Asn  
 405 410 415  
 5 Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile Pro Gly Ile Glu  
 420 425 430  
 Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln Val Pro Leu Glu  
 435 440 445  
 10 Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro Val Lys Asn Ala  
 450 455 460  
 Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala Lys Ile Pro Ser  
 465 470 475 480  
 Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg Gln Gln Lys Val  
 485 490 495  
 15 Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu Met Glu Lys Ala  
 500 505 510  
 Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp Gln Lys Phe Gly  
 515 520 525  
 20 Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys  
 530 535 540  
 Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly  
 545 550 555 560  
 Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser  
 565 570 575  
 25 Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp  
 580 585 590  
 Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro Leu Ser Leu  
 595 600 605  
 30 Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr  
 610 615 620  
 Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro  
 625 630 635 640  
 Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn  
 645 650 655  
 35 Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser Ile Arg His Thr  
 660 665 670  
 Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys Ala Ala Asp Val  
 675 680 685  
 40 Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr Asn Glu Arg Phe  
 690 695 700  
 Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly Asn Leu Asp Glu  
 705 710 715 720  
 Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala Ser Leu Pro Asn  
 725 730 735  
 45 Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val Pro Ala Ala Arg  
 740 745 750  
 Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met Asp Thr Pro Ser  
 755 760 765  
 50 Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu Tyr Thr Leu Lys  
 770 775 780  
 Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met Asp Gln Val Tyr  
 785 790 795 800  
 Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr Ser Val Ala Ala  
 805 810 815  
 55 Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala Leu Met Gln Ile  
 820 825 830  
 Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met Asn Ala Ile Val  
 835 840 845  
 60 Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro Asn Val Glu Tyr  
 850 855 860  
 Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His Lys Glu Ser Leu  
 865 870 875 880  
 Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala Ser Phe Phe Glu  
 885 890 895  
 65 Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu Asn Gly Leu Thr  
 900 905 910  
 Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu Lys Gln Gln Asn  
 915 920 925  
 70 Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala Gln  
 930 935 940

(2) INFORMATION FOR SEQ ID NO:407

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Met	Ser	Lys	Lys	Gly	Thr	Ile	Gly	Val	Thr	Ser	Asp	Asn	Ile	Phe	Pro	1	5	10	15
Val	Ile	Lys	Lys	Phe	Leu	Tyr	Ser	Asp	His	Glu	Ile	Phe	Leu	Arg	Glu	20	25	30	35
Ile	Val	Ser	Asn	Ala	Val	Asp	Ala	Thr	Gln	Lys	Leu	Lys	Thr	Leu	Thr	40	45	50	55
Ser	Val	Gly	Glu	Phe	Lys	Gly	Glu	Thr	Gly	Asp	Leu	Arg	Val	Thr	Val	60	65	70	75
Ser	Val	Asp	Glu	Val	Ala	Arg	Thr	Ile	Thr	Val	Ser	Asp	Arg	Gly	Val	80	85	90	95
Gly	Met	Thr	Glu	Glu	Val	Glu	Lys	Tyr	Ile	Asn	Gln	Ile	Ala	Phe		100	105	110	115
Ser	Ser	Ala	Glu	Glu	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Asp	Lys	Ala	Ala	120	125	130	135
Ile	Ile	Gly	His	Phe	Gly	Leu	Gly	Phe	Tyr	Ser	Ala	Phe	Met	Val	Ser	140	145	150	155
Glu	Arg	Val	Asp	Val	Ile	Thr	Arg	Ser	Phe	Arg	Glu	Asp	Ala	Thr	Ala	160	165	170	175
Val	Lys	Trp	Ser	Cys	Asp	Gly	Ser	Pro	Glu	Tyr	Thr	Leu	Glu	Pro	Ala	180	185	190	195
Asp	Lys	Ala	Asp	Arg	Gly	Thr	Asp	Ile	Val	Met	His	Ile	Asp	Glu	Glu	200	205	210	215
Asn	Ser	Glu	Phe	Leu	Lys	Lys	Glu	Lys	Ile	Glu	Gly	Leu	Leu	Gly	Lys	220	225	230	235
Tyr	Cys	Lys	Phe	Leu	Thr	Val	Pro	Ile	Ile	Phe	Gly	Lys	Lys	Gln	Glu	240	245	250	255
Trp	Lys	Asp	Gly	Lys	Met	Gln	Asp	Thr	Asp	Glu	Asp	Asn	Gln	Ile	Asn	260	265	270	275
Asp	Thr	His	Pro	Ala	Trp	Thr	Lys	Lys	Pro	Ala	Asp	Leu	Lys	Asp	Glu	280	285	290	295
Asp	Tyr	Lys	Glu	Phe	Tyr	Arg	Ser	Leu	Tyr	Pro	Met	Ser	Glu	Glu	Pro	300	305	310	315
Leu	Phe	Trp	Ile	His	Leu	Asn	Val	Asp	Tyr	Pro	Phe	Asn	Leu	Thr	Gly	320	325	330	335
Ile	Leu	Tyr	Phe	Pro	Lys	Ile	Lys	Asn	Asn	Leu	Asp	Leu	Gln	Arg	Asn	340	345	350	355
Lys	Ile	Gln	Leu	Tyr	Cys	Asn	Gln	Val	Tyr	Val	Thr	Asp	Glu	Val	Gln	360	365	370	375
Gly	Ile	Val	Pro	Asp	Phe	Leu	Thr	Leu	Leu	His	Gly	Val	Ile	Asp	Ser	380	385	390	395
Pro	Asp	Ile	Pro	Leu	Asn	Val	Ser	Arg	Ser	Tyr	Leu	Gln	Ser	Asp	Ala	400	405	410	415
Asn	Val	Lys	Lys	Ile	Ser	Ser	His	Ile	Thr	Lys	Lys	Val	Ala	Asp	Arg	420	425	430	435
Leu	Glu	Glu	Ile	Phe	Lys	Asn	Asp	Arg	Pro	Thr	Phe	Glu	Glu	Lys	Trp	440	445	450	455
Asp	Ser	Leu	Lys	Leu	Phe	Val	Glu	Tyr	Gly	Met	Leu	Thr	Asp	Glu	Lys	460	465	470	475
Phe	Tyr	Glu	Arg	Ala	Ala	Lys	Phe	Phe	Leu	Phe	Thr	Asp	Met	Asp	Gly	480	485	490	495
His	Lys	Tyr	Thr	Phe	Asp	Glu	Tyr	Arg	Thr	Leu	Val	Glu	Gly	Val	Gln	500	505	510	515
Thr	Asp	Lys	Asp	Gly	Gln	Val	Val	Tyr	Leu	Tyr	Ala	Thr	Asp	Lys	His	520	525	530	535
Gly	Gln	Tyr	Ser	His	Val	Lys	Arg	Ala	Ser	Asp	Lys	Gly	Tyr	Ser	Val	540	545	550	555
Met	Leu	Leu	Asp	Gly	Gln	Leu	Asp	Pro	His	Ile	Val	Ser	Leu	Leu	Glu	560	565	570	575
Gln	Lys	Leu	Glu	Lys	Thr	His	Phe	Val	Arg	Val	Asp	Ser	Asp	Thr	Ile	580	585	590	595



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210 215 220  
 Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly Ala Phe  
 225 230 235 240  
 Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala Asp Gly  
 245 250 255  
 5 Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly Asn Gln  
 260 265 270  
 Val Lys Leu Leu Arg Val Leu Gln Glu Thr Phe Glu Pro Leu Gly  
 275 280 285  
 10 Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala Thr Asn  
 290 295 300  
 Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp Leu  
 305 310 315 320  
 Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu Arg Glu  
 325 330 335  
 15 Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu Ala Phe  
 340 345 350  
 Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu Ala Met  
 355 360 365  
 20 Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu Leu Lys  
 370 375 380  
 Asn Val Val Glu Arg Thr Leu Leu Ser Gly Ser Arg Glu Ile Ser  
 385 390 395 400  
 25 Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala Asp His  
 405 410 415  
 Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile Arg Glu  
 420 425 430  
 Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg Ala Leu  
 435 440 445  
 30 Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr Gly Leu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:409

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...250  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile  
 1 5 10 15  
 55 Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile  
 20 25 30  
 Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val  
 35 40 45  
 60 Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly  
 50 55 60  
 Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu  
 65 70 75 80  
 Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val  
 85 90 95  
 65 Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala  
 100 105 110  
 Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg  
 115 120 125  
 70 Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu  
 130 135 140  
 Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala  
 145 150 155 160  
 Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu  
 165 170 175  
 75 Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg

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180 185 190  
 Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu  
 195 200 205  
 Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile  
 210 215 220  
 Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly  
 225 230 235 240  
 Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu  
 245 250

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(2) INFORMATION FOR SEQ ID NO:410  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...461  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys  
 1 5 10 15  
 Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys  
 20 25 30  
 Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala  
 35 40 45  
 Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln  
 50 55 60  
 Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu  
 65 70 75 80  
 Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu  
 85 90 95  
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr  
 100 105 110  
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu  
 115 120 125  
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met  
 130 135 140  
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser  
 145 150 155 160  
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln  
 165 170 175  
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln  
 180 185 190  
 Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr Gly  
 195 200 205  
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala  
 210 215 220  
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp  
 225 230 235 240  
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg  
 245 250 255  
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly  
 260 265 270  
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg  
 275 280 285  
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg  
 290 295 300  
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala  
 305 310 315 320  
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met  
 325 330 335  
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys  
 340 345 350  
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala

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355 360 365  
 Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp Ile  
 370 375 380  
 Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser Gly  
 385 390 395 400  
 5 Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala Arg  
 405 410 415  
 Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg Gln  
 420 425 430  
 10 Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys Val  
 435 440 445  
 Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450 455 460

## 15 (2) INFORMATION FOR SEQ ID NO:411

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

35 Met Asn Ser Arg His Leu Thr Ile Thr Ile Ile Ala Gly Leu Ser Leu  
 1 5 10 15  
 Phe Val Leu Thr Leu Gly Gly Cys Ser Val Ala Gln Gln Asp Thr Gln  
 20 25 30  
 40 Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser Ala Trp Ile Gln Arg Ser  
 35 40 45  
 Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala Tyr Asn Ile Ala Thr Glu  
 50 55 60  
 Arg Val Asp Ala Leu Pro Ala Glu Arg Lys Gln Gly Asp Arg Pro Tyr  
 65 70 75 80  
 45 Ala Ile Val Thr Asp Ile Arg Glu Thr Ile Leu Asp Asn Thr Pro Asn  
 85 90 95  
 Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp Tyr Asp Glu Glu Thr Trp  
 100 105 110  
 50 Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp Thr Leu Ala Gly Ala Leu  
 115 120 125  
 Ser Phe Phe Leu His Ala Ala Asn Lys Gly Ile Glu Val Phe Tyr Val  
 130 135 140  
 Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala Thr Leu Gln Asn Leu Gln  
 145 150 155 160  
 55 Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu His Leu Leu Thr Thr His  
 165 170 175  
 Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu Lys Ile Gln Glu Gln Tyr  
 180 185 190  
 60 Glu Ile Val Leu Leu Ile Gly Asp Asn Leu Gly Asp Phe His His Phe  
 195 200 205  
 Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys Gln Ala Leu Gly Leu Thr  
 210 215 220  
 Ala Gly Glu Phe Gly Arg His Phe Ile Met Leu Pro Asn Pro Asn Tyr  
 225 230 235 240  
 65 Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly Lys Tyr Pro Pro Leu Pro  
 245 250 255  
 Glu Arg Asp Lys Ala Leu Lys Gln Leu His Ser Gln Asn Ser Arg  
 260 265 270

## 70 (2) INFORMATION FOR SEQ ID NO:412

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

Met Ser Thr Asn Ile Asp Val Gln Gln Ile Lys Gln Arg Phe Gly Ile  
1 5 10 15  
Ile Gly Ser Ser Pro Leu Met Glu His Ala Thr Arg Val Ala Ala Gln  
20 25 30  
Val Ala Pro Thr Asp Met Ser Val Leu Val Thr Gly Glu Ser Gly Ser  
35 40 45  
Gly Lys Glu Phe Phe Pro Gln Ile Ile His Tyr Tyr Ser Ala Arg Lys  
50 55 60  
His His Ser Tyr Ile Ala Val Asn Cys Gly Ala Ile Pro Glu Gly Thr  
65 70 75 80  
Ile Asp Ser Glu Leu Phe Gly His Arg Lys Gly Ser Phe Thr Gly Ala  
85 90 95  
Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile  
100 105 110  
Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu  
115 120 125  
Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln  
130 135 140  
Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Thr Asn Val Asn Leu  
145 150 155 160  
Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg  
165 170 175  
Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp  
180 185 190  
Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys  
195 200 205  
Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu  
210 215 220  
Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr  
225 230 235 240  
Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr  
245 250 255  
Ile Thr Arg Tyr Leu Asp Ala Glu Gly Met Gln Asp Leu His Pro Val  
260 265 270  
Val Ile Arg Arg Asn Glu Thr Thr Glu Ala Asp Lys Gln Ile Pro His  
275 280 285  
Tyr Glu Arg Glu Ile Ile Tyr Gln Val Leu Tyr Asp Met Lys Lys Glu  
290 295 300  
Ile Ala Asp Leu Lys Gly Met Met Asn Arg Leu Ala His His Glu Gln  
305 310 315 320  
Pro Ser Trp Pro Val Gly Ser Asp Val Trp Gly Asn Asp Asp Lys Arg  
325 330 335  
Thr Ala Asp Pro Lys Trp Gly Val Ser Thr His Lys Ala Pro Ile Ala  
340 345 350  
Asn Ala Ala Glu Pro Val Glu Pro Ile Gln Glu Ala Ser Glu Tyr Thr  
355 360 365  
Glu Asp Pro Val Ser Leu Glu Glu Val Glu Lys Lys Met Ile Ser Leu  
370 375 380  
Ala Leu Glu Arg His Gly Gly Arg Arg Lys Gln Thr Ala Glu Glu Leu  
385 390 395 400  
Lys Ile Ser Glu Arg Thr Leu Tyr Arg Lys Ile Lys Glu Tyr Gly Leu  
405 410 415  
Glu

(2) INFORMATION FOR SEQ ID NO:413

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 602 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala Ala Ala Arg  
1 5 10 15  
Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr Lys Gly Asn  
20 25 30  
Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr Gly Ala Met  
35 40 45  
Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Ile Arg Leu  
50 55 60  
Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His Ala Ser Val  
65 70 75 80  
Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg Tyr Glu Arg  
85 90 95  
Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala Asn Tyr Asp  
100 105 110  
Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg Leu Leu Met  
115 120 125  
Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe Trp Lys Glu  
130 135 140  
Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser Val Ala Leu  
145 150 155 160  
Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe Phe Glu Pro  
165 170 175  
His Ala Asp Glu Glu Leu Met Gln Ala Val Arg Pro Asp Ala Ile Ile  
180 185 190  
Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys Ile Glu Ala  
195 200 205  
Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Val Arg Pro Pro Leu  
210 215 220  
Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu Arg Arg Ala  
225 230 235 240  
Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser Gly Phe Thr  
245 250 255  
Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met Tyr Arg Leu  
260 265 270  
Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu Pro Ser Gly  
275 280 285  
Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu Glu Asp Ala  
290 295 300  
Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro Asp Val Thr  
305 310 315 320  
Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro Glu His Glu  
325 330 335  
Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val Thr Leu Pro  
340 345 350  
Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu Val Pro Arg  
355 360 365  
Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln Gly Gly Val  
370 375 380  
Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala Thr Gln Thr  
385 390 395 400  
Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile Ile Gly Thr  
405 410 415  
Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val Gly Ala Ile  
420 425 430  
Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn His Ile Val  
435 440 445  
Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly Ala Tyr Pro  
450 455 460  
Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe Val Gly Glu  
465 470 475 480  
Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser Val Thr Val



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	305				310				315			320				
	Pro	Glu	Asn	Thr	Gly	Lys	Ile	Ile	Gly	Gly	Pro	Met	Met	Gly	Arg	
					325				330					335		
5	Ala	Leu	Leu	Ser	Pro	Asp	Val	Pro	Val	Thr	Lys	Gly	Ser	Ser	Gly	Val
				340					345					350		
	Leu	Ile	Leu	Asp	Arg	Glu	Glu	Ala	Val	Arg	Lys	Pro	Met	Arg	Asp	Cys
			355					360					365			
	Ile	Arg	Cys	Ala	Lys	Cys	Val	Gly	Val	Cys	Pro	Met	Gly	Leu	Asn	Pro
			370				375					380				
10	Ala	Phe	Leu	Met	Arg	Asp	Thr	Leu	Tyr	Lys	Ser	Trp	Glu	Thr	Ala	Glu
	385					390					395					400
	Lys	Gly	Asn	Val	Val	Asp	Cys	Ile	Glu	Cys	Gly	Ser	Cys	Ser	Phe	Thr
					405				410						415	
15	Cys	Pro	Ala	Asn	Arg	Pro	Leu	Leu	Asp	Tyr	Ile	Arg	Gln	Ala	Lys	Lys
				420					425					430		
	Thr	Val	Met	Gly	Ile	Gln	Arg	Ala	Arg	Lys	Gln					
			435					440								

(2) INFORMATION FOR SEQ ID NO:415

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 479 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...479
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

[illegible]

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290 295 300  
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu  
 305 310 315 320  
 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile  
 5 325 330 335  
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg  
 340 345 350  
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys  
 355 360 365  
 10 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu  
 370 375 380  
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe  
 385 390 395 400  
 15 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn  
 405 410 415  
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr  
 420 425 430  
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly  
 435 440 445  
 20 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly  
 450 455 460  
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys  
 465 470 475  
 25 (2) INFORMATION FOR SEQ ID NO:416  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...383  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416  
 45 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn  
 1 5 10 15  
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln  
 20 25 30  
 50 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe  
 35 40 45  
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg  
 50 55 60  
 Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly  
 65 70 75 80  
 55 Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg  
 85 90 95  
 Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser Asp  
 100 105 110  
 60 Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg  
 115 120 125  
 Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys  
 130 135 140  
 Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp  
 145 150 155 160  
 65 Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly  
 165 170 175  
 Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln  
 180 185 190  
 70 Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr  
 195 200 205  
 Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu  
 210 215 220  
 Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln Met  
 225 230 235 240  
 75 Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly

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245 250 255  
 Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile Arg  
 260 265 270  
 Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu Ala  
 275 280 285  
 Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala Lys  
 290 295 300  
 Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu Arg  
 305 310 315 320  
 Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln Leu  
 325 330 335  
 Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp Glu  
 340 345 350  
 Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr Asp  
 355 360 365  
 Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:417

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met  
 1 5 10 15  
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala  
 20 25 30  
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr  
 35 40 45  
 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Tyr Pro Asp Gln Arg  
 50 55 60  
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln  
 65 70 75 80  
 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala  
 85 90 95  
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro  
 100 105 110  
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala  
 115 120 125  
 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr  
 130 135 140  
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln  
 145 150 155 160  
 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr  
 165 170 175  
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys  
 180 185 190  
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser  
 195 200 205  
 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val  
 210 215 220  
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp  
 225 230 235 240  
 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala  
 245 250 255  
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala  
 260 265 270  
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys  
 275 280 285  
 Ala Thr Ser Ala Arg

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(2) INFORMATION FOR SEQ ID NO:418

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...356

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu  
 1 5 10 15  
 25 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe  
 20 25 30  
 Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe  
 35 40 45  
 30 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu  
 50 55 60  
 Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala  
 65 70 75 80  
 Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro  
 85 90 95  
 35 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly  
 100 105 110  
 Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Gly Val Ala Leu  
 115 120 125  
 40 Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala  
 130 135 140  
 Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys  
 145 150 155 160  
 Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr  
 165 170 175  
 45 Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu  
 180 185 190  
 Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala  
 195 200 205  
 50 Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile  
 210 215 220  
 Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly  
 225 230 235 240  
 Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu  
 245 250 255  
 55 Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr  
 260 265 270  
 Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg  
 275 280 285  
 60 Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys  
 290 295 300  
 Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met  
 305 310 315 320  
 Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val  
 325 330 335  
 65 Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys  
 340 345 350  
 Glu Glu Thr Asp  
 355

70

(2) INFORMATION FOR SEQ ID NO:419

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 757 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

75



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485 490 495  
 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly  
 500 505 510  
 5 10 15 20 25 30 35  
 Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn Gly Tyr Lys Thr Pro Thr  
 515 520 525 530  
 Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu Thr Thr Met Gly Ser His  
 535 540 545  
 Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr  
 550 555 560  
 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala  
 565 570 575  
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile  
 580 585 590  
 15 20 25 30 35  
 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln  
 595 600 605  
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys  
 610 615 620  
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu  
 625 630 635 640  
 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala  
 645 650 655  
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln  
 660 665 670  
 25 30 35  
 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr  
 675 680 685  
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr  
 690 695 700  
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu  
 705 710 715 720  
 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val  
 725 730 735  
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala  
 740 745 750  
 35  
 Ile Arg Phe Asn Asn  
 755

(2) INFORMATION FOR SEQ ID NO:420

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...331  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420  
 60 Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu  
 1 5 10 15  
 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu  
 20 25 30  
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr  
 35 40 45  
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser  
 50 55 60  
 65 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala  
 65 70 75 80  
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala  
 85 90 95  
 70 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln  
 100 105 110  
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala  
 115 120 125  
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly  
 130 135 140  
 75 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala



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145 150 155 160  
 Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met Ala Arg  
 165 170 175  
 Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu Val Asp  
 180 185 190  
 Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn Glu Thr  
 195 200 205  
 Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe Pro Lys  
 210 215 220  
 10 Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile Ala Glu  
 225 230 235 240  
 Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe Leu Ser  
 245 250 255  
 15 Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala Leu Asn  
 260 265 270  
 Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met Gly Thr  
 275 280 285  
 Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp Leu Lys  
 290 295 300  
 20 Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala Gln Lys  
 305 310 315 320  
 Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys  
 325 330

25 (2) INFORMATION FOR SEQ ID NO:421

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

45 Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser Phe Ser Val Leu Leu  
 1 5 10 15  
 Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val Val Tyr Leu Gln Asp  
 20 25 30  
 50 Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys Pro Tyr Asp Val Lys  
 35 40 45  
 Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val Ser Ser Arg Asp Pro  
 50 55 60  
 Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr Thr Arg Ala Leu Ala  
 65 70 75 80  
 55 Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly Phe Leu Val Asp Ser  
 85 90 95  
 Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln Ile Tyr Val Glu Gly  
 100 105 110  
 60 Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln Lys Arg Ile Ile Ser  
 115 120 125  
 Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val Gln Leu Gln Asn Phe  
 130 135 140  
 Lys Val Ser Val Leu Gly Glu Val Asn His Pro Gly Ser Met Ser Val  
 145 150 155 160  
 65 Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile Gly Met Ala Gly Asp  
 165 170 175  
 Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe Val Ile Arg Glu Thr  
 180 185 190  
 70 Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu Arg Lys Ala Asp Leu  
 195 200 205  
 Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn Asp Val Ile Tyr Val  
 210 215 220  
 Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu Ile Asn Gln Asn Asn  
 225 230 235 240  
 75 Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr Leu Val Ser Ile Ser

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245 250 255  
 Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 260 265

5 (2) INFORMATION FOR SEQ ID NO:422  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 569 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 10  
 (ii) MOLECULE TYPE: protein  
 15 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...569  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

25 Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr  
 1 5 10 15  
 Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu  
 20 25 30  
 Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val  
 30 35 40 45  
 Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile  
 50 55 60  
 Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly  
 65 70 75 80  
 35 Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu  
 85 90 95  
 Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser  
 100 105 110  
 40 Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met  
 115 120 125  
 Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile  
 130 135 140  
 Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala  
 145 150 155 160  
 45 Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr  
 165 170 175  
 Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile  
 180 185 190  
 50 Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr  
 195 200 205  
 Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr  
 210 215 220  
 Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu  
 225 230 235 240  
 55 Asp Leu Arg Gly Asn Gly Gly Leu Met Gln Ala Ala Ile Glu Ile  
 245 250 255  
 Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly  
 260 265 270  
 60 Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile  
 275 280 285  
 Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser  
 290 295 300  
 Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val  
 305 310 315 320  
 65 Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg  
 325 330 335  
 Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr  
 340 345 350  
 70 Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn  
 355 360 365  
 Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe  
 370 375 380  
 Tyr Thr Ala Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro  
 385 390 395 400  
 75 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met

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405 410 415  
 Ala Ile Asn Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys  
 420 425 430  
 His Lys Thr Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp  
 435 440 445  
 Tyr Ala Ala Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp  
 450 455 460  
 Arg Gln Ser Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile  
 465 470 475 480  
 10 Glu Gly Tyr Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu  
 485 490 495  
 Lys Leu Lys Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu  
 500 505 510  
 15 Ile Thr Asn Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu  
 515 520 525  
 Arg Gly Ser Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu  
 530 535 540  
 Ala Ile Lys Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu  
 545 550 555 560  
 20 Ala Ala Pro Lys Ala Glu Asn Lys Gly  
 565

## (2) INFORMATION FOR SEQ ID NO:423

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 981 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...981  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser Ala Leu Ala Ile  
 1 5 10 15  
 45 Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr Asn Arg Tyr Glu  
 20 25 30  
 Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met Ala Tyr Leu Asp  
 35 40 45  
 50 Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr Leu Lys Glu Ala  
 50 55 60  
 Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys Gly Gly Met Asn  
 65 70 75 80  
 Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg Asn Leu Ser Asn  
 85 90 95  
 55 Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu Asn Ala Ala Lys  
 100 105 110  
 Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val Lys Glu Tyr Arg  
 115 120 125  
 60 Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe Gly Ser Gly Asp  
 130 135 140  
 Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala Asp Val Val Arg  
 145 150 155 160  
 Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala Ser Phe Asn Val  
 165 170 175  
 65 Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala Pro Asn Leu Gln  
 180 185 190  
 Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu Pro Gly Val Lys  
 195 200 205  
 70 Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser Ala Asn Leu Gln  
 210 215 220  
 Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly Asp Leu Ile Ala  
 225 230 235 240  
 Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn Thr Asp Ala Thr  
 245 250 255  
 75 Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala Ala Thr Ala Asp

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		260		265		270
	Ser	Ala	Ala	Val	Gln	Ala
		275		280		285
5	Glu	Ala	Lys	Asp	Ala	Thr
		290		295		300
	Pro	Val	Asn	Arg	Gly	Ala
		305		310		315
	Met	Ala	Gln	Ile	Ser	Glu
		320		325		330
10	Thr	Arg	Glu	Asp	Val	Leu
		335		340		345
	Pro	Glu	Thr	Lys	Glu	Thr
		350		355		360
15	Thr	Asn	Arg	Thr	Gly	Asp
		365		370		375
	Ala	Lys	Ser	Asp	Ile	Gln
		380		385		390
	Ser	Met	Thr	Met	Asn	Glu
		395		400		405
20	Lys	Asp	Asn	Val	Gly	Arg
		410		415		420
	Tyr	Ser	Ala	Pro	Asn	Val
		425		430		435
25	Ile	Ser	Gly	His	Phe	Thr
		440		445		450
	Leu	Asn	Ser	Gly	Lys	Met
		455		460		465
	Val	Ile	Gly	Pro	Thr	Leu
		470		475		480
30	Ser	Phe	Leu	Leu	Ala	Leu
		485		490		495
	Tyr	Gly	Phe	Leu	Pro	Gly
		500		505		510
35	Ser	Phe	Thr	Leu	Gly	Val
		515		520		525
	Leu	Ser	Gly	Ile	Ala	Gly
		530		535		540
	Ala	Asn	Val	Leu	Ile	Phe
		545		550		555
40	Lys	Thr	Pro	Ile	Arg	Ala
		560		565		570
	Ala	Ile	Phe	Asp	Ser	Asn
		575		580		585
45	Phe	Leu	Tyr	Gly	Thr	Gly
		590		595		600
	Ile	Gly	Leu	Ile	Ala	Ser
		605		610		615
	Val	Phe	Glu	Lys	Leu	Ala
		620		625		630
50	Thr	Thr	Ser	Ile	Thr	Arg
		635		640		645
	Leu	Gly	Lys	Arg	Lys	Thr
		650		655		660
55	Leu	Gly	Leu	Ile	Ala	Ser
		665		670		675
	Phe	Ser	Gly	Gly	Arg	Asn
		680		685		690
	Ser	Glu	Ala	Val	Arg	Ser
		695		700		705
60	Leu	Val	Thr	Ser	Ile	Gly
		710		715		720
	Asn	Tyr	Lys	Ile	Gln	Glu
		725		730		735
65	Asp	Lys	Leu	Tyr	Gln	Ser
		740		745		750
	Ala	Asp	Gln	Phe	Leu	Asp
		755		760		765
	Ser	Met	Ser	Ser	Asp	Ile
		770		775		780
70	Ser	Met	Ile	Phe	Met	Ala
		785		790		795
	Ser	Phe	Ser	Ala	Gly	Val
		800		805		810
	Ile	Ile	Ala	Leu	Tyr	Ala
		815		820		825
75	Ile	Ile	Ala	Leu	Tyr	Ala
		830		835		840
	Leu	Leu	Trp	Lys	Ile	Leu
		845		850		855

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Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala Ile Ile Gly Tyr  
 865 870 875 880  
 Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile Arg Glu Thr Met  
 885 890 895  
 5 Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile Asn Asp Ala Leu  
 900 905 910  
 Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu Thr Thr Phe Ile  
 915 920 925  
 10 Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe  
 930 935 940  
 Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu  
 945 950 955 960  
 Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn  
 965 970 975  
 15 Lys Ala Ala Lys Lys  
 980

(2) INFORMATION FOR SEQ ID NO:424

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1017 amino acids  
 (ii) TYPE: amino acid  
 (iii) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1017  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

Met Lys Arg Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly  
 1 5 10 15  
 40 Trp Ala Met Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser  
 20 25 30  
 Glu Asp Asn Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn  
 35 40 45  
 45 Thr Thr Ile Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser  
 50 55 60  
 Val Pro Ala Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr  
 65 70 75 80  
 Thr Lys Glu Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro  
 85 90 95  
 50 Asp Ser Lys Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly  
 100 105 110  
 Gln Lys Leu Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu  
 115 120 125  
 55 Lys Leu Ala Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly  
 130 135 140  
 Gln Val Ala Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala  
 145 150 155 160  
 Val Ala Ser Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser  
 165 170 175  
 60 Ala Pro Leu Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val  
 180 185 190  
 Ala Thr Met Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp  
 195 200 205  
 65 Ala Ser Ala Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val  
 210 215 220  
 Phe Ile Gln Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr  
 225 230 235 240  
 Phe Asn Ala Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu  
 245 250 255  
 70 Asp Asn Met Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala  
 260 265 270  
 Gly Phe Trp Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile  
 275 280 285  
 75 Leu Ala Gly Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp  
 290 295 300

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Glu Tyr Gly Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp  
 305 310 315 320  
 Trp Leu Lys Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile  
 325 330 335  
 5 Ser Phe Ser Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly  
 340 345 350  
 Tyr Phe Asp Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg  
 355 360 365  
 10 Tyr Ser Gly Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys  
 370 375 380  
 Val Gly Ala Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp  
 385 390 395 400  
 Tyr Phe Gly Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr  
 405 410 415  
 15 Met Pro Arg Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp  
 420 425 430  
 Val Tyr Tyr Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr  
 435 440 445  
 20 Phe Ala Lys Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val  
 450 455 460  
 Asn Gly Phe Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala  
 465 470 475 480  
 Gln Ala Gly Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met  
 485 490 495  
 25 Pro Asn Asn Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg  
 500 505 510  
 Ala Tyr Arg Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys  
 515 520 525  
 30 Phe Ser Ile Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu  
 530 535 540  
 Tyr Ile Glu Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe  
 545 550 555 560  
 Glu Ser Asp Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser  
 565 570 575  
 35 Leu Ser Leu Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe  
 580 585 590  
 Phe Ser Arg Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe  
 595 600 605  
 40 Ser Val Arg Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser  
 610 615 620  
 Ala Trp Phe Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe  
 625 630 635 640  
 Ile Gln Glu Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr  
 645 650 655  
 45 Gly Thr Thr Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu  
 660 665 670  
 Val Thr Val Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser  
 675 680 685  
 50 Thr Ala Gly Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn  
 690 695 700  
 Phe Gly Leu Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val  
 705 710 715 720  
 Asp Phe Tyr Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met  
 725 730 735  
 55 Pro Tyr Ile Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met  
 740 745 750  
 Lys Asn Thr Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn  
 755 760 765  
 60 Lys Asp Trp Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln  
 770 775 780  
 Glu Ile Thr Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn  
 785 790 795 800  
 Thr Gly Thr Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala  
 805 810 815  
 65 Glu Tyr Ala Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val  
 820 825 830  
 Pro Gly Gln Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr  
 835 840 845  
 70 Ser Ala Asp Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Pro Ile  
 850 855 860  
 Thr Gly Gly Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp  
 865 870 875 880  
 Ala Asp Phe Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg  
 885 890 895  
 75 Tyr Phe Thr Glu Asn Ala Gly Gly Leu Met Gln Leu Asn Lys Asp Lys

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5 Met Leu 900 Asn Ala Trp Thr 905 Glu Asp Asn Lys Glu Thr Asp Val Pro 910  
 915 Lys Leu Gly Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala 925  
 930 Ser Phe Leu Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn 940  
 945 Ser Leu Phe Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu 955  
 960  
 10 Met Ala Arg Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro 970  
 980 Glu Ala Gly Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln 990  
 995 1000 1005  
 15 Tyr Val Ala Gly Ile Gln Leu Ser Phe 1010 1015

(2) INFORMATION FOR SEQ ID NO:425  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1014 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1014  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met  
 1 5 10 15  
 40 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
 20 25 30  
 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
 35 40 45  
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
 50 55 60  
 45 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
 65 70 75 80  
 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
 85 90 95  
 50 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
 100 105 110  
 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
 115 120 125  
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
 130 135 140  
 55 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
 145 150 155 160  
 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
 165 170 175  
 60 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
 180 185 190  
 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
 195 200 205  
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
 210 215 220  
 65 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
 225 230 235 240  
 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met  
 245 250 255  
 70 Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp  
 260 265 270  
 Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly  
 275 280 285  
 Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly  
 290 295 300  
 75 Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys

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 Ala Leu Phe Lys Thr 310  
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Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly  
 915 920 925  
 Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu  
 930 935 940  
 5 Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe  
 945 950 955 960  
 Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg  
 965 970 975  
 10 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly  
 980 985 990  
 Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala  
 995 1000 1005  
 Gly Ile Gln Leu Ser Phe  
 1010  
 15  
 (2) INFORMATION FOR SEQ ID NO:426  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 821 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20  
 (ii) MOLECULE TYPE: protein  
 25 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...821  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426  
 35 Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu  
 1 5 10 15  
 Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn  
 20 25 30  
 40 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg  
 35 40 45  
 Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp  
 50 55 60  
 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu  
 45 65 70 75 80  
 Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser  
 85 90 95  
 Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr  
 100 105 110  
 50 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu  
 115 120 125  
 Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly  
 130 135 140  
 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser  
 145 150 155 160  
 55 Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His  
 165 170 175  
 Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His  
 180 185 190  
 60 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp  
 195 200 205  
 Lys Thr Gln Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr  
 210 215 220  
 65 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn  
 225 230 235 240  
 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His  
 245 250 255  
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu  
 260 265 270  
 70 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr  
 275 280 285  
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp  
 290 295 300  
 75 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln  
 305 310 315 320

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Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile  
 325 330 335  
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala  
 340 345 350  
 5 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr  
 355 360 365  
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys  
 370 375 380  
 10 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly  
 385 390 395 400  
 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu  
 405 410 415  
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr  
 420 425 430  
 15 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys  
 435 440 445  
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys  
 450 455 460  
 20 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro  
 465 470 475 480  
 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly  
 485 490 495  
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp  
 500 505 510  
 25 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn  
 515 520 525  
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys  
 530 535 540  
 30 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile  
 545 550 555 560  
 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr  
 565 570 575  
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn  
 580 585 590  
 35 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser  
 595 600 605  
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp  
 610 615 620  
 40 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys  
 625 630 635 640  
 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala  
 645 650 655  
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr  
 660 665 670  
 45 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe  
 675 680 685  
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr  
 690 695 700  
 50 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu  
 705 710 715 720  
 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu  
 725 730 735  
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg  
 740 745 750  
 55 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile  
 755 760 765  
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr  
 770 775 780  
 60 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu  
 785 790 795 800  
 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu  
 805 810 815  
 Lys Ile His Ile Gly  
 820

(2) INFORMATION FOR SEQ ID NO:427

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

10 Met Arg Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Pro Ile  
1 5 10 15  
Phe Phe Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg  
20 25 30  
15 Phe Thr Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr  
35 40 45  
Gly Pro Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys  
50 55 60  
20 His Pro Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:428

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 859 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
35 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...859

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu Tyr Ser  
1 5 10 15  
45 Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln Asp Met  
20 25 30  
Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile Asp Ile  
35 40 45  
Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu Ile Glu  
50 55 60  
Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly Ser Pro  
65 70 75 80  
Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr Asp Ile  
85 90 95  
55 Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu Leu  
100 105 110  
Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile Phe Met  
115 120 125  
Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe Gly Gln  
130 135 140  
60 Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile Leu Asp  
145 150 155  
Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser Ser Pro  
165 170 175  
Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala Pro Glu  
180 185 190  
65 Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Arg Ser Gly Gly  
195 200 205  
Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala Met Ala  
210 215 220  
70 Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu Ile Glu  
225 230 235  
Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro Val Leu  
245 250 255  
75 Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly Leu Ala  
260 265 270

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	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp	Lys	Arg
			275					280					285			
	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys	Tyr	Arg
			290				295					300				
5	Gly	Gln	Phe	Glu	Glu	Arg	Ile	Lys	Ala	Val	Leu	Asp	Glu	Leu	Lys	Lys
			305			310					315				320	
	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile	Val	Gly
				325						330					335	
10	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu	Lys	Pro
				340					345					350		
	Ala	Leu	Ala	Arg	Gly	Gln	Val	Gln	Cys	Ile	Gly	Ala	Thr	Thr	Leu	Asp
			355				360						365			
	Glu	Tyr	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Gly	Ala	Leu	Glu	Arg	Arg	Phe
			370				375					380				
15	Gln	Lys	Val	Pro	Ile	Ala	Pro	Ser	Thr	Ala	Glu	Glu	Thr	Leu	Thr	Ile
			385			390					395				400	
	Leu	Gln	Asn	Ile	Lys	Glu	Lys	Tyr	Glu	Asp	Tyr	His	Gly	Val	Arg	Tyr
				405						410					415	
20	Thr	Asp	Glu	Ala	Ile	Lys	Ala	Ala	Val	Glu	Leu	Thr	Asp	Arg	Tyr	Val
				420					425					430		
	Ser	Asp	Arg	Phe	Phe	Pro	Asp	Lys	Ala	Ile	Asp	Ala	Met	Asp	Glu	Ala
			435					440					445			
	Gly	Ala	Ser	Val	His	Ile	Thr	Asn	Val	Val	Ala	Pro	Lys	Glu	Ile	Glu
			450				455					460				
25	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Ser	Val	Arg	Glu	Asn	Lys	Leu	Ser	Ala
			465			470					475				480	
	Val	Lys	Ala	Gln	Asn	Tyr	Glu	Leu	Ala	Ala	Ser	Phe	Arg	Asp	Gln	Glu
				485						490					495	
30	Arg	Arg	Thr	Gln	Gln	Gln	Ile	Ala	Glu	Glu	Lys	Lys	Lys	Trp	Glu	Glu
				500					505					510		
	Gln	Met	Ser	Lys	His	Arg	Glu	Thr	Val	Asp	Glu	Asn	Val	Val	Ala	His
			515					520					525			
	Val	Val	Ala	Leu	Met	Thr	Gly	Val	Pro	Ala	Glu	Arg	Leu	Ser	Thr	Gly
				530			535						540			
35	Glu	Gly	Glu	Arg	Leu	Arg	Thr	Met	Ala	Asp	Asp	Leu	Lys	Thr	Lys	Val
			545			550					555				560	
	Val	Gly	Gln	Asp	Thr	Ala	Ile	Glu	Lys	Met	Val	His	Ala	Ile	Gln	Arg
				565						570					575	
40	Asn	Arg	Leu	Gly	Leu	Arg	Asn	Glu	Lys	Lys	Pro	Ile	Gly	Ser	Phe	Leu
			580					585					590			
	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Tyr	Leu	Ala	Lys	Lys	Leu
			595					600					605			
	Ala	Glu	Tyr	Leu	Phe	Glu	Asp	Glu	Asn	Ala	Met	Ile	Arg	Val	Asp	Met
			610				615					620				
45	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ser	Val	Ser	Arg	Leu	Val	Gly	Ala	Pro
			625			630					635				640	
	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Arg	Val
				645						650					655	
50	Arg	Arg	Lys	Pro	Tyr	Ser	Val	Val	Leu	Leu	Asp	Glu	Ile	Glu	Lys	Ala
				660					665				670			
	His	Ala	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Met	Asp	Glu	Gly	Gln
			675					680					685			
	Leu	Thr	Asp	Ser	Leu	Gly	Arg	Arg	Val	Asn	Phe	Lys	Asn	Thr	Val	Ile
			690				695					700				
55	Ile	Ile	Thr	Ser	Asn	Val	Gly	Thr	Arg	Gln	Leu	Lys	Asp	Phe	Gly	Gln
			705			710					715				720	
	Gly	Ile	Gly	Phe	Arg	Ser	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Lys	Glu	His
				725						730					735	
60	Ser	Arg	Ser	Val	Ile	Gln	Lys	Ala	Leu	Asn	Lys	Thr	Phe	Ser	Pro	Glu
				740				745					750			
	Phe	Leu	Asn	Arg	Leu	Asp	Asp	Ile	Ile	Leu	Phe	Asp	Gln	Leu	Gly	Lys
			755				760						765			
	Thr	Glu	Ile	Arg	Arg	Met	Val	Asp	Ile	Glu	Leu	Lys	Ala	Val	Leu	Ala
				770			775						780			
65	Arg	Ile	His	Arg	Ala	Gly	Tyr	Asp	Leu	Val	Leu	Thr	Asp	Glu	Ala	Lys
				785		790					795				800	
	Asp	Val	Ile	Ala	Thr	Lys	Gly	Tyr	Asp	Leu	Gln	Tyr	Gly	Ala	Arg	Pro
				805						810					815	
70	Leu	Lys	Arg	Thr	Leu	Gln	Asn	Glu	Val	Glu	Asp	Arg	Leu	Thr	Asp	Leu
				820				825						830		
	Ile	Leu	Ser	Gly	Gln	Ile	Glu	Lys	Gly	Gln	Thr	Leu	Thr	Leu	Ser	Ala
				835				840						845		
	Arg	Asp	Gly	Glu	Ile	Ile	Val	Gln	Glu	Gln	Ala					
				850			855									
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(2) INFORMATION FOR SEQ ID NO:429

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iiii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

5 Met Asn Tyr Leu Tyr Ile Leu Ile Thr Leu Leu Leu Ser Gly Phe Phe  
 1 5 10 15  
 Ser Gly Ala Glu Ile Ala Phe Leu Ser Ser Asp Lys Leu Arg Leu Glu  
 20 25 30  
 25 Leu Asp Arg Asn Arg Gly Asp Leu Thr Gly Arg Ala Leu Asn Leu Leu  
 35 40 45  
 Tyr Arg His Pro Asp Gln Leu Val Thr Thr Leu Leu Val Gly Asn Asn  
 50 55 60  
 30 Ile Val Leu Val Val Tyr Gly Leu Leu Met Ala Gly Leu Leu Ala Ala  
 65 70 75 80  
 Pro Leu Ala Gln Trp Ile Asp Asn Asp Ala Met Ile Val Val Leu Gln  
 85 90 95  
 Ser Val Leu Ser Thr Ile Ile Ile Leu Phe Thr Gly Glu Phe Leu Pro  
 100 105 110  
 35 Lys Ala Ile Phe Lys Thr Asn Ala Asn Met Met Met Arg Val Phe Ala  
 115 120 125  
 Leu Pro Ile Val Ala Ile Tyr Tyr Leu Leu Tyr Pro Leu Ser Lys Leu  
 130 135 140  
 40 Phe Thr Gly Leu Ser Arg Ser Phe Ile Arg Leu Val Asp Lys Asn Tyr  
 145 150 155 160  
 Val Pro Thr Thr Val Gly Leu Gly Arg Val Asp Leu Asp His Tyr Leu  
 165 170 175  
 Ala Glu Asn Met Ser Gly Glu Asn Glu Gln Asn Asp Leu Thr Thr Glu  
 180 185 190  
 45 Val Lys Ile Ile Gln Asn Ala Leu Asp Phe Ser Gly Ile Gln Val Arg  
 195 200 205  
 Asp Cys Met Ile Pro Arg Asn Glu Met Ile Ala Cys Glu Leu Gln Thr  
 210 215 220  
 50 Asp Ile Glu Val Leu Lys Thr Thr Phe Ile Asp Thr Gly Leu Ser Lys  
 225 230 235 240  
 Ile Ile Ile Tyr Arg Gln Asn Ile Asp Asp Val Val Gly Tyr Ile His  
 245 250 255  
 Ser Ser Glu Met Phe Arg Gly Gln Asp Trp Gln Lys Arg Ile Asn Thr  
 260 265 270  
 55 Thr Val Phe Val Pro Glu Ser Met Tyr Ala Asn Lys Leu Met Arg Leu  
 275 280 285  
 Leu Met Gln Arg Lys Lys Ser Ile Ala Ile Val Ile Asp Glu Leu Gly  
 290 295 300  
 60 Gly Thr Ala Gly Met Val Thr Leu Glu Asp Leu Val Glu Glu Ile Phe  
 305 310 315 320  
 Gly Asp Ile Glu Asp Glu His Asp Thr Arg Lys Ile Ile Ala Lys Gln  
 325 330 335  
 Leu Gly Pro His Thr Tyr Leu Val Ser Gly Arg Met Glu Ile Asp Asp  
 340 345 350  
 65 Val Asn Glu Arg Phe Gly Leu Ser Leu Pro Glu Ser Asp Asp Tyr Leu  
 355 360 365  
 Thr Val Ala Gly Phe Ile Leu Asn Ser His Gln Asn Ile Pro Gln Ala  
 370 375 380  
 70 Asn Glu Val Val Glu Ile Ala Pro Tyr Thr Phe Thr Ile Leu Arg Ser  
 385 390 395 400  
 Ser Ser Thr Lys Ile Glu Leu Val Lys Met Ser Ile Asp Asp Gln Ser  
 405 410 415  
 Asn

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## (2) INFORMATION FOR SEQ ID NO:430

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 293 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

## (iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

15 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...293

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:430

20 Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val  
1 5 10 15  
Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile  
20 25 30  
25 Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu  
35 40 45  
Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val  
50 55 60  
30 Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr  
65 70 75 80  
Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr  
85 90 95  
Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu  
100 105 110  
35 Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu  
115 120 125  
Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn  
130 135 140  
40 Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu  
145 150 155 160  
Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr  
165 170 175  
Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala  
180 185 190  
45 Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val  
195 200 205  
Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser  
210 215 220  
50 Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys  
225 230 235 240  
Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly  
245 250 255  
Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr  
260 265 270  
55 Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser  
275 280 285  
Lys Ile Gln Val Arg  
290

## 60 (2) INFORMATION FOR SEQ ID NO:431

## (i) SEQUENCE CHARACTERISTICS:

65 (A) LENGTH: 312 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

70 (iii) HYPOTHETICAL: YES

## (iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

75 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

5 Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp  
 1 5 10 15  
 Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr  
 20 25 30  
 Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile  
 35 40 45  
 10 Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu  
 50 55 60  
 Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val Cys  
 65 70 75 80  
 15 Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser  
 85 90 95  
 Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu  
 100 105 110  
 Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn  
 115 120 125  
 20 Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp  
 130 135 140  
 Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp  
 145 150 155 160  
 25 Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg  
 165 170 175  
 Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Arg  
 180 185 190  
 Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr  
 195 200 205  
 30 Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu  
 210 215 220  
 Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser  
 225 230 235  
 35 Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly  
 245 250 255  
 Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp  
 260 265 270  
 Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys  
 275 280 285  
 40 Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val  
 290 295 300  
 Tyr Thr Glu Lys Ile Gln Ile Gln  
 305 310

(2) INFORMATION FOR SEQ ID NO:432

(1) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 843 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

60 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

65 Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala  
 1 5 10 15  
 Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu  
 20 25 30  
 70 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala  
 35 40 45  
 Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala  
 50 55 60  
 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr  
 65 70 75 80

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Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp  
 85 90 95  
 Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp  
 100 105 110  
 5 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp  
 115 120 125  
 Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu  
 130 135 140  
 10 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp  
 145 150 155 160  
 Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro  
 165 170 175  
 Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr  
 180 185 190  
 15 Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp  
 195 200 205  
 Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val  
 210 215 220  
 20 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met  
 225 230 235 240  
 Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala  
 245 250 255  
 Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe  
 260 265 270  
 25 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu  
 275 280 285  
 Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala  
 290 295 300  
 30 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala  
 305 310 315 320  
 Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His  
 325 330 335  
 Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn  
 340 345 350  
 35 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu  
 355 360 365  
 Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile  
 370 375 380  
 40 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu  
 385 390 395 400  
 Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala  
 405 410 415  
 Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn  
 420 425 430  
 45 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys  
 435 440 445  
 Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser  
 450 455 460  
 50 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn  
 465 470 475 480  
 Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr  
 485 490 495  
 Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val  
 500 505 510  
 55 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr  
 515 520 525  
 Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val  
 530 535 540  
 60 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn  
 545 550 555 560  
 Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser  
 565 570 575  
 Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala  
 580 585 590  
 65 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp  
 595 600 605  
 Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser  
 610 615 620  
 70 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val  
 625 630 635 640  
 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn  
 645 650 655  
 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro  
 660 665 670  
 75 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val





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260 265 270  
 Phe Glu Val Tyr Asp Val Val His Val Lys Ile Asn Pro Gln Ser Asp  
 275 280 295  
 Gly Lys  
 290

5

(2) INFORMATION FOR SEQ ID NO:434

10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...223

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

Met Lys Lys Ser Ser Val Val Ala Ser Val Leu Ala Val Ala Leu Val  
 1 5 10 15  
 Phe Ala Gly Cys Gly Leu Asn Asn Met Ala Lys Gly Gly Leu Ile Gly  
 20 25 30  
 Ala Gly Val Gly Gly Ala Ile Gly Ala Gly Val Gly Asn Val Ala Gly  
 35 40 45  
 Asn Thr Ala Val Gly Ala Ile Val Gly Thr Ala Val Gly Gly Ala Ala  
 50 55 60  
 Gly Ala Leu Ile Gly Lys Lys Met Asp Lys Gln Lys Lys Glu Leu Glu  
 65 70 75 80  
 Ala Ala Val Pro Asp Ala Thr Ile Gln Thr Val Asn Asp Gly Glu Ala  
 85 90 95  
 Ile Leu Val Thr Phe Asp Ser Gly Ile Leu Phe Ala Thr Asn Ser Ser  
 100 105 110  
 Thr Leu Ser Pro Asn Ser Arg Thr Ala Leu Thr Lys Phe Ala Ala Asn  
 115 120 125  
 Met Asn Lys Asn Pro Asp Thr Asp Ile Arg Ile Val Gly His Thr Asp  
 130 135 140  
 Asn Thr Gly Ser Asp Lys Ile Asn Asp Pro Leu Ser Glu Arg Arg Ala  
 145 150 155 160  
 Ala Ser Val Tyr Ser Phe Leu Asn Ser Gln Gly Val Ser Met Ser Arg  
 165 170 175  
 Met Ala Ala Glu Gly Arg Gly Ser His Glu Pro Val Ala Asp Asn Ser  
 180 185 190  
 Thr Val Ala Gly Arg Ser Ala Asn Arg Arg Val Glu Val Tyr Ile Leu  
 195 200 205  
 Pro Asn Ala Lys Met Ile Glu Gln Ala Gln Gln Gly Thr Leu Lys  
 210 215 220

55

(2) INFORMATION FOR SEQ ID NO:435

60 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...337

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

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Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
1      5      10      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
20      25      30
5 Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
35      40      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
50      55      60
10 Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
65      70      75      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
85      90      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
100      105      110
15 Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
115      120      125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
130      135      140
20 Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
145      150      155      160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
165      170      175
Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
180      185      190
25 Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
195      200      205
Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
210      215      220
30 Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
225      230      235      240
Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
245      250      255
Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
260      265      270
35 Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala
275      280      285
Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
290      295      300
40 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
305      310      315      320
Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
325      330      335
Lys

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- 45 (2) INFORMATION FOR SEQ ID NO:436
- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (11) MOLECULE TYPE: protein
- 55 (111) HYPOTHETICAL: YES
- (11) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis
- 60 (12) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION: 1...151
- 65 (11) SEQUENCE DESCRIPTION: SEQ ID NO:436

```

Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
1      5      10      15
Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
20      25      30
70 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
35      40      45
Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
50      55      60
75 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
65      70      75      80

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Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu  
 85 90 95  
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His  
 100 105 110  
 5 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg  
 115 120 125  
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser  
 130 135 140  
 10 Glu Leu Ser Leu Leu His Thr  
 145 150

## (2) INFORMATION FOR SEQ ID NO:437

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...391
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu  
 1 5 10 15  
 35 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro  
 20 25 30  
 Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe  
 35 40 45  
 Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn  
 50 55 60  
 40 Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val  
 65 70 75 80  
 Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly  
 85 90 95  
 45 Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn  
 100 105 110  
 Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn  
 115 120 125  
 Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp  
 130 135 140  
 50 Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys  
 145 150 155 160  
 Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe  
 165 170 175  
 55 Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala Ala His  
 180 185 190  
 Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val  
 195 200 205  
 Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala  
 210 215 220  
 60 Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile  
 225 230 235 240  
 Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn  
 245 250 255  
 65 Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys  
 260 265 270  
 Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu  
 275 280 285  
 Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys  
 290 295 300  
 70 Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr  
 305 310 315 320  
 Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr  
 325 330 335  
 75 Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp  
 340 345 350

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Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu  
 355 360 365  
 Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg  
 370 375 380  
 5 Val Val Ile Val Arg Ser Lys  
 385 390

(2) INFORMATION FOR SEQ ID NO:438

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...385

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala  
 1 5 10 15  
 30 Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln  
 20 25 30  
 Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp  
 35 35 40 45  
 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly  
 50 55 60  
 Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr  
 65 70 75 80  
 Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln  
 85 90 95  
 40 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg  
 100 105 110  
 Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu  
 115 120 125  
 45 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile  
 130 135 140  
 Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala  
 145 150 155 160  
 Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn  
 165 170 175  
 50 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn  
 180 185 190  
 Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys  
 195 200 205  
 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe  
 210 215 220  
 55 Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala  
 225 230 235 240  
 Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val  
 245 250 255  
 60 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro  
 260 265 270  
 Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe  
 275 280 285  
 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr  
 290 295 300  
 65 Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val  
 305 310 315 320  
 Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu  
 325 330 335  
 70 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly  
 340 345 350  
 Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln  
 355 360 365  
 75 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala  
 370 375 380

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Glu  
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## 5 (2) INFORMATION FOR SEQ ID NO:439

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...190

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val  
 1 5 10 15  
 Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys  
 20 25 30  
 Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu  
 35 40 45  
 Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp  
 50 55 60  
 Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile  
 65 70 75 80  
 Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro  
 85 90 95  
 Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn  
 100 105 110  
 Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr  
 115 120 125  
 Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr  
 130 135 140  
 Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr  
 145 150 155 160  
 Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala  
 165 170 175  
 Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala  
 180 185 190

## 50 (2) INFORMATION FOR SEQ ID NO:440

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 186 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...186

## 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln  
 1 5 10 15  
 Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr  
 20 25 30  
 Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr  
 35 40 45  
 Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu

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50 55 60  
 Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val  
 65 70 75 80  
 Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln  
 85 90 95  
 Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu  
 100 105 110  
 Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser  
 115 120 125  
 Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr Leu Ala Met Val  
 130 135 140  
 Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys  
 145 150 155 160  
 Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala  
 165 170 175  
 Met Ala Phe Met Gly Phe Ser Gly Ile Ala  
 180 185

(2) INFORMATION FOR SEQ ID NO:441

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

40 Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu  
 1 5 10 15  
 Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr  
 20 25 30  
 Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe  
 35 40 45  
 Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr  
 50 55 60  
 Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu  
 65 70 75 80  
 Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly  
 85 90 95  
 Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp  
 100 105 110  
 Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala  
 115 120 125  
 Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn  
 130 135 140  
 Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val  
 145 150 155 160  
 Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly  
 165 170 175  
 Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe  
 180 185 190  
 Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met  
 195 200 205  
 Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly  
 210 215 220  
 Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu  
 225 230 235 240  
 Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala  
 245 250 255  
 Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met  
 260 265 270  
 Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn  
 275 280 285  
 Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro

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290 295 300  
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly  
 305 310 315 320  
 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg  
 325 330 335  
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala  
 340 345 350  
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln  
 355 360 365  
 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln  
 370 375 380  
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn  
 385 390 395 400  
 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr  
 405 410 415  
 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe  
 420 425 430  
 Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp  
 435 440 445  
 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg  
 450 455 460  
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser  
 465 470 475 480  
 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile  
 485 490 495  
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr  
 500 505 510  
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn  
 515 520 525  
 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg  
 530 535 540  
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly  
 545 550 555 560  
 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser  
 565 570 575  
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp  
 580 585 590  
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln  
 595 600 605  
 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp  
 610 615 620  
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr  
 625 630 635 640  
 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu  
 645 650 655  
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr  
 660 665 670  
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys  
 675 680 685  
 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val  
 690 695 700  
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly  
 705 710 715 720  
 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu  
 725 730 735  
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln  
 740 745 750  
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala  
 755 760 765  
 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser  
 770 775 780  
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser  
 785 790 795 800  
 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val  
 805 810 815  
 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn  
 820 825 830  
 Phe

70

(2) INFORMATION FOR SEQ ID NO:442

75

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 891 amino acids  
 (B) TYPE: amino acid



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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

15 Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile  
1 5 10 15  
Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile  
20 25 30  
Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala  
35 40 45  
Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg  
50 55 60  
Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Leu Ile Pro Gly Asp  
25 65 70 75 80  
Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser  
85 90 95  
Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu  
100 105 110  
30 Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser  
115 120 125  
Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu  
130 135 140  
Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln  
35 145 150 155 160  
Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile  
165 170 175  
Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val  
180 185 190  
40 Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr  
195 200 205  
Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met  
210 215 220  
45 Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser  
225 230 235 240  
Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg  
245 250 255  
Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg  
260 265 270  
50 Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys  
275 280 285  
Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile  
290 295 300  
Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu  
305 310 315 320  
55 Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg  
325 330 335  
Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr  
340 345 350  
60 Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn  
355 360 365  
Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys  
370 375 380  
Gln Ala Asn Ile Asn Lys Val Ile Ile Lys Gly Asn Thr Val Val Tyr  
385 390 395 400  
65 Glu Asp Val Val Arg Arg Glu Leu Tyr Thr Lys Pro Gly Gln Leu Phe  
405 410 415  
Ser Arg Glu Asp Ile Ile Asn Ser Ile Arg Leu Ile Asn Gln Leu Gly  
420 425 430  
70 His Phe Asp Ala Glu Lys Ser Ile Pro Arg Pro Ile Pro Asn Pro Glu  
435 440 445  
Thr Gly Thr Val Asp Ile Glu Tyr Asp Leu Val Pro Arg Ser Ser Asp  
450 455 460  
75 Gln Leu Glu Leu Ser Val Gly Trp Ser Gln Ser Gly Leu Leu Phe Arg  
465 470 475 480

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Gly Ala Ile Lys Phe Thr Asn Phe Ser Val Gly Asn Leu Leu His Pro  
 485 490  
 Ser Met Tyr Lys Lys Gly Ile Ile Pro Gln Gly Asp Gly Gln Thr Leu  
 500 505 510  
 5 Ser Leu Ser Ala Gln Thr Asn Gly Lys Tyr Tyr Gln Gln Tyr Ser Val  
 515 520 525  
 Thr Phe Met Asp Pro Trp Phe Gly Gly Lys Arg Pro Asp Met Phe Ser  
 530 535 540  
 10 Phe Ser Ala Phe Tyr Ser Lys Thr Thr Ala Ile Asp Ser Lys Phe Tyr  
 545 550 555 560  
 Asn Ser Asn Ala Gly Asn Tyr Tyr Asn Ala Tyr Tyr Asn Ser Tyr Tyr  
 565 570 575  
 Asn Asn Tyr Asn Ser Tyr Tyr Asn Gly Met Ser Asn Tyr Thr Gly Asp  
 580 585 590  
 15 Leu Tyr Thr Gln Ala Ser Asp Pro Asp Arg Ser Leu Gln Met Leu Gly  
 595 600 605  
 Thr Ser Ile Gly Tyr Gly Lys Arg Leu Thr Trp Pro Asp Asn Trp Phe  
 610 615 620  
 20 Gln Ile Tyr Thr Ser Leu Asn Tyr Thr Tyr Tyr Arg Leu Arg Asn Trp  
 625 630 635 640  
 Ser Tyr Asn Thr Phe Gln Asn Phe His His Gly Ser Ala Asn Asp Leu  
 645 650 655  
 Asn Leu Glu Leu Arg Leu Ser Arg Thr Ser Ile Asp Asn Pro Ile Tyr  
 660 665 670  
 25 Thr Arg Ser Gly Ser Asp Phe Met Val Ser Val Ala Ala Thr Leu Pro  
 675 680 685  
 Tyr Ser Leu Trp Asp Asn His Asp Tyr Ala Ser Gln Asn Leu Ser Val  
 690 695 700  
 30 Ser Asp Arg Tyr Arg Phe Ile Glu Tyr His Lys Trp Lys Phe Arg Gly  
 705 710 715 720  
 Arg Val Phe Thr Pro Leu Leu Asn Pro Ala Thr His Lys Tyr Thr Pro  
 725 730 735  
 Val Leu Met Ser Arg Val Glu Gly Ala Val Leu Gly Ser Tyr Asn Ser  
 740 745 750  
 35 Asn Lys Lys Ser Pro Phe Gly Thr Phe Tyr Met Gly Gly Asp Gly Met  
 755 760 765  
 Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly  
 770 775 780  
 40 Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala  
 785 790 795 800  
 Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn  
 805 810 815  
 Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp  
 820 825 830  
 45 Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly  
 835 840 845  
 Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp  
 850 855 860  
 50 Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly  
 865 870 875 880  
 Ser Asn Val His Phe Val Leu Gly Gln Glu Phe  
 885 890

(2) INFORMATION FOR SEQ ID NO:443

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu  
 1 5 10 15

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Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met  
 20 25 30  
 Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln  
 35 40 45  
 5 Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu  
 50 55 60  
 Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe  
 65 70 75 80  
 10 Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Ala Ile Val Lys Lys  
 85 90 95  
 Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly  
 100 105 110  
 Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu  
 115 120 125  
 15 Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met  
 130 135 140  
 Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile  
 145 150 155 160  
 20 Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe  
 1 5 10 15  
 45 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu  
 20 25 30  
 Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val  
 35 40 45  
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln  
 50 55 60  
 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala  
 65 70 75 80  
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala  
 85 90 95  
 55 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys  
 100 105 110  
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala  
 115 120 125  
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg  
 130 135 140  
 60 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp  
 145 150 155 160  
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

10 Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
    1      5      10      15
    Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
        20      25      30
15 Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
    35      40      45
    Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
    50      55      60
    Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Leu Glu Asn Ile Arg
    65      70      75      80
20 Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
    85      90      95
    Ser Tyr Gln Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Gln Leu
    100      105      110
    Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
    115      120      125
25 Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
    130      135      140
    Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
    145      150      155      160
30 Gly Ile Lys

```

(2) INFORMATION FOR SEQ ID NO:446

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 827 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...827

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1      5      10      15
55 Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
    20      25      30
    Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
    35      40      45
60 Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
    50      55      60
    Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
    65      70      75      80
    Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
    85      90      95
65 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
    100      105      110
    Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
    115      120      125
70 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
    130      135      140
    Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
    145      150      155      160
    Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
    165      170      175
75 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val

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		180		185		190
	Glu	Val	Tyr	Arg	Pro	Leu
		195		200		205
	Ser	Phe	Val	Asn	Pro	Asp
5		210		215		220
	Gly	Phe	Thr	Ala	Asp	Tyr
		225		230		235
	Arg	Tyr	Lys	Gln	Pro	Gln
		245		250		255
10		260		265		270
	Ile	Thr	Gly	Val	Arg	Tyr
		275		280		285
	Asp	Thr	Lys	Ala	Glu	Tyr
15		290		295		300
	Met	Thr	Tyr	Arg	Phe	Ser
		305		310		315
	Ile	Ser	Gln	Thr	Arg	Tyr
		325		330		335
20		340		345		350
	Gln	Glu	Gln	Asp	Arg	Phe
		355		360		365
	Phe	Val	Pro	Asp	Asp	Lys
25		370		375		380
	Asn	Ser	Asn	Glu	Arg	Glu
		385		390		395
	Asn	Asp	Val	Gln	Leu	Gly
		405		410		415
30		420		425		430
	Arg	Asn	Arg	Leu	Ser	Tyr
		435		440		445
	Met	Lys	Leu	Asn	Glu	Lys
35		450		455		460
	Met	Glu	Lys	Ile	Ala	Asp
		465		470		475
	Val	Gly	Tyr	Asn	Leu	Pro
		485		490		495
40		500		505		510
	Val	Gln	Asp	Arg	Phe	Asn
		515		520		525
	Ile	Pro	Gly	Ile	Arg	Ala
45		530		535		540
	Val	Ser	Pro	Arg	Ile	Ser
		545		550		555
	Leu	Val	Leu	Arg	Ala	Ala
		565		570		575
50		580		585		590
	Val	Leu	Asn	Glu	Lys	Ile
		595		600		605
	Gly	Ala	Asp	Tyr	Thr	Phe
55		610		615		620
	Ala	Glu	Ala	Tyr	Tyr	Lys
		625		630		635
	Glu	Asn	Val	Lys	Ile	Arg
		645		650		655
60		660		665		670
	Asp	Ser	Trp	Leu	Thr	Ala
		675		680		685
	Gly	Tyr	Gly	Ser	Leu	Pro
65		690		695		700
	Phe	Phe	Leu	Gln	Glu	Tyr
		705		710		715
	Leu	Arg	Ala	Ala	Leu	Ser
		725		730		735
70		740		745		750
	Gly	Leu	Ser	Ser	Pro	Ala
		755		760		765
	Leu	Gly	Val	Met	Tyr	Lys
75		770		775		780
	Arg	Ser	Lys	Trp	Leu	Met

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Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp Val  
 785 790 795 800  
 Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr Arg  
 805 810 815  
 5 Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe  
 820 825

(2) INFORMATION FOR SEQ ID NO:447

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 672 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...672
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

Met Tyr Ser Gly His His Lys Ile His Tyr Pro Phe Leu Ile Leu Leu  
 1 5 10 15  
 30 Val Cys Leu Ala Phe Ala Ala Cys Lys Ser Val Lys Leu Lys Asp Ala  
 20 25 30  
 Glu Lys Ala His Asp Arg Gln Glu Tyr Thr Lys Ala Ala Asp Met Tyr  
 35 35 40 45  
 Asn Thr Leu Tyr Arg Arg Thr Arg Arg Lys Gln Val Glu Met Lys Ala  
 50 50 55 60  
 Tyr Thr Ala Phe Arg Ser Gly Glu Asn Tyr Arg Ala Ala Gly Arg Gln  
 65 70 75 80  
 Ala Lys Ala Leu Arg Gly Tyr Leu Asn Ala Arg Arg Tyr Gly Tyr Pro  
 85 90 95  
 40 Asp Ser Val Val Leu Leu Arg Leu Ala Gln Thr Tyr Gln Gln Gly Gly  
 100 105 110  
 Asn Tyr Lys Glu Ala Glu Val Leu Phe Arg Gly Tyr Leu Glu Ala Tyr  
 115 120 125  
 Pro Lys Ser Tyr Phe Ala Ala Ile Gly Leu Glu Gly Cys Leu Phe Ala  
 130 135 140  
 45 Arg Gln Gln Lys Glu Tyr Pro Thr Arg Tyr Arg Ile Arg Arg Ala Ala  
 145 150 155 160  
 Glu Trp Asn Ser Ala Arg Gly Asp Phe Gly Pro Ala Tyr Ala Pro Asp  
 165 170 175  
 50 Ala Ser Ala Leu Tyr Phe Thr Ser Ser Arg Ser Lys Asp Asp Gly Leu  
 180 185 190  
 Asp Asn Ser Ser Ile Thr Gly Leu Lys Pro Asn Asp Ile Tyr Ile Ile  
 195 200 205  
 Lys Arg Asp Ala Gln Gly Arg Trp Gly Arg Pro Asp Ser Val Ser Gly  
 210 215 220  
 55 Gly Ile Asn Thr Pro Trp Asp Glu Gly Val Pro Thr Ile Thr Pro Asp  
 225 230 235 240  
 Gly Ser Thr Ile Tyr Tyr Thr Leu Ala Gln Gln Gly Ala Asp Tyr Asp  
 245 250 255  
 60 Arg Thr Val Gln Ile Tyr Ser Ala Ala Arg Ser Gly Glu Gly Gly Trp  
 260 265 270  
 Ser Asn Gly Ser Leu Val Asp Ile Met Arg Asp Ser Leu Arg Met Ala  
 275 280 285  
 Ala His Pro Ser Met Ser Ala Ser Gly Asp Tyr Leu Tyr Phe Val Ser  
 290 295 300  
 65 Asn Ile Gly Gly Ser Tyr Gly Gly Lys Asp Ile Tyr Arg Val Lys Val  
 305 310 315 320  
 Ser Asp Arg Ser Tyr Gly Ser Pro Glu Asn Leu Gly Pro Asp Ile Asn  
 325 330 335  
 70 Thr Pro Gly Asp Glu Met Phe Pro Phe Ile Asp Gly Asp Ser Thr Leu  
 340 345 350  
 Phe Phe Ala Ser Asp Gly His Ala Gly Leu Gly Gly Leu Asp Ile Phe  
 355 360 365  
 75 Lys Ala Thr Leu Asp Ser Thr Gly Gln Trp His Val Val Asn Met Gly  
 370 375 380

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Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro  
 385 390 395 400  
 Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly  
 405 410 415  
 5 Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe  
 420 425 430  
 His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met  
 435 440 445  
 10 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly  
 450 455 460  
 Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly  
 465 470 475 480  
 Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala  
 485 490 495  
 15 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Thr Asp Thr  
 500 505 510  
 Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg  
 515 520 525  
 20 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala  
 530 535 540  
 Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile  
 545 550 555 560  
 Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp  
 565 570 575  
 25 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala  
 580 585 590  
 Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg  
 595 600 605  
 30 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala  
 610 615 620  
 Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr  
 625 630 635 640  
 Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp  
 645 650 655  
 35 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg  
 660 665 670

(2) INFORMATION FOR SEQ ID NO:448

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 708 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...708  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln  
 1 5 10 15  
 60 Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His  
 20 25 30  
 Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu  
 35 40 45  
 65 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys  
 50 55 60  
 Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser  
 65 70 75 80  
 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg  
 85 90 95  
 70 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile  
 100 105 110  
 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu  
 115 120 125  
 75 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn  
 130 135 140

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Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys  
 145 150 155 160  
 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala  
 165 170 175  
 5 Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp  
 180 185 190  
 Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser  
 195 200 205  
 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val  
 210 215 220  
 10 Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala  
 225 230 235 240  
 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu  
 245 250 255  
 15 Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly  
 260 265 270  
 Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser  
 275 280 285  
 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln  
 290 295 300  
 20 Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala  
 305 310 315 320  
 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly  
 325 330 335  
 25 Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu  
 340 345 350  
 Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln  
 355 360 365  
 30 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn  
 370 375 380  
 Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu  
 385 390 395 400  
 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys  
 405 410 415  
 35 Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val  
 420 425 430  
 Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr  
 435 440 445  
 40 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln  
 450 455 460  
 Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro  
 465 470 475 480  
 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr  
 485 490 495  
 45 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe  
 500 505 510  
 His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn  
 515 520 525  
 50 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile  
 530 535 540  
 Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe  
 545 550 555 560  
 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met  
 565 570 575  
 55 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg  
 580 585 590  
 Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu  
 595 600 605  
 60 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn  
 610 615 620  
 Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu  
 625 630 635 640  
 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro  
 645 650 655  
 65 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr  
 660 665 670  
 Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr  
 675 680 685  
 70 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val  
 690 695 700  
 Met Val Asn Phe  
 705

(2) INFORMATION FOR SEQ ID NO: 449

75



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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 462 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...462

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

20 Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val  
 1 5 10 15  
 Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu  
 20 25 30  
 Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp  
 35 40 45  
 25 Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp  
 50 55 60  
 Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp  
 65 70 75 80  
 30 Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys  
 85 90 95  
 Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly  
 100 105 110  
 Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser  
 115 120 125  
 35 Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly  
 130 135 140  
 Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp  
 145 150 155 160  
 40 Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu  
 165 170 175  
 Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn  
 180 185 190  
 Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr  
 195 200 205  
 45 Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu  
 210 215 220  
 Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val  
 225 230 235 240  
 50 Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu  
 245 250 255  
 Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr  
 260 265 270  
 Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg  
 275 280 285  
 55 Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr  
 290 295 300  
 Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile  
 305 310 315 320  
 60 Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser  
 325 330 335  
 Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn  
 340 345 350  
 Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg  
 355 360 365  
 65 His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg  
 370 375 380  
 Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg  
 385 390 395 400  
 70 Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg Tyr Gln Thr Gly  
 405 410 415  
 Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln  
 420 425 430  
 Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys  
 435 440 445  
 75 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln



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420 425 430  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
 435 440 445  
 5 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 450 455 460  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 465 470 475 480  
 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
 485 490

10

(2) INFORMATION FOR SEQ ID NO:451

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

20

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...245

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe  
 1 5 10 15  
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg  
 20 25 30  
 35 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys  
 35 40 45  
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp  
 50 55 60  
 40 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala  
 65 70 75 80  
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser  
 85 90 95  
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln  
 100 105 110  
 45 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val  
 115 120 125  
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp  
 130 135 140  
 50 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro  
 145 150 155 160  
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg  
 165 170 175  
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly  
 180 185 190  
 55 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe  
 195 200 205  
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser  
 210 215 220  
 60 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala  
 225 230 235 240  
 Ser Phe Ala Leu Lys  
 245

65

(2) INFORMATION FOR SEQ ID NO:452

70

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

75

(iii) HYPOTHETICAL: YES

75

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...276

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

10 Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly  
1 5 10 15  
Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys  
20 25 30  
Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala  
35 40 45  
15 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val  
50 55 60  
Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser  
65 70 75 80  
Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala  
85 90 95  
20 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala  
100 105 110  
Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln  
115 120 125  
25 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met  
130 135 140  
Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr  
145 150 155 160  
Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr Gly Leu Ala Tyr  
165 170 175  
30 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr  
180 185 190  
Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp  
195 200 205  
35 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly  
210 215 220  
Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val  
225 230 235 240  
Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile  
245 250 255  
40 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys  
260 265 270  
Pro Gly Lys Lys  
275

45

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

65

Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu  
1 5 10 15  
Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu  
20 25 30  
70 Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His  
35 40 45  
Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr  
50 55 60  
Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile  
65 70 75 80

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Pro Phe Gly Leu Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val  
 85 90 95  
 Ile Ser Lys Trp Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile  
 100 105 110  
 5 Ser Gln Val Lys Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu  
 115 120 125  
 Arg Glu His Gly Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr  
 130 135 140  
 10 Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met  
 145 150 155 160  
 Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr  
 165 170 175  
 Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg  
 180 185 190  
 15 Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr  
 195 200 205  
 Ile Ser Ala Leu Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln  
 210 215 220  
 20 Asp Ile Ile Tyr Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys  
 225 230 235 240  
 Leu Arg Ala Lys Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro  
 245 250 255  
 Trp Arg Ile Gly Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu  
 260 265 270  
 25 Ser Pro Thr Asp Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr  
 275 280 285  
 Arg Lys Met Pro Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe  
 290 295 300  
 30 Phe Ser Gly Asn Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys  
 305 310 315 320  
 Ser Leu Ala Arg Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu  
 325 330 335  
 Gln Arg Asp Ser Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr  
 340 345 350  
 35 Leu Asp Lys Pro Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys  
 355 360 365  
 Ser Asn Asp Phe Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg  
 370 375 380  
 40 Asn Val Phe Gly Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser  
 385 390 395 400  
 Tyr Glu Trp Glu Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu  
 405 410 415  
 Ile Asp Ile Asn Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe  
 420 425 430  
 45 Pro Ser Ile Val Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Pro  
 435 440 445  
 Thr Thr Thr Thr Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His  
 450 455 460  
 50 Tyr Phe Ser Met Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln  
 465 470 475 480  
 Pro Ser Lys Glu His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr  
 485 490 495  
 Asn Leu Leu Gly His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn  
 500 505 510  
 55 Asn Pro Pro Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met  
 515 520 525  
 Gly Tyr Ile Tyr Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His  
 530 535 540  
 60 His Leu Trp Met Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn  
 545 550 555 560  
 Leu Ile Tyr Leu Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe  
 565 570 575  
 Val Gly Val Pro Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg  
 580 585 590  
 65 Tyr Ser Tyr Thr Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly  
 595 600 605  
 Thr Gly Val Ile Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser  
 610 615 620  
 70 Glu Gln Phe Tyr Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val  
 625 630 635 640  
 Arg Ser Ile Gly Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr  
 645 650 655  
 Ser Tyr Leu Asp Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu  
 660 665 670  
 75 Tyr Arg Gly Lys Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp

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675 680 685  
 Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly  
 690 695 700  
 5 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala  
 705 710 715 720  
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val  
 725 730 735  
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys  
 740 745 750  
 10 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His  
 755 760 765  
 Leu Ala Val Gly Tyr Pro Phe  
 770 775  
 15 (2) INFORMATION FOR SEQ ID NO:454  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (E) LOCATION 1...774  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454  
 35 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gly Ile Ala Gly Cys Leu  
 1 5 10 15  
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp  
 20 25 30  
 40 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser  
 35 40 45  
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn  
 50 55 60  
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser  
 65 70 75 80  
 45 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met  
 85 90 95  
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala  
 100 105 110  
 50 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr  
 115 120 125  
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr  
 130 135 140  
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu  
 145 150 155 160  
 55 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu  
 165 170 175  
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro  
 180 185 190  
 60 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn  
 195 200 205  
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp  
 210 215 220  
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu  
 225 230 235 240  
 65 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe  
 245 250 255  
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu  
 260 265 270  
 70 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr  
 275 280 285  
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val  
 290 295 300  
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser  
 305 310 315 320  
 75 Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg

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5 Phe Val Glu His 325 Asn Gly Lys Asp Glu Ile Ala Leu Ala 335 Asp Ser Ser  
 340 345 350  
 Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser  
 355 360 365  
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala  
 370 375 380  
 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu  
 385 390 395 400  
 10 Met Phe Asn Ile Lys Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly  
 405 410 415  
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro  
 420 425 430  
 15 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Leu Arg  
 435 440 445  
 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu  
 450 455 460  
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr  
 465 470 475 480  
 20 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp  
 485 490 495  
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro  
 500 505 510  
 25 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Glu Gln Phe Ile Leu Gly Ser  
 515 520 525  
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val  
 530 535 540  
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu  
 545 550 555 560  
 30 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly  
 565 570 575  
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp  
 580 585 590  
 35 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala  
 595 600 605  
 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Asn Ala Arg His  
 610 615 620  
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg  
 625 630 635 640  
 40 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro  
 645 650 655  
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn  
 660 665 670  
 45 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Phe  
 675 680 685  
 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu  
 690 695 700  
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala  
 705 710 715 720  
 50 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu  
 725 730 735  
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys  
 740 745 750  
 55 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile  
 755 760 765  
 Ala Val Gly Tyr Pro Phe  
 770

(2) INFORMATION FOR SEQ ID NO:455

60

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 867 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

70

- (iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

75

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...867

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:455

5	Met	Arg	Lys	Arg	Ile	Leu	Gln	Leu	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Ala
	1				5					10					15	
	Leu	Gly	Ser	Ser	Leu	Ala	Ile	Ala	Gln	Thr	Val	Val	Thr	Gly	Lys	Val
			20					25						30		
	Ile	Asp	Ser	Glu	Thr	Ser	Glu	Pro	Leu	Ile	Gly	Val	Ser	Val	Ser	Thr
			35					40						45		
10	Gly	Gln	Gly	Ala	Ser	Leu	Arg	Gly	Val	Thr	Thr	Asp	Met	Asp	Gly	Gly
		50					55					60				
	Phe	Arg	Phe	Glu	Val	Pro	Ala	Lys	Ser	Val	Leu	Thr	Phe	Arg	Cys	Val
		65				70				75					80	
	Gly	Tyr	Ala	Thr	Val	Thr	Arg	Ser	Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp
				85						90				95		
15	Leu	Gly	Thr	Ile	Leu	Leu	Asp	Pro	Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile
									105					110		
	Gln	Val	Ile	Ala	Ser	Val	Val	Pro	Lys	Asp	Arg	Met	Thr	Pro	Val	Pro
		115						120					125			
20	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp	Ile	Gln	Ala	Ala	Ser	Leu	Asn	Val
		130					135					140				
	Glu	Phe	Pro	Glu	Leu	Val	Lys	Ser	Thr	Pro	Ser	Thr	Tyr	Thr	Thr	Lys
		145				150					155				160	
	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp
				165						170				175		
25	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	Asn	Gly	Val	Pro	Val	Asn	Gly	Met
			180						185					190		
	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln
		195						200					205			
30	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly
		210					215					220				
	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp
		225					230					235			240	
	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu
				245						250				255		
35	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala
					260				265					270		
	Ile	Thr	Ile	Ala	Gly	Ser	His	Met	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly
			275				280						285			
40	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe
		290					295					300				
	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp
		305				310					315				320	
	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr
				325						330				335		
45	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr
								345					350			
	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu
		355						360					365			
50	Asn	His	Phe	Trp	Lys	Met	Asp	Glu	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk
		370					375					380				
	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn	
		385				390				395				400		
	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln
				405						410				415		
55	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala
				420						425				430		
	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly
			435					440					445			
60	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys
		450					455					460				
	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr
		465				470				475				480		
	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr
				485						490				495		
65	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln
				500						505				510		
	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile
				515						520				525		
70	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	Met	Glu	His	Ser	Ser	Glu	Trp	Ile
		530					535					540				
	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His
					545					550				555		560
	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro
					565					570				575		
75																



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Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys  
 590 585 590  
 Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg  
 595 600 605  
 5 Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn  
 610 615 620  
 Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly  
 625 630 635 640  
 10 Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr  
 645 650 655  
 Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val  
 660 665 670  
 Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val  
 675 680 685  
 15 Ser Tyr Arg Pro Ile Arg Gln Ile Asp Leu Arg Gly Met Phe Ser Leu  
 690 695 700  
 Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu  
 705 710 715 720  
 20 Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His  
 725 730 735  
 Val Gly Asp Ala Ala Gln Met Thr Ala Val Ser Ala Asp Ile Glu  
 740 745 750  
 Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys  
 755 760 765  
 25 Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu  
 770 775 780  
 Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly  
 785 790 795 800  
 30 Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser  
 805 810 815  
 Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val  
 820 825 830  
 Ser Asp Ala Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser  
 835 840 845  
 35 Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg  
 850 855 860  
 Val Asn Phe  
 865  
 40 (2) INFORMATION FOR SEQ ID NO:456  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...431  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456  
 60 Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser  
 1 5 10 15  
 Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg  
 20 25 30  
 65 Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp  
 35 40 45  
 Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His  
 50 55 60  
 Leu Asn Leu Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln  
 65 70 75 80  
 70 Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met  
 85 90 95  
 Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp  
 100 105 110  
 75 Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu  
 115 120 125

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Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met  
 130 135 140  
 Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala  
 145 150 155 160  
 5 Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala  
 165 170 175  
 Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg  
 180 185 190  
 10 Glu Glu Glu Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg  
 195 200 205  
 Gln Val Gln Ala Leu Gly Ala Lys Lys Asp Leu Glu Ala Gln Leu  
 210 215 220  
 Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys  
 225 230 235 240  
 15 Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu  
 245 250 255  
 Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro  
 260 265 270  
 20 Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp  
 275 280 285  
 Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg  
 290 295 300  
 Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly  
 305 310 315 320  
 25 Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly  
 325 330 335  
 Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp  
 340 345 350  
 30 Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val  
 355 360 365  
 Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys  
 370 375 380  
 Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly  
 385 390 395 400  
 35 Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu  
 405 410 415  
 Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg  
 420 425 430  
 40 (2) INFORMATION FOR SEQ ID NO:457  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...333  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457  
 60 Met Lys Lys Tyr Leu Leu Tyr Ala Ser Leu Leu Thr Ser Val Leu Leu  
 1 5 10 15  
 Phe Ser Cys Ser Lys Asn Asn Pro Asn Glu Pro Val Glu Asp Arg Ser  
 20 25 30  
 65 Ile Glu Ile Ser Ile Arg Val Asp Phe Thr Lys Thr Gly Glu Ala  
 35 40 45  
 Val Arg Tyr Glu Arg Asn Gln Gly Ser Ala Ala Glu Arg Leu Ile Thr  
 50 55 60  
 Asn Leu Tyr Leu Leu Phe Asp Gln Ser Gly Ala Asn Pro Ala Lys  
 65 70 75 80  
 70 Tyr Tyr Ile Thr Gly Asn Thr Phe Thr Gly Gly Thr Trp Leu Pro Asp  
 85 90 95  
 Asp Met Lys Val Lys Leu Asp Met Thr Gln Ser Glu Ala Gly Glu Arg  
 100 105 110  
 75 Lys Val Tyr Val Val Ala Asn Val Asp Asn Ala Val Lys Thr Ala Leu  
 115 120 125

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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Asp Ala Val Ala Asn Glu Ser Asp Leu Gln Thr Val Lys Arg Thr Thr  
 130 135 140  
 Ala Met Pro Trp Ser Thr Asp Ile Ala Ser Pro Phe Leu Met Ser Gly  
 145 150 155 160  
 5 Asn Lys Thr His Asp Phe Leu Ala Asn Arg Leu Leu Asp Asn Val Pro  
 165 170 175  
 Leu Val Arg Ala Ile Ala Lys Val Glu Leu Asn Ile Ser Leu Ser Glu  
 180 185 190  
 10 Lys Phe Gln Ile Val Pro Ile Ile Val Asn Gly Ser Leu Ser Glu Phe  
 195 200 205  
 Lys Phe Arg Tyr Val Asn Phe Asp Lys Glu Thr Tyr Val Val Lys Pro  
 210 215 220  
 Thr Thr Lys Pro Asp Asn Leu Ile Ser Ser Ala Asn Gly Val Trp Pro  
 225 230 235 240  
 15 Gln Ile Thr Asp Trp Thr Val Trp Gly Ala Ser Leu Asn Thr Ser Pro  
 245 250 255  
 Ala Pro Asp Ala Gly Thr Gly Tyr Thr Leu Asp Ala Asn Gly Lys Val  
 260 265 270  
 20 Thr Ala Leu Arg Ile Val Thr Tyr Leu Asn Glu Arg Asp Ser Lys Gly  
 275 280 285  
 Ala Thr Val Glu Val Ala Leu Pro Arg Val Asp Asp Gly Thr Leu Pro  
 290 295 300  
 Pro Pro Glu Phe Gly Pro Glu Leu Tyr Arg Leu Pro Leu Pro Asp Lys  
 305 310 315 320  
 25 Ile Leu Arg Asn His Trp Tyr Lys Tyr Glu Val Glu Ile  
 325 330

(2) INFORMATION FOR SEQ ID NO:458

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...315  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser  
 1 5 10 15  
 50 Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala  
 20 25 30  
 Ala Thr Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp  
 35 40 45  
 55 Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser  
 50 55 60  
 Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser  
 65 70 75 80  
 Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser  
 85 90 95  
 60 Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg  
 100 105 110  
 Asn Leu Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu  
 115 120 125  
 65 Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser  
 130 135 140  
 Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr  
 145 150 155 160  
 Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp  
 165 170 175  
 70 Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly  
 180 185 190  
 His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp  
 195 200 205  
 75 Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His  
 210 215 220

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Pro Ser Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val  
 225 230 235 240  
 Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val  
 245 250 255  
 5 Ile Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro  
 260 265 270  
 Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala  
 275 280 285  
 10 Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile  
 290 295 300  
 Leu His Ile Ala Arg Ala Leu Ala His Glu Arg  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:459

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 30 (B) LOCATION 1...848  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe  
 1 5 10 15  
 35 Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp  
 20 25 30  
 Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu  
 35 40 45  
 40 Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr  
 50 55 60  
 Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile  
 65 70 75 80  
 45 Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val  
 85 90 95  
 Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu  
 100 105 110  
 Asp Ala Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu  
 115 120 125  
 50 Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys  
 130 135 140  
 Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe  
 145 150 155 160  
 55 Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn  
 165 170 175  
 Gln Val Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile  
 180 185 190  
 Asp Ser Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu  
 195 200 205  
 60 Gln Ile Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly  
 210 215 220  
 Gly Ser Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile  
 225 230 235 240  
 Ile Thr Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu  
 245 250 255  
 65 Ser Phe Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala  
 260 265 270  
 Ser Ile Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln  
 275 280 285  
 70 Ala Arg Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu  
 290 295 300  
 Leu Gly Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg  
 305 310 315 320  
 75 Leu Ser Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu  
 325 330 335

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Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly  
 340 345 350  
 Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr  
 355 360 365  
 5 Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser  
 370 375 380  
 Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile  
 385 390 395 400  
 10 Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln  
 405 410 415  
 Asp Gln Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met  
 420 425 430  
 Gly Gly Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro  
 435 440 445  
 15 Ser Gln Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp  
 450 455 460  
 Val Met Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn  
 465 470 475 480  
 20 Thr Ile Pro Leu Tyr Pro Gln Leu Asp Gln Asn Ile Asn Asn Tyr Ser  
 485 490 495  
 Leu Phe Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val  
 500 505 510  
 Gly Ala Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser  
 515 520 525  
 25 Pro Arg Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg  
 530 535 540  
 Ala Thr Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp  
 545 550 555 560  
 30 Leu His Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp  
 565 570 575  
 Pro Asn Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp  
 580 585 590  
 Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly  
 595 600 605  
 35 Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp  
 610 615 620  
 Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala  
 625 630 635 640  
 40 Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe  
 645 650 655  
 Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala  
 660 665 670  
 Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val  
 675 680 685  
 45 Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met  
 690 695 700  
 Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr  
 705 710 715 720  
 50 Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala  
 725 730 735  
 Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys  
 740 745 750  
 Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu  
 755 760 765  
 55 Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe  
 770 775 780  
 Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala  
 785 790 795 800  
 60 Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe  
 805 810 815  
 Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr  
 820 825 830  
 Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 835 840 845

(2) INFORMATION FOR SEQ ID NO:460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

10 Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly  
1 5 10 15  
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser  
20 25 30  
15 Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser  
35 40 45  
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro  
50 55 60  
Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro  
65 70 75 80  
20 Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr  
85 90 95  
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala  
100 105 110  
25 Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg  
115 120 125  
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg  
130 135 140  
30 Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr  
145 150 155 160  
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn  
165 170 175  
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro  
180 185 190  
35 Gly Ala Lys Arg Val Ile Pro Arg Lys Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:461

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...455

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

60 Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu  
1 5 10 15  
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met  
20 25 30  
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn  
35 40 45  
65 Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser  
50 55 60  
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile  
65 70 75 80  
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr  
85 90 95  
70 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val  
100 105 110  
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys  
115 120 125  
75 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp  
130 135 140

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Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln  
 145 150 155 160  
 Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln  
 165 170 175  
 5 Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly  
 180 185 190  
 Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu  
 195 200 205  
 10 Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln  
 210 215 220  
 Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp  
 225 230 235 240  
 Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu  
 245 250 255  
 15 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser  
 260 265 270  
 Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala  
 275 280 285  
 20 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr  
 290 295 300  
 Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser  
 305 310 315 320  
 Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn  
 325 330 335  
 25 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser  
 340 345 350  
 Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys  
 355 360 365  
 30 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala  
 370 375 380  
 Asp Lys Ala Ile Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys  
 385 390 395 400  
 Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala  
 405 410 415  
 35 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu  
 420 425 430  
 Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp  
 435 440 445  
 40 Phe Tyr Gln Gly Lys Asp Phe  
 450 455

## (2) INFORMATION FOR SEQ ID NO:462

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 444 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...444  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu  
 1 5 10 15  
 65 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Cys  
 20 25 30  
 Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala  
 35 40 45  
 Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe  
 50 55 60  
 70 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg  
 65 70 75 80  
 Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn  
 85 90 95  
 75 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln  
 100 105 110

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Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg  
 115 120 125  
 Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu  
 130 135 140  
 5 Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met  
 145 150 155 160  
 Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met  
 165 170 175  
 10 Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser  
 180 185 190  
 Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys  
 195 200 205  
 Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp  
 210 215 220  
 15 Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp  
 225 230 235 240  
 Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His  
 245 250 255  
 20 His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr  
 260 265 270  
 Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val  
 275 280 285  
 Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp  
 290 295 300  
 25 Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val  
 305 310 315 320  
 Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser  
 325 330 335  
 30 His Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg  
 340 345 350  
 Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala  
 355 360 365  
 Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr  
 370 375 380  
 35 Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu  
 385 390 395 400  
 Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu  
 405 410 415  
 40 Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys  
 420 425 430  
 Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp  
 435 440

## (2) INFORMATION FOR SEQ ID NO:463

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 940 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...940  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

65 Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe  
 5 10 15  
 Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly  
 20 25 30  
 Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe  
 35 40 45  
 70 Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp  
 50 55 60  
 Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val  
 65 70 75 80  
 75 Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala  
 85 90 95



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Ser His Ile Ser Ser Ile Gly Asp Val Asp Val Tyr Arg Leu Gln Phe  
 100 105 110  
 Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu Tyr Tyr Asp Ala Phe Asn  
 115 120 125  
 5 Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr Thr Pro Asp His Glu Ile  
 130 135 140  
 Val Leu Gly Ala Tyr Thr Asn Ala Thr His Arg Arg Asn Gly Ala Phe  
 145 150 155 160  
 10 Ala Thr Glu Pro Val Pro Gly Ser Glu Leu Ile Met Asp Tyr Glu Val  
 165 170 175  
 Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys Ile Ser Gly Ala Gly Tyr  
 180 185 190  
 Ile Phe Asp Lys Val Gly Gly Arg Pro Val Thr Asp Asn His Tyr Gly  
 195 200 205  
 15 Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys Glu Ile Asn Ile Asn Cys  
 210 215 220  
 Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys Asn Gly Val Val Gln Met  
 225 230 235 240  
 20 Ile Met Val Lys Gly Gln Tyr Ile Ser Met Cys Ser Gly Asn Leu Leu  
 245 250 255  
 Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu Ile Ile Ser Ala Gly His  
 260 265 270  
 Cys Ala Ser Ile Thr Thr Asn Phe Gly Val Thr Gln Ser Glu Leu Asp  
 275 280 285  
 25 Lys Trp Ile Phe Thr Phe His Tyr Glu Lys Arg Gly Cys Ser Asn Gly  
 290 295 300  
 Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile Ile Gly Ala Ser Met Lys  
 305 310 315 320  
 Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp Gly Leu Leu Leu Gln Leu  
 325 330 335  
 30 Asn Asp Glu Val Pro Leu Arg Tyr Arg Val Tyr Tyr Asn Gly Trp Asp  
 340 345 350  
 Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala Gly Ile His His Pro Ala  
 355 360 365  
 35 Gly Asp Ala Met Lys Ile Ser Ile Leu Lys Lys Thr Pro Ala Leu Asn  
 370 375 380  
 Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly Thr Asp Asp His Phe Tyr  
 385 390 395 400  
 40 Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly Gly Ser Ser Gly Ser Ser  
 405 410 415  
 Leu Phe Asn Gln Asn Lys His Val Val Gly Thr Leu Thr Gly Gly Ala  
 420 425 430  
 Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly Arg Leu Asn Ser His Trp  
 435 440 445  
 45 Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser Arg Met Asp Ile Tyr Leu  
 450 455 460  
 Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile Leu Asn Gly Thr Tyr Arg  
 465 470 475 480  
 50 Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro Arg Leu Leu Leu Gln Ser  
 485 490 495  
 Thr Gly Asp Gln Val Glu Leu Asn Trp Thr Ala Val Pro Ala Asp Gln  
 500 505 510  
 Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His Ile Phe Arg Asn Gly Lys  
 515 520 525  
 55 Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr Ser Asp Ala Ile Asp Glu  
 530 535 540  
 Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe  
 545 550 555 560  
 60 Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp  
 565 570 575  
 Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys  
 580 585 590  
 Pro Asp Val Thr Pro Leu Pro Gly Gly Gly Val Ser Leu Ser Trp Lys  
 595 600 605  
 65 Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn  
 610 615 620  
 Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala  
 625 630 635 640  
 70 Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met  
 645 650 655  
 Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile Ala Ala Val Tyr Val Met  
 660 665 670  
 Pro Ser Ala Pro Asp Ser Thr Phe His Leu Phe Leu Lys Ser Asn Thr  
 675 680 685  
 75 Asn Arg Arg Leu Gln Lys Val Thr Thr Pro Ser Asp Trp Gln Ala Gly



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180 185 190  
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly  
 195 200 205  
 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys  
 210 215 220  
 5 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile  
 225 230 235 240  
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys  
 245 250 255  
 10 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro  
 260 265 270  
 Asp Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln  
 275 280 285  
 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile  
 290 295 300  
 15 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly  
 305 310 315 320  
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu  
 325 330 335  
 20 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn  
 340 345 350  
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile  
 355 360 365  
 25 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly  
 370 375 380  
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr  
 385 390 395 400  
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val  
 405 410 415  
 30 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala  
 420 425 430  
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile  
 435 440 445  
 35 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu  
 450 455 460  
 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val  
 465 470 475 480  
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr  
 485 490 495  
 40 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr  
 500 505 510  
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr  
 515 520 525  
 45 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala  
 530 535 540  
 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu  
 545 550 555 560  
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn  
 565 570 575  
 50 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys  
 580 585 590  
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp  
 595 600 605  
 55 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly  
 610 615 620  
 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln  
 625 630 635 640  
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val  
 645 650 655  
 60 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys  
 660 665 670

(2) INFORMATION FOR SEQ ID NO:465

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1282 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 75 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1282

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

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Met Arg Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly
1      5      10      15
10  Leu Gln Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu
    20      25      30
    Pro Ser Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu
    35      40      45
    Val Val Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln
    50      55      60
15  Val Phe Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu
    65      70      75
    Gly Glu Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu
    85      90      95
20  Phe Ser Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe
    100     105     110
    Asp Asn Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu
    115     120     125
25  Pro Glu Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp
    130     135     140
    Tyr Tyr Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser
    145     150     155
    Gln Asp Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr
    165     170     175
30  Pro Phe Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys
    180     185     190
    Ile Glu Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys
    195     200     205
35  Asn Thr Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr
    210     215     220
    Glu Ala Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg
    225     230     235
    Gly Thr Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln
    245     250     255
40  Asn Cys Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln
    260     265     270
    Gln Pro His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr
    275     280     285
45  Asn Gly Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser
    290     295     300
    Phe Pro Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn
    305     310     315
    Phe Ile Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp
    325     330     335
50  Gly Lys Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr
    340     345     350
    Leu Ala Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn
    355     360     365
    Val Ser Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser
    370     375     380
55  Asp Tyr Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu
    385     390     395
    Phe Ile Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu
    405     410     415
60  Ile Glu Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His
    420     425     430
    Lys Asn Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu
    435     440     445
65  Arg Leu Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile
    450     455     460
    Leu Lys Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu
    465     470     475
    Asn Asn Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr
    485     490     495
70  Val Trp Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg
    500     505     510
    Leu Asn Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser
    515     520     525
75  Ser Ala Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr
    530     535     540

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	Thr	Tyr	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg
	545				550						555					560
	Ala	Thr	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu
				565						570					575	
5	Phe	Tyr	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val
			580						585				590			
	Val	Gly	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp
			595				600					605				
10	Thr	Tyr	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn
	610				615							620				
	Ile	Met	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn
	625				630						635				640	
	Asn	Thr	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu
				645						650					655	
15	Lys	Ile	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile
			660						665					670		
	Gln	Val	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile
			675					680				685				
20	Ser	Gly	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp
	690				695							700				
	Gly	Leu	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu
	705				710						715				720	
	Asn	Leu	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser
				725						730					735	
25	Val	Lys	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu
			740						745					750		
	Ile	Ser	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn
			755						760				765			
30	Cys	Asp	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr
	770						775					780				
	Val	Phe	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys
					790						795				800	
	Ala	Lys	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr
				805						810					815	
35	His	Ile	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile
			820						825					830		
	Lys	Leu	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val
			835						840				845			
40	Asn	Cys	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn
	850						855					860				
	Arg	Leu	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly
	865					870					875				880	
	Ser	Thr	Leu	Tyr	Asn	Ser	Tyr	Gly	Ile	Tyr	Asn	Arg	Asn	Lys	Ile	Ser
				885						890				895		
45	Asn	Asn	His	Ile	Gly	Val	Arg	Leu	Leu	Asn	Asn	Ser	Cys	Phe	Tyr	Phe
			900						905					910		
	Asp	Asn	Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser
			915						920				925			
50	Asn	Arg	Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn
	930					935						940				
	Phe	His	Tyr	Asn	Ser	Leu	Gln	Gly	Gly	Asp	Thr	Asp	Thr	Trp	Ile	Tyr
	945					950					955				960	
	Asn	Asp	Thr	Tyr	Thr	Asn	Arg	Tyr	Ile	Asp	Val	Ser	Asn	Asn	His	Trp
				965						970					975	
55	Gly	Asn	Asn	Asp	Leu	Phe	Asp	Pro	Asn	Gln	Val	Phe	Asn	Thr	Pro	Asp
			980						985					990		
	Leu	Phe	Ile	Trp	Ile	Pro	Phe	Trp	Asp	Gly	Leu	Pro	Asn	Gly	Arg	Ser
			995					1000					1005			
60	Gly	Asn	Ser	Ser	Ala	Glu	Ala	Val	Glu	Phe	Gln	Thr	Ala	Leu	Asp	Cys
	1010						1015						1020			
	Ile	Gly	Asn	Ser	Asp	Tyr	Leu	Ser	Ala	Lys	Val	Ala	Leu	Lys	Met	Met
					1025							1030				1040
	Val	Glu	Thr	Tyr	Pro	Glu	Ser	Asp	Phe	Ala	Ile	Ala	Ala	Leu	Lys	Glu
				1045							1050				1055	
65	Leu	Phe	Arg	Ile	Glu	Lys	Met	Ser	Gly	Asn	Asp	Tyr	Glu	Gly	Leu	Lys
				1060						1065				1070		
	Asp	Tyr	Phe	Arg	Ser	Asn	Pro	Thr	Ile	Ile	Ser	Ser	Gln	Asn	Leu	Phe
			1075						1080					1085		
70	Pro	Thr	Ala	Asp	Phe	Leu	Ser	Ala	Arg	Cys	Asp	Ile	Val	Cys	Glu	Asn
				1090					1095					1100		
	Tyr	Gln	Ser	Ala	Ile	Asp	Trp	Tyr	Glu	Asn	Arg	Leu	Asn	Ser	Glu	Ile
	1105					1110						1115				1120
	Ser	Tyr	Gln	Asp	Ser	Val	Phe	Ala	Val	Ile	Asp	Leu	Gly	Asp	Ile	Tyr
					1125						1130				1135	
75	Trp	Asn	Met	Gln	Leu	Asp	Ser	Leu	Arg	Gly	Thr	Gly	Ile	Asp	Leu	Asn

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1140      1145      1150
Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val
1155      1160      1165
Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu
5 1170      1175      1180
Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile
1185      1190      1195      1200
Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr
1205      1210      1215
10 Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly
1220      1225      1230
Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr
1235      1240      1245
Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu
15 1250      1255      1260
Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg
1265      1270      1275      1280
Ile Lys

```

20

(2) INFORMATION FOR SEQ ID NO:466

```

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1274 amino acids
25 (B) TYPE: amino acid
(D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

```

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

```

```

35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1274

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```

40 Met Met Cys Ser Leu His Leu Gly Leu Gln Ser Gln Thr Trp His Gly
1 5 10 15
Asp Pro Asp Ser Val Ala Ala Leu Pro Ser Ile Gly Ile Gln Glu Ser
20 25 30
45 Ser Cys Thr Arg Ile Thr Phe Glu Val Val Phe Pro Gly Phe Tyr Ser
35 40 45
Val Glu Lys Arg Glu Gly Asn Gln Val Phe Gln Arg Ile Ser Met Pro
50 55 60
Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu Ala Glu Leu Pro Val Leu
65 70 75 80
Lys Lys Met Ile Ala Val Pro Glu Phe Ser Thr Ala Asn Val Ala Val
85 90 95
Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn Tyr Asn Ile Tyr Pro Asn
100 105 110
55 Pro Thr Tyr Val Val Glu Glu Leu Pro Glu Gly Gly Thr Tyr Leu Val
115 120 125
Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr Ser Gln Asn Val Ser Leu
130 135 140
60 Pro Ser Thr His Tyr Val Tyr Ser Gln Asp Gly Tyr Phe Arg Ser Gln
145 150 155 160
Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe Arg Tyr Asn Pro Val Arg
165 170 175
Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu Val Thr Ile Thr Phe Asp
180 185 190
65 Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr Gly Ile Phe Asn Lys Val
195 200 205
Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala Asp Gly Lys Ser Ala Ile
210 215 220
70 Glu Asn Asp Met Val Phe Ser Arg Gly Thr Thr Thr Tyr Ile Ser Gly
225 230 235 240
Asn Val Ala Ser Asn Leu Pro Gln Asn Cys Asp Tyr Leu Val Ile Tyr
245 250 255
Asp Asp Met Phe Asn Val Asn Gln Gln Pro His Asp Glu Ile Lys Arg
260 265 270
75 Leu Cys Glu His Arg Ala Phe Tyr Asn Gly Phe Asp Val Ala Ala Val

```

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		275				280				285				
		Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser	Phe	Pro	Ser	Asn	Ala
		290												
		Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn	Phe	Ile	Arg	Ser	Val
5		305												
		Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp	Gly	Lys	Leu	Gly	Tyr
		Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr	Leu	Ala	Asp	Thr	Asp
10		Val	Pro	Thr	Ser	Phe	Ile	His	Asn	Val	Ser	Leu	Ile	Pro
		Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser	Asp	Tyr	Phe	Phe	Ser
15		Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu	Phe	Ile	Gly	Arg	Phe
		Asn	Ala	His	Glu	Leu	His	Asn	Leu	Ile	Glu	Lys	Thr	Ile
20		Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His	Lys	Asn	Ile	Leu	Tyr
		Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu	Arg	Leu	Phe	Leu	Lys
		Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Lys	Ser	Asn	Gln
25		Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu	Asn	Asn	Gly	Ser	His
		Phe	Asn	Thr	His	Gly	Met	Pro	Thr	Val	Trp	Gly	Ile	Gly
		Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg	Leu	Asn	Asn	Thr	Ser
30		Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala	Val	Ala	Asp
		Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr	Ala	Pro	Asn
35		Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	Ala	Thr	Gln	Tyr	Ala
		Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	Phe	Tyr	Glu	Tyr	Leu
		Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly	Glu	Met	Leu
40		Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	Thr	Tyr	Ser	Lys	Phe
		Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met	Ala	His	Gly
45		Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	Asn	Thr	Ile	Ile	Ser
		Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	Lys	Ile	Pro	Glu	Lys
		His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val	Met	Ser	Gly
50		Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	Ser	Gly	Glu	Thr	Gly
		Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	Gly	Leu	Ala	Ile	Asn
55		Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	Asn	Leu	Phe	Ser	Thr
		Met	Pro	Lys	Phe	His	Phe	Asp	Ser	Val	Lys	Phe	Asn	Ser
		Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	Ile	Ser	Asn	Cys	Glu
60		Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	Cys	Asp	Leu	Ser	Val
		Met	Phe	Ser	Ser	Gly	Ile	Thr	Val	Phe	Lys	Pro	Met	Ala
65		Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	Ala	Lys	Ile	Thr	Asp
		Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	His	Ile	Thr	Asn	Thr
		Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	Lys	Leu	Asp	Asn	Ile
70		Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	Asn	Cys	Asp	Glu	Ala
		Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	Arg	Leu	His	Asn	Ile
75		Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	Ser	Thr	Leu	Tyr	Asn

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Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu  
 885 890 895  
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu  
 900 905 910  
 5 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser  
 915 920 925  
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly  
 930 935 940  
 10 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr  
 945 950 955 960  
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro  
 965 970 975  
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp  
 980 985 990  
 15 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val  
 995 1000 1005  
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser  
 1010 1015 1020  
 20 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp  
 1025 1030 1035 1040  
 Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser  
 1045 1050 1055  
 Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr  
 1060 1065 1070  
 25 Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala  
 1075 1080 1085  
 Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr  
 1090 1095 1100  
 30 Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala  
 1105 1110 1115 1120  
 Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu  
 1125 1130 1135  
 Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys  
 1140 1145 1150  
 35 Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu  
 1155 1160 1165  
 Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser  
 1170 1175 1180  
 40 Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys  
 1185 1190 1195 1200  
 Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val  
 1205 1210 1215  
 Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu  
 1220 1225 1230  
 45 Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser  
 1235 1240 1245  
 Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys  
 1250 1255 1260  
 50 Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys  
 1265 1270

(2) INFORMATION FOR SEQ ID NO:467

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 925 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 60 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...925  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile  
 1 5 10 15  
 75 Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser  
 20 25 30



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Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile  
 35 40 45  
 Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu  
 50 55 60  
 5 Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser  
 65 70 75 80  
 Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile  
 85 90 95  
 10 Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile  
 100 105 110  
 Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr  
 115 120 125  
 Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile  
 130 135 140  
 15 Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr  
 145 150 155 160  
 Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys  
 165 170 175  
 20 Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe  
 180 185 190  
 Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu  
 195 200 205  
 Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg  
 210 215 220  
 25 Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn  
 225 230 235 240  
 Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu  
 245 250 255  
 30 Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr  
 260 265 270  
 Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala  
 275 280 285  
 Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His  
 290 295 300  
 35 Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val  
 305 310 315 320  
 Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp  
 325 330 335  
 40 Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly  
 340 345 350  
 His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr  
 355 360 365  
 Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val  
 370 375 380  
 45 Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr  
 385 390 395 400  
 Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile  
 405 410 415  
 50 Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu  
 420 425 430  
 Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His  
 435 440 445  
 Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val  
 450 455 460  
 55 Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val  
 465 470 475 480  
 Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn  
 485 490 495  
 60 Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala  
 500 505 510  
 Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp  
 515 520 525  
 Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp  
 530 535 540  
 65 Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile  
 545 550 555 560  
 Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp  
 565 570 575  
 70 Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp  
 580 585 590  
 Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro  
 595 600 605  
 Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser  
 610 615 620  
 75 Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr

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130 135 140  
 Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val  
 145 150 155 160  
 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala  
 165 170 175  
 5 Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu  
 180 185 190  
 Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr  
 195 200 205  
 10 Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp  
 210 215 220  
 Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu  
 225 230 235 240  
 15 Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln  
 245 250 255  
 Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu  
 260 265 270  
 Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp  
 275 280 285  
 20 Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr  
 290 295 300  
 Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly  
 305 310 315 320  
 25 Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr  
 325 330 335  
 Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser  
 340 345 350  
 Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn  
 355 360 365  
 30 Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp  
 370 375 380  
 Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met  
 385 390 395 400  
 35 Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu  
 405 410 415  
 Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile  
 420 425 430  
 Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys  
 435 440 445  
 40 Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr  
 450 455 460  
 Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile  
 465 470 475 480  
 45 Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu  
 485 490 495  
 Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn  
 500 505 510  
 Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val  
 515 520 525  
 50 Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu  
 530 535 540  
 Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln  
 545 550 555 560  
 55 Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu  
 565 570 575  
 Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile  
 580 585 590  
 Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met  
 595 600 605  
 60 Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro  
 610 615 620  
 Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu  
 625 630 635 640  
 65 Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val  
 645 650 655  
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala  
 660 665 670  
 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala  
 675 680 685  
 70 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys  
 690 695 700  
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu  
 705 710 715 720  
 75 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro  
 725 730 735

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Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu  
 740 745 750  
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys  
 755 760 765  
 5 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 770 775 780  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 785 790 795 800  
 10 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 805 810 815  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 820 825 830  
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 835 840 845  
 15 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 850 855 860  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 865 870 875 880  
 20 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 885 890 895  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 900 905 910  
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920  
 25 (2) INFORMATION FOR SEQ ID NO:469  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 921 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...921  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469  
 45 Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp  
 1 5 10 15  
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala  
 20 25 30  
 50 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser  
 35 40 45  
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp  
 50 55 60  
 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro  
 65 70 75 80  
 55 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile  
 85 90 95  
 Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys  
 100 105 110  
 60 Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His  
 115 120 125  
 Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val  
 130 135 140  
 65 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp  
 145 150 155 160  
 Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp  
 165 170 175  
 Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp  
 180 185 190  
 70 Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp  
 195 200 205  
 Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn  
 210 215 220  
 75 Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln  
 225 230 235 240



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835 840 845  
 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg  
 850 855 860  
 Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu  
 865 870 875 880  
 Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu  
 885 890 895  
 Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr  
 900 905 910  
 10 Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920

(2) INFORMATION FOR SEQ ID NO:470

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 593 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...593  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Met Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala  
 1 5 10 15  
 35 Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr  
 20 25 30  
 Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln  
 35 40 45  
 Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala  
 40 50 55 60  
 Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr  
 65 70 75 80  
 Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro  
 85 90 95  
 45 Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn  
 100 105 110  
 Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg  
 115 120 125  
 50 Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg  
 130 135 140  
 Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys  
 145 150 155 160  
 Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser  
 165 170 175  
 55 Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn  
 180 185 190  
 Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser  
 195 200 205  
 60 Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val  
 210 215 220  
 Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg  
 225 230 235 240  
 Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu  
 245 250 255  
 65 Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser  
 260 265 270  
 Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe  
 275 280 285  
 Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp  
 290 295 300  
 70 Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly  
 305 310 315 320  
 Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser  
 325 330 335  
 75 Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp

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      340      345      350
Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe
      355      360      365
5 Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met
      370      375      380
Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu
      385      390      395      400
Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met
      405      410      415
10 Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr
      420      425      430
Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val
      435      440      445
15 Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly
      450      455      460
Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala
      465      470      475      480
Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln
      485      490      495
20 Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro
      500      505      510
Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr
      515      520      525
25 Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His
      530      535      540
Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu
      545      550      555      560
Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly
      565      570      575
30 Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr
      580      585      590
Phe

```

35 (2) INFORMATION FOR SEQ ID NO:471

```

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 589 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

```

40 (ii) MOLECULE TYPE: protein

45 (iii) HYPOTHETICAL: YES

```

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

```

50 (ix) FEATURE:
 (A) NAME/KEY: misc\_feature
 (B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

```

55 Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser
      1      5      10      15
Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp
      20      25      30
Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met
      35      40      45
60 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg
      50      55      60
Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val
      65      70      75      80
65 Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro
      85      90      95
Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly
      100      105      110
His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala
      115      120      125
70 Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser
      130      135      140
Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg Met
      145      150      155      160
75 Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

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165 170 175  
 Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly  
 180 185 190  
 Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr  
 195 200 205  
 Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala  
 210 215 220  
 Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser  
 225 230 235 240  
 10 Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr  
 245 250 255  
 Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys  
 260 265 270  
 Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser  
 275 280 285  
 15 Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr  
 290 295 300  
 Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn  
 305 310 315 320  
 20 Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly  
 325 330 335  
 Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser  
 340 345 350  
 25 Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile  
 355 360 365  
 Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met  
 370 375 380  
 Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu  
 385 390 395 400  
 30 Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly  
 405 410 415  
 Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro  
 420 425 430  
 35 Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro  
 435 440 445  
 Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr  
 450 455 460  
 Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys  
 465 470 475 480  
 40 Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile  
 485 490 495  
 Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg  
 500 505 510  
 45 Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser  
 515 520 525  
 Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala  
 530 535 540  
 Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile  
 545 550 555 560  
 50 Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met  
 565 570 575  
 Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe  
 580 585

55 (2) INFORMATION FOR SEQ ID NO:472

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...346

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

75

Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe



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1      5      10      15
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
20      25      30
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
35      40      45
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
50      55      60
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
65      70      75      80
10 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
85      90      95
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
100      105      110
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
115      120      125
15 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
130      135      140
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
145      150      155      160
20 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
165      170      175
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180      185      190
25 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
195      200      205
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
210      215      220
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
225      230      235      240
30 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
245      250      255
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
260      265      270
35 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
275      280      285
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
290      295      300
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
305      310      315      320
40 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
325      330      335
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
340      345

```

## (2) INFORMATION FOR SEQ ID NO:473

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```

65 Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
1      5      10      15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
20      25      30
70 Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His-Phe Leu Asn Leu
35      40      45
Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
50      55      60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
65      70      75      80
75 Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser

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5 Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg  
 100 105 110  
 Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln  
 115 120 125  
 Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp  
 130 135 140  
 Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg  
 145 150 155 160  
 10 Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser  
 165 170 175  
 Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp  
 180 185 190  
 15 Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu  
 195 200 205  
 Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu  
 210 215 220  
 Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr  
 225 230 235 240  
 20 Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp  
 245 250 255  
 Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu  
 260 265 270  
 25 Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln  
 275 280 285  
 Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu  
 290 295 300  
 Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser  
 305 310 315 320  
 30 Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly  
 325 330 335  
 Ile Arg Leu Asp Asp Lys Ser Ile Phe  
 340 345  
 35 (2) INFORMATION FOR SEQ ID NO:474  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...330  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474  
 55 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val  
 1 5 10 15  
 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn  
 20 25 30  
 60 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr  
 35 40 45  
 Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu  
 50 55 60  
 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met  
 65 70 75 80  
 Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu  
 85 90 95  
 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met  
 100 105 110  
 70 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser  
 115 120 125  
 Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe  
 130 135 140  
 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr  
 145 150 155 160  
 75 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp

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      165      170      175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
      180      185      190
5  Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
      195      200      205
    Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
      210      215      220
    Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
      225      230      235
10  Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
      245      250      255
    Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
      260      265      270
    Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
      275      280      285
15  Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
      290      295      300
    Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
      305      310      315
20  Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
      325      330

```

(2) INFORMATION FOR SEQ ID NO:475

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...324
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

```

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu
1      5      10      15
45  Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly
      20      25      30
    Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys
      35      40      45
50  Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly
      50      55      60
    Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser
      65      70      75      80
    Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly
      85      90      95
55  Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly
      100      105      110
    Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe
      115      120      125
60  Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val
      130      135      140
    Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val
      145      150      155      160
    Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro
      165      170      175
65  Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp
      180      185      190
    Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser
      195      200      205
70  Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile
      210      215      220
    Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn
      225      230      235      240
    Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro
      245      250      255
75  Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe

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260 265 270  
 Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile  
 275 280 285  
 Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile  
 290 295 300  
 Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser  
 305 310 315 320  
 Asn Gly Arg Ser

10 (2) INFORMATION FOR SEQ ID NO:476  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 547 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...547  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe  
 1 5 10 15  
 Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn  
 20 25 30  
 Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg  
 35 40 45  
 Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp  
 50 55 60  
 Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe  
 65 70 75 80  
 Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly  
 85 90 95  
 Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val  
 100 105 110  
 Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser Arg Gly Met  
 115 120 125  
 His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu Ala Tyr Tyr  
 130 135 140  
 Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His Phe Glu Asp  
 145 150 155 160  
 Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg Leu Pro Leu  
 165 170 175  
 Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg Leu Thr Asp  
 180 185 190  
 Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser Cys Ala Thr  
 195 200 205  
 Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser Ala Ala Tyr  
 210 215 220  
 Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg Pro Gly Gln  
 225 230 235 240  
 Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val Asp Val Ser  
 245 250 255  
 Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr Val Asn Gly  
 260 265 270  
 Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp Ala Ile Gly  
 275 280 285  
 Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile  
 290 295 300  
 Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp  
 305 310 315 320  
 His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr Ala Leu Arg  
 325 330 335  
 Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asn Tyr  
 340 345 350  
 His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu

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355 360 365  
 Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp  
 370 375 380  
 5 Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr  
 385 390 395 400  
 Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu  
 405 410 415  
 Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp  
 420 425 430  
 10 Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser  
 435 440 445  
 Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala  
 450 455 460  
 15 Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser  
 465 470 475 480  
 Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr  
 485 490 495  
 Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala  
 500 505 510  
 20 Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln  
 515 520 525  
 Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser  
 530 535 540  
 25 Tyr Leu Phe  
 545

(2) INFORMATION FOR SEQ ID NO:477

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...750  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys  
 1 5 10 15  
 50 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser  
 20 25 30  
 Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala  
 35 40 45  
 Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys  
 50 55 60  
 55 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser  
 65 70 75 80  
 Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe  
 85 90 95  
 60 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly  
 100 105 110  
 Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met  
 115 120 125  
 Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val  
 130 135 140  
 65 Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met  
 145 150 155 160  
 Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser  
 165 170 175  
 70 Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly  
 180 185 190  
 Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly  
 195 200 205  
 Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe  
 210 215 220  
 75 Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr

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(2) INFORMATION FOR SEQ ID NO:478

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 494 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

5 Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser  
 1 5 10 15  
 15 Ile Ser Asn Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu  
 20 20 25 30  
 Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile  
 35 40 45  
 Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe  
 50 55 60  
 20 Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser  
 65 70 75 80  
 Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn  
 85 90 95  
 25 Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg  
 100 105 110  
 Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Gly  
 115 120 125  
 Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn  
 130 135 140  
 30 Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly  
 145 150 155 160  
 His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu  
 165 170 175  
 Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe  
 180 185 190  
 35 Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser  
 195 200 205  
 Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly  
 210 215 220  
 40 Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala  
 225 230 235 240  
 Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu  
 245 250 255  
 Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe  
 260 265 270  
 45 Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu  
 275 280 285  
 Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly  
 290 295 300  
 50 Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys  
 305 310 315 320  
 Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala  
 325 330 335  
 55 Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg  
 340 345 350  
 Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met  
 355 360 365  
 Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn  
 370 375 380  
 60 Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn  
 385 390 395 400  
 Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr  
 405 410 415  
 Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser  
 420 425 430  
 65 Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser  
 435 440 445  
 Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala  
 450 455 460  
 70 Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser  
 465 470 475 480  
 Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe  
 485 490

75 (2) INFORMATION FOR SEQ ID NO:479

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 294 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr  
 1 5 10 15  
 Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys  
 20 25 30  
 Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser  
 35 40 45  
 Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu  
 50 55 60  
 Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp  
 65 70 75 80  
 Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys  
 85 90 95  
 Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr  
 100 105 110  
 Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser  
 115 120 125  
 Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val  
 130 135 140  
 Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile  
 145 150 155 160  
 Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro  
 165 170 175  
 Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu  
 180 185 190  
 Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly  
 195 200 205  
 Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn  
 210 215 220  
 Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly  
 225 230 235 240  
 Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys  
 245 250 255  
 Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val  
 260 265 270  
 Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val  
 275 280 285  
 Gly Val Ala Tyr Thr Phe  
 290

(2) INFORMATION FOR SEQ ID NO:480

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...204



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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:480

5 Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly  
 1 5 10 15  
 Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe  
 20 25 30  
 Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn  
 35 40 45  
 10 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu  
 50 55 60  
 Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg  
 65 70 75 80  
 15 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr  
 85 90 95  
 Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn  
 100 105 110  
 Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala  
 115 120 125  
 20 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala  
 130 135 140  
 Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser  
 145 150 155 160  
 25 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His  
 165 170 175  
 Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg  
 180 185 190  
 Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 195 200

## (2) INFORMATION FOR SEQ ID NO:481

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
 40 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...243

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:481

50 Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr  
 1 5 10 15  
 Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe  
 20 25 30  
 55 Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr  
 35 40 45  
 Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile  
 50 55 60  
 60 Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys  
 65 70 75 80  
 Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr  
 85 90 95  
 Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn  
 100 105 110  
 65 Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu  
 115 120 125  
 Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys  
 130 135 140  
 70 Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Glu Phe Phe Gly Pro  
 145 150 155 160  
 Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile  
 165 170 175  
 Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu  
 180 185 190  
 75 His Gly Phe Val Asp Ile Val Ser Gly Gly Gly Ser Asp Ile Pro Arg



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Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val  
 1 5 10 15  
 Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro  
 20 25 30  
 5 Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser  
 35 40 45  
 Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp  
 50 55 60  
 10 Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg  
 65 70 75 80  
 Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu  
 85 90 95  
 Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr  
 100 105 110  
 15 Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala  
 115 120 125  
 Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr  
 130 135 140  
 20 Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp  
 145 150 155 160  
 Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr  
 165 170 175  
 Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr  
 180 185 190  
 25 Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met  
 195 200 205  
 Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe  
 210 215 220  
 30 Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val  
 225 230 235 240  
 Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly  
 245 250 255  
 Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile  
 260 265 270  
 35 Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg  
 275 280 285  
 Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu  
 290 295 300  
 40 Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser  
 305 310 315 320  
 Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr  
 325 330 335  
 Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr Ser Lys  
 340 345 350  
 45 Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro Lys Ala  
 355 360 365  
 Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr Gly Ser  
 370 375 380  
 50 Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala Arg Thr  
 385 390 395 400  
 Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe Pro Gly  
 405 410 415  
 Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn Met Arg  
 420 425 430  
 55 Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn Met Ser  
 435 440 445  
 Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu Arg Trp  
 450 455 460  
 60 Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn Ser Ile  
 465 470 475 480  
 Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg Asp Trp  
 485 490 495  
 Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val Pro Leu  
 500 505 510  
 65 Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu Trp Trp  
 515 520 525  
 Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe  
 530 535 540  
 70 Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser  
 545 550 555 560  
 Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp  
 565 570 575  
 Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe  
 580 585 590  
 75 Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg

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595 600 605  
 Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu  
 610 615 620  
 5 His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro  
 625 630 635 640  
 Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu  
 645 650 655  
 Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile  
 660 665 670  
 10 Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala  
 675 680 685  
 Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu  
 690 695 700  
 15 Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu  
 705 710 715 720  
 Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser  
 725 730 735  
 Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser  
 740 745 750  
 20 Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly  
 755 760 765  
 Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys  
 770 775 780  
 25 Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu  
 785 790 795 800  
 Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg  
 805 810 815  
 Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser  
 820 825 830  
 30 Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp  
 835 840 845  
 Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr  
 850 855 860  
 35 Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser  
 865 870 875 880  
 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser  
 885 890 895  
 Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala  
 900 905 910  
 40 Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser  
 915 920 925  
 Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg  
 930 935 940  
 45 Pro Ile Thr Asn Thr Trp Tyr  
 945 950

(2) INFORMATION FOR SEQ ID NO:484

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1226 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1226  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

Met Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys  
 1 5 10 15  
 70 Thr Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr-Glu Arg Phe Ala  
 20 25 30  
 Asp Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu  
 35 40 45  
 Val Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln  
 50 55 60  
 75 Ser Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile

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	65		70		75		80
	Arg	Pro	Ala	Asn	Arg	Phe	Pro
				85			
					90		
						95	
5	Asn	Leu	Arg	Ala	Ser	Pro	Pro
				100			
					105		
						110	
							115
							120
							125
							130
10	Val	Val	Met	Val	Ile	Asp	Gln
						150	
							155
							160
							165
							170
							175
							180
							185
							190
15	Ser	Tyr	Asp	His	Glu	Pro	His
							200
							205
							210
							215
							220
20	His	Thr	Gln	Gly	Gly	Leu	Lys
							230
							235
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Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu  
 675 680 685  
 Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro  
 690 695 700  
 5 Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly  
 705 710 715 720  
 Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser  
 725 730 735  
 10 Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly  
 740 745 750  
 Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu  
 755 760 765  
 Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe  
 770 775 780  
 15 Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser  
 785 790 795 800  
 Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn  
 805 810 815  
 20 Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn  
 820 825 830  
 Gly Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln  
 835 840 845  
 Lys Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr  
 850 855 860  
 25 Gly Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu  
 865 870 875 880  
 Asn Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile  
 885 890 895  
 30 Gly Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe  
 900 905 910  
 Pro Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg  
 915 920 925  
 Asp Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala  
 930 935 940  
 35 Gly Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu  
 945 950 955 960  
 Pro Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn  
 965 970 975  
 40 Gly Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn  
 980 985 990  
 Thr Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly  
 995 1000 1005  
 Asn Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly  
 1010 1015 1020  
 45 Asn Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser  
 1025 1030 1035 1040  
 Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly  
 1045 1050 1055  
 Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln  
 1060 1065 1070  
 50 Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala  
 1075 1080 1085  
 Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe  
 1090 1095 1100  
 55 Ala Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His  
 1105 1110 1115 1120  
 Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp  
 1125 1130 1135  
 60 Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp  
 1140 1145 1150  
 Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn  
 1155 1160 1165  
 Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys  
 1170 1175 1180  
 65 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys  
 1185 1190 1195 1200  
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr  
 1205 1210 1215  
 70 Asn Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:485

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1225 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met	Lys	Arg	Tyr	Thr	Ile	Ile	Leu	Ala	Val	Phe	Leu	Leu	Phe	Cys	Thr
1				5					10					15	
Val	Phe	Thr	Phe	Gln	Ile	Lys	Ala	Arg	Pro	Tyr	Glu	Arg	Phe	Ala	Asp
			20				25						30		
Val	Glu	Lys	Pro	Trp	Ile	Gln	Lys	His	Ser	Met	Asp	Ser	Lys	Leu	Val
		35				40					45				
Pro	Ala	Asn	Lys	Gly	Asn	Leu	Ile	Gln	Ala	Glu	Ile	Val	Tyr	Gln	Ser
	50				55					60					
Val	Ser	Glu	His	Ser	Asp	Leu	Val	Ile	Ser	Pro	Val	Asn	Glu	Ile	Arg
65				70					75					80	
Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu	Asn
		85						90						95	
Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr	Ala
		100						105					110		
Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp	Asp
	115						120					125			
Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp	Val
	130				135					140					
Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile	Ala	
145					150				155					160	
Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys	Met
		165						170					175		
Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val	Ser
	180						185						190		
Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr	Ala
	195						200					205			
Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr	His
	210					215					220				
Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser	Thr
225					230				235					240	
Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr	Glu
		245						250					255		
Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr
	260						265						270		
Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile	Asn
	275						280					285			
Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr	Pro
	290					295					300				
Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro	Glu
305					310				315					320	
Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp	Gly
		325							330				335		
Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr	Tyr
		340					345						350		
Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala	Lys
	355					360						365			
Asn	Ser	Gly	Tyr	Thr	Ile	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp	Phe
	370				375						380				
Ala	Leu	Ala	Asn	Asn	Ser	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn	His
385					390				395					400	
Phe	Phe	Thr	Ala	Thr	Pro	Ala	Asn	Leu	Ala	Ala	Phe	Asp	Asn	Ile	
		405							410				415		
Ala	Gln	Thr	Ile	Asn	Ile	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp	Phe
	420						425						430		
Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp	Val
	435					440						445			
Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser
	450					455					460				
Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu

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465 470 475 480  
 Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn  
 485 490 495  
 Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly  
 500 505 510  
 Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn  
 515 520 525  
 Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu  
 530 535 540  
 10 Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly  
 545 550 555 560  
 Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala  
 565 570 575  
 15 His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His  
 580 585 590  
 Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln  
 595 600 605  
 Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly  
 610 615 620  
 20 Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly  
 625 630 635 640  
 Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala  
 645 650 655  
 25 Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser  
 660 665 670  
 Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr  
 675 680 685  
 Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala  
 690 695 700  
 30 Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn  
 705 710 715 720  
 Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser Gln  
 725 730 735  
 35 Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr  
 740 745 750  
 Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe  
 755 760 765  
 Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr  
 770 775 780  
 40 Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp  
 785 790 795 800  
 Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp  
 805 810 815  
 45 Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly  
 820 825 830  
 Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys  
 835 840 845  
 Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly  
 850 855 860  
 50 Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn  
 865 870 875 880  
 Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly  
 885 890 895  
 55 Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro  
 900 905 910  
 Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp  
 915 920 925  
 Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly  
 930 935 940  
 60 Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro  
 945 950 955 960  
 Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly  
 965 970 975  
 65 Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr  
 980 985 990  
 Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn  
 995 1000 1005  
 Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn  
 1010 1015 1020  
 70 Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe  
 1025 1030 1035 1040  
 Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu  
 1045 1050 1055  
 75 Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val  
 1060 1065 1070



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Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp  
 1075 1080 1085  
 Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala  
 1090 1095 1100  
 5 Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg  
 1105 1110 1115 1120  
 Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser  
 1125 1130 1135  
 10 Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp  
 1140 1145 1150  
 Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln  
 1155 1160 1165  
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu  
 1170 1175 1180  
 15 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val  
 1185 1190 1195 1200  
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn  
 1205 1210 1215  
 20 Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:486

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe  
 1 5 10 15  
 45 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly  
 20 25 30  
 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His  
 35 40 45  
 Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg  
 50 55 60  
 Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val  
 65 70 75 80  
 Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu  
 85 90 95  
 55 Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu  
 100 105 110  
 Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg  
 115 120 125  
 Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln  
 130 135 140  
 60 Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val  
 145 150 155 160  
 Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe Glu  
 165 170 175  
 65 Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser  
 180 185 190  
 Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala  
 195 200 205  
 Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp  
 210 215 220  
 70 Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr  
 225 230 235 240  
 Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu  
 245 250 255  
 75 Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Asp  
 260 265 270

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Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe  
 275 280 285  
 Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly  
 290 295 300  
 5 Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly  
 305 310 315 320  
 Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr  
 325 330 335  
 10 Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn  
 340 345 350  
 Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr  
 355 360 365  
 Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp  
 370 375 380  
 15 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe  
 385 390 395 400  
 Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu  
 405 410 415  
 20 Leu Trp Phe Lys Ala Arg Tyr Ser Phe  
 420 425

(2) INFORMATION FOR SEQ ID NO:487

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 404 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...404  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu  
 1 5 10 15  
 45 Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn  
 20 25 30  
 Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn  
 35 40 45  
 Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu  
 50 55 60  
 Gln Thr Phe Val Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr  
 65 70 75 80  
 Ile Leu Leu Thr Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys  
 85 90 95  
 Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala  
 100 105 110  
 55 Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu  
 115 120 125  
 Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Tyr  
 130 135 140  
 60 Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr  
 145 150 155 160  
 Glu Gly Glu Pro Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe  
 165 170 175  
 Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val  
 180 185 190  
 65 Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val  
 195 200 205  
 Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn  
 210 215 220  
 70 Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys  
 225 230 235 240  
 Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val  
 245 250 255  
 75 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn  
 260 265 270

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Lys Val His Val Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly  
 275 280 285  
 Leu Ile Thr Met Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr  
 290 295 300  
 5 Asp Glu Tyr Asp Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly  
 305 310 315 320  
 Ser Tyr Leu Phe Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr  
 325 330 335  
 10 Leu Asp Leu Pro Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp  
 340 345 350  
 Thr Leu Ser Gly Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val  
 355 360 365  
 Gly Asp Thr Ala Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met  
 370 375 380  
 15 Asp Lys Arg Arg Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr  
 385 390 395 400  
 Trp Glu Val Glu

20 (2) INFORMATION FOR SEQ ID NO:488

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

40 Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro  
 1 5 10 15  
 Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp  
 20 25 30  
 45 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys  
 35 40 45  
 Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn  
 50 55 60  
 Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu  
 65 70 75 80  
 Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His  
 85 90 95  
 Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr  
 100 105 110  
 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser  
 115 120 125  
 55 Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu  
 130 135 140  
 Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln  
 145 150 155 160  
 60 Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile  
 165 170 175  
 Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp  
 180 185 190  
 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe  
 195 200 205  
 65 Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr  
 210 215 220  
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala  
 225 230 235 240  
 70 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile  
 245 250 255  
 Asp Ile Ser Phe  
 260

75 (2) INFORMATION FOR SEQ ID NO:489

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu  
 1 5 10 15  
 Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr  
 20 25 30  
 Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser  
 35 40 45  
 Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr  
 50 55 60  
 Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr  
 65 70 75 80  
 His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile  
 85 90 95  
 Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu  
 100 105 110  
 Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg  
 115 120 125  
 Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp  
 130 135 140  
 Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val  
 145 150 155 160  
 Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser  
 165 170 175  
 Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser  
 180 185 190  
 Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys  
 195 200 205  
 Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly  
 210 215 220  
 Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu  
 225 230 235 240  
 Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala  
 245 250 255  
 Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr  
 260 265 270  
 Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe  
 275 280 285  
 Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly  
 290 295 300  
 Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu  
 305 310 315 320  
 Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp  
 325 330 335  
 Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser  
 340 345 350  
 Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala  
 355 360 365  
 Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro  
 370 375 380  
 Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn  
 385 390 395 400  
 Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala  
 405 410 415  
 Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met  
 420 425 430  
 Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala  
 435 440 445

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His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser  
 450 455 460  
 Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro  
 465 470 475 480  
 5 Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp  
 485 490 495  
 Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln  
 500 505 510  
 10 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala  
 515 520 525  
 Leu Phe Pro Glu Asn Ala Ala Ala Asp Phe Ser His Asn Ser Phe Asp  
 530 535 540  
 Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln  
 545 550 555 560  
 15 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln  
 565 570 575  
 Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly  
 580 585 590  
 20 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr  
 595 600 605  
 Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp  
 610 615 620  
 Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn  
 625 630 635 640  
 25 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser  
 645 650 655  
 Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg  
 660 665 670  
 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala  
 675 680 685  
 30 Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu  
 690 695 700  
 Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr  
 705 710 715 720  
 35 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe  
 725 730 735  
 Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val  
 740 745 750  
 40 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser  
 755 760 765  
 Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile  
 770 775 780  
 Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn  
 785 790 795 800  
 45 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys  
 805 810 815  
 Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gln Gly Asn Pro Thr  
 820 825 830  
 Gly Asn

## (2) INFORMATION FOR SEQ ID NO:490

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 60 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...399  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala  
 1 5 10 15  
 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu  
 20 25 30

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Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala  
 35 40 45  
 Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr  
 50 55 60  
 5 Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro  
 65 70 75 80  
 Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr  
 85 90 95  
 10 Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro  
 100 105 110  
 Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr  
 115 120 125  
 Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly  
 130 135 140  
 15 Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn  
 145 150 155 160  
 Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg  
 165 170 175  
 20 Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser  
 180 185 190  
 Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu  
 195 200 205  
 Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu  
 210 215 220  
 25 Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp  
 225 230 235 240  
 Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu  
 245 250 255  
 Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly  
 260 265 270  
 30 Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr  
 275 280 285  
 Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His  
 290 295 300  
 35 Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro  
 305 310 315 320  
 Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu  
 325 330 335  
 40 Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp  
 340 345 350  
 Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg Val Trp Phe  
 355 360 365  
 Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met  
 370 375 380  
 45 Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:491

- 50 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...382  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met  
 1 5 10 15  
 70 Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro  
 20 25 30  
 Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu  
 35 40 45  
 Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp  
 50 55 60

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    Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
    65      70      75      80
    Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
    85      90      95
5   Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
    100      105      110
    Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
    115      120      125
10  Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
    130      135      140
    Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
    145      150      155      160
    Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
    165      170      175
15  Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
    180      185      190
    Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
    195      200      205
20  Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
    210      215      220
    His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
    225      230      235      240
    Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
    245      250      255
25  Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
    260      265      270
    Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
    275      280      285
30  Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
    290      295      300
    Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
    305      310      315      320
    Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
    325      330      335
35  Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
    340      345      350
    Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
    355      360      365
40  Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
    370      375      380

```

## (2) INFORMATION FOR SEQ ID NO:492

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...222
- (x) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1      5      10      15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
20      25      30
65 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
    35      40      45
    Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
    50      55      60
70 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
    65      70      75      80
    Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
    85      90      95
75 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
    100      105      110

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Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe  
 115 120 125  
 Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His  
 130 135 140  
 5 Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys  
 145 150 155 160  
 Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His  
 165 170 175  
 10 Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys  
 180 185 190  
 Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe  
 195 200 205  
 15 Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu  
 210 215 220  
 (2) INFORMATION FOR SEQ ID NO:493  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 25 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...391  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493  
 35 Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile  
 1 5 10 15  
 Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn  
 20 25 30  
 40 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg  
 35 40 45  
 Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr  
 50 55 60  
 45 Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala  
 65 70 75 80  
 Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp  
 85 90 95  
 Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu  
 100 105 110  
 50 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu  
 115 120 125  
 Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn  
 130 135 140  
 55 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe  
 145 150 155 160  
 Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His  
 165 170 175  
 Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala  
 180 185 190  
 60 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp  
 195 200 205  
 Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp  
 210 215 220  
 65 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr  
 225 230 235 240  
 Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu  
 245 250 255  
 Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Ile Met Asp Gln Asn  
 260 265 270  
 70 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser  
 275 280 285  
 Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu  
 290 295 300  
 75 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser  
 305 310 315 320

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Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro  
 325 330 335  
 Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met  
 340 345 350  
 5 Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser  
 355 360 365  
 Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp  
 370 375 380  
 10 Gly Leu Arg Asn Leu Phe His  
 385 390

(2) INFORMATION FOR SEQ ID NO:494

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 446 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...446
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met  
 1 5 10 15  
 35 Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala  
 20 25 30  
 Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn  
 35 40 45  
 Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg  
 50 55 60  
 40 Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr  
 65 70 75 80  
 Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe  
 85 90 95  
 45 Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val  
 100 105 110  
 Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile  
 115 120 125  
 Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr  
 130 135 140  
 50 Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr  
 145 150 155 160  
 Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu  
 165 170 175  
 55 Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala  
 180 185 190  
 Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr  
 195 200 205  
 Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp  
 210 215 220  
 60 Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser  
 225 230 235 240  
 Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe  
 245 250 255  
 65 Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln  
 260 265 270  
 Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met  
 275 280 285  
 Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly  
 290 295 300  
 70 Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp  
 305 310 315 320  
 Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr  
 325 330 335  
 75 Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly  
 340 345 350

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Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro  
 355 360 365  
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg  
 370 375 380  
 5 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala  
 385 390 395 400  
 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp  
 405 410 415  
 10 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val  
 420 425 430  
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val  
 435 440 445

(2) INFORMATION FOR SEQ ID NO:495

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly  
 1 5 10 15  
 Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys  
 20 25 30  
 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu  
 35 40 45  
 40 Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe  
 50 55 60  
 Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp  
 65 70 75 80  
 45 Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn  
 85 90 95  
 Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu  
 100 105 110  
 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp  
 115 120 125  
 50 Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu  
 130 135 140  
 Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe  
 145 150 155 160  
 55 Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln  
 165 170 175  
 Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp  
 180 185 190  
 Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln  
 195 200 205  
 60 Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser  
 210 215 220  
 Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser  
 225 230 235 240  
 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro  
 245 250 255  
 65 Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val  
 260 265 270  
 Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile  
 275 280 285  
 70 Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr  
 290 295 300  
 Gly Asp Lys Lys  
 305

(2) INFORMATION FOR SEQ ID NO:496

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Met Lys Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu  
 1 5 10 15  
 Thr Gly Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr  
 20 25 30  
 Ala Phe Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser  
 35 40 45  
 Ala Tyr Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Ser Ile  
 50 55 60  
 Thr Arg Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu  
 65 70 75 80  
 Asn Leu Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg  
 85 90 95  
 Trp Met Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn  
 100 105 110  
 Pro Ala Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala  
 115 120 125  
 Ala Ala Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met  
 130 135 140  
 Asp Asn Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly  
 145 150 155 160  
 Gly Ile Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu  
 165 170 175  
 Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser  
 180 185 190  
 Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe  
 195 200 205  
 Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe  
 210 215 220  
 Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly  
 225 230 235 240  
 Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg  
 245 250 255  
 Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser  
 260 265 270  
 Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile  
 275 280 285  
 Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn  
 290 295 300  
 Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

5 Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg  
1 5 10 15  
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala  
20 25 30  
10 Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr  
35 40 45  
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala  
50 55 60  
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser  
65 70 75 80  
15 Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His  
85 90 95  
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala  
100 105 110  
20 Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser  
115 120 125  
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser  
130 135 140  
25 Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe  
145 150 155 160  
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg  
165 170 175  
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile  
180 185 190  
30 Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr  
195 200 205  
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Ile Gly  
210 215 220  
35 Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val  
225 230 235 240  
Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu  
245 250 255  
Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly  
260 265 270  
40 Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
275 280 285

(2) INFORMATION FOR SEQ ID NO:498

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 599 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
50 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
(vi) ORIGINAL SOURCE:  
55 (A) ORGANISM: Porphyromonas gingivalis  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...599  
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

Met Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu  
1 5 10 15  
65 Glu Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln  
20 25 30  
Glu Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val  
35 40 45  
70 Val Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn  
50 55 60  
Val Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr  
65 70 75 80  
Asn Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn  
85 90 95  
75 Gln Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg

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100 105 110  
 Ala Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu  
 115 120 125  
 5 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val  
 130 135 140  
 Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val  
 145 150 155 160  
 Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe  
 165 170 175  
 10 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His  
 180 185 190  
 Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile  
 195 200 205  
 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile  
 210 215 220  
 15 Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile  
 225 230 235 240  
 His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile  
 245 250 255  
 20 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu  
 260 265 270  
 Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro  
 275 280 285  
 25 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly  
 290 295 300  
 Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln  
 305 310 315 320  
 Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His  
 325 330 335  
 30 Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala  
 340 345 350  
 Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu  
 355 360 365  
 35 Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro  
 370 375 380  
 Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly  
 385 390 395 400  
 Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser  
 405 410 415  
 40 Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu  
 420 425 430  
 Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn  
 435 440 445  
 Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp  
 450 455 460  
 45 Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val  
 465 470 475 480  
 Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val  
 485 490 495  
 50 Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln  
 500 505 510  
 Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys  
 515 520 525  
 55 Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu  
 530 535 540  
 Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala  
 545 550 555 560  
 Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln  
 565 570 575  
 60 Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu  
 580 585 590  
 Lys Glu Lys Leu Ser Glu Asn  
 595

65 (2) INFORMATION FOR SEQ ID NO:499

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

5  
 10 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 1 5 10 15  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 20 25 30  
 15 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 35 40 45  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 50 55 60  
 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 65 70 75 80  
 20 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 85 90 95  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 100 105 110  
 25 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 115 120 125  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 130 135 140  
 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 145 150 155 160  
 30 Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 165 170 175  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 180 185 190  
 35 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val  
 195 200 205  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 210 215 220  
 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 225 230 235 240  
 40 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 245 250 255  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 260 265 270  
 45 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 275 280 285  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 290 295 300  
 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys  
 305 310 315 320  
 50 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 325 330 335  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 340 345 350  
 55 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 355 360 365  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 370 375 380  
 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 385 390 395 400  
 60 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 405 410 415  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 420 425 430  
 65 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 435 440 445  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 450 455 460  
 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 465 470 475 480  
 70 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 485 490 495  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 500 505 510  
 75 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 515 520 525

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Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 530 535 540  
 Glu Lys Leu Ser Glu Asn  
 545 550

5

(2) INFORMATION FOR SEQ ID NO:500

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 458 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

25

Met Ile Val Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln  
 1 5 10 15  
 Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr  
 20 25 30  
 Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val  
 35 40 45  
 Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys  
 50 55 60  
 Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val  
 65 70 75 80  
 Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp  
 85 90 95  
 Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro  
 100 105 110  
 Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp  
 115 120 125  
 Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met  
 130 135 140  
 Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys  
 145 150 155 160  
 Val Lys Gly Lys Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu  
 165 170 175  
 Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp  
 180 185 190  
 Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu  
 195 200 205  
 Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser  
 210 215 220  
 Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr  
 225 230 235 240  
 Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr  
 245 250 255  
 Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile  
 260 265 270  
 His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu  
 275 280 285  
 Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp  
 290 295 300  
 Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn  
 305 310 315 320  
 Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu  
 325 330 335  
 Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro  
 340 345 350  
 Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp  
 355 360 365  
 Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu  
 370 375 380  
 Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe  
 385 390 395 400

75

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```

10      (2) INFORMATION FOR SEQ ID NO:501
           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 426 amino acids
               (B) TYPE: amino acid
15          (D) TOPOLOGY: linear
           (ii) MOLECULE TYPE: protein
           (iii) HYPOTHETICAL: YES
20          (vi) ORIGINAL SOURCE:
               (A) ORGANISM: Porphyromonas gingivalis
           (ix) FEATURE:
25          (A) NAME/KEY: misc_feature
               (B) LOCATION 1...426

```

75



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Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys  
 370 375 380  
 Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn  
 385 390 395 400  
 5 Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu  
 405 410 415  
 Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn  
 420 425

## 10 (2) INFORMATION FOR SEQ ID NO:502

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...240

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

30 Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys  
 1 5 10 15  
 Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile  
 20 25 30  
 35 Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn  
 35 40 45  
 Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp  
 50 55 60  
 Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu  
 65 70 75 80  
 40 Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly  
 85 90 95  
 Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala  
 100 105 110  
 Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr  
 115 120 125  
 45 Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile  
 130 135 140  
 Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn  
 145 150 155 160  
 50 Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly  
 165 170 175  
 Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln  
 180 185 190  
 Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn  
 195 200 205  
 55 Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met  
 210 215 220  
 Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn  
 225 230 235 240

## 60 (2) INFORMATION FOR SEQ ID NO:503

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:







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Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr  
 50 55 60  
 Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly  
 65 70 75 80  
 5 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser  
 85 90 95  
 Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe  
 100 105 110  
 10 Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val  
 115 120 125  
 Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp  
 130 135 140  
 Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe  
 145 150 155 160  
 15 Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr  
 165 170 175  
 Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly  
 180 185 190  
 20 Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe  
 195 200 205  
 Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp  
 210 215 220  
 Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr  
 225 230 235 240  
 25 His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala  
 245 250 255  
 Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly  
 260 265 270  
 30 Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser  
 275 280 285  
 Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu  
 290 295 300  
 Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn  
 305 310 315 320  
 35 Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val  
 325 330 335  
 Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile  
 340 345 350  
 40 Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro  
 355 360 365  
 Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser  
 370 375 380  
 Ser Gly Ser Met Ser Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu  
 1 5 10 15  
 Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp  
 20 25 30  
 70 Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp  
 35 40 45  
 Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val  
 50 55 60  
 75 Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser  
 65 70 75 80

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Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg  
 85 90 95  
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys  
 100 105 110  
 5 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp  
 115 120 125  
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser  
 130 135 140  
 10 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr  
 145 150 155 160  
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn  
 165 170 175  
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr  
 180 185 190  
 15 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn  
 195 200 205  
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser  
 210 215 220  
 20 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His  
 225 230 235 240  
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr  
 245 250 255  
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys  
 260 265 270  
 25 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys  
 275 280 285  
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn  
 290 295 300  
 30 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu  
 305 310 315 320  
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln  
 325 330 335  
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser  
 340 345 350  
 35 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg  
 355 360 365  
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly  
 370 375 380  
 40 Ser Met Ser Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...581  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser  
 1 5 10 15  
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg  
 20 25 30  
 65 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro  
 35 40 45  
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met  
 50 55 60  
 70 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser  
 65 70 75 80  
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg  
 85 90 95  
 75 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly  
 100 105 110

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Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu  
 115 120 125  
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe  
 130 135 140  
 5 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly  
 145 150 155 160  
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile  
 165 170 175  
 10 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn  
 180 185 190  
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu  
 195 200 205  
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly  
 210 215 220  
 15 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly  
 225 230 235 240  
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile  
 245 250 255  
 20 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala  
 260 265 270  
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile  
 275 280 285  
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys  
 290 295 300  
 25 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe  
 305 310 315 320  
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met  
 325 330 335  
 30 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro  
 340 345 350  
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg  
 355 360 365  
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly  
 370 375 380  
 35 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu  
 385 390 395 400  
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser  
 405 410 415  
 40 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile  
 420 425 430  
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn  
 435 440 445  
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro  
 450 455 460  
 45 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu  
 465 470 475 480  
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys  
 485 490 495  
 50 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu  
 500 505 510  
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr  
 515 520 525  
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His  
 530 535 540  
 55 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser  
 545 550 555 560  
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser  
 565 570 575  
 60 Tyr Ser Thr Asn Leu  
 580

(2) INFORMATION FOR SEQ ID NO:508

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...239

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Met Arg Ser Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly
1      5      10      15
Ser Glu Arg Arg Ser Arg Ile Ser Ser Val Val Met Ser Ile Arg
10     20     25     30
Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp
35     40     45
His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp
50     55     60
Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr
65     70     75     80
His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg
85     90     95
Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser
100    105    110
Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala
115    120    125
Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val
130    135    140
Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys
145    150    155    160
Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val
165    170    175
Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr
180    185    190
His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg
195    200    205
Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe
210    215    220
Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
225    230    235

```

## (2) INFORMATION FOR SEQ ID NO:509

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...211

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
1      5      10      15
Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe
20     25     30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
35     40     45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
50     55     60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
65     70     75     80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
85     90     95
Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
100    105    110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
115    120    125
Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
130    135    140

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Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln  
 145 150 155 160  
 Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu  
 165 170 175  
 5 Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile  
 180 185 190  
 Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly  
 195 200 205  
 10 Leu Asn His  
 210

(2) INFORMATION FOR SEQ ID NO:510

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 781 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu  
 1 5 10 15  
 Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr  
 20 25 30  
 35 Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly  
 35 40 45  
 Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr  
 50 55 60  
 40 Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala  
 65 70 75 80  
 His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile  
 85 90 95  
 45 Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys  
 100 105 110  
 Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu  
 115 120 125  
 Phe Ser Asp Glu Gln Thr Ser Trp Phe Ser His Lys Ala Glu Thr Ala  
 130 135 140  
 50 Thr Pro Tyr Tyr Tyr Ser Val Tyr Leu Ala Asp Tyr Asp Thr Arg Val  
 145 150 155 160  
 Glu Met Ala Pro Thr Glu Arg Ala Ala Ile Phe Arg Ile Arg Tyr Ser  
 165 170 175  
 55 Gly Asn Thr Glu Ser Gly Ser Gly Arg Trp Leu Arg Leu Asp Ala Phe  
 180 185 190  
 Thr Gly Gly Ser Glu Ile Ser Ile Val Asp Pro His Thr Val Val Gly  
 195 200 205  
 Ile Ser Arg Lys Asn Ser Gly Gly Val Pro Ala Asn Phe Ala Cys Tyr  
 210 215 220  
 60 Phe Ile Leu Gln Ser Asp Thr Pro Met Ala Asp Val Leu Leu Glu Thr  
 225 230 235 240  
 Asp Thr Gly Lys Ser Asp Glu Gly Thr Arg Ala Trp Ala Ala Cys Arg  
 245 250 255  
 65 Phe Asp Ser Gln Glu Val Thr Val Arg Val Ala Ser Ser Phe Ile Ser  
 260 265 270  
 Val Glu Gln Ala Glu Arg Asn Leu Ala Glu Val Lys Gly Gln Ser Phe  
 275 280 285  
 Asp Arg Ile Arg Leu Ala Gly Arg Glu Ala Trp Asn Lys Val Leu Gly  
 290 295 300  
 70 Arg Ile His Val Glu Gly Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr  
 305 310 315 320  
 Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu  
 325 330 335  
 75 Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val  
 340 345 350

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5 Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg  
 355 360 365  
 Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys  
 370 375 380  
 10 Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro  
 385 390 395 400  
 Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser  
 405 410 415  
 15 Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp  
 420 425 430  
 Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His  
 435 440 445  
 Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser  
 450 455 460  
 20 Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg  
 465 470 475 480  
 Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg  
 485 490 495  
 25 Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser  
 500 505 510  
 Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly  
 515 520 525  
 Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp  
 530 535 540  
 30 Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val  
 545 550 555 560  
 Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro  
 565 570 575  
 35 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp  
 580 585 590  
 Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile  
 595 600 605  
 Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met  
 610 615 620  
 40 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg  
 625 630 635 640  
 Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr  
 645 650 655  
 45 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser  
 660 665 670  
 Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu  
 675 680 685  
 Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His  
 690 695 700  
 50 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile  
 705 710 715 720  
 Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr  
 725 730 735  
 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr  
 740 745 750  
 Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser  
 755 760 765  
 Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn  
 770 775 780

## (2) INFORMATION FOR SEQ ID NO:511

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
  
 65 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271  
  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

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Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Phe Pro Leu Ser  
 1 5 10 15  
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys  
 20 25 30  
 5 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg  
 35 40 45  
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr  
 50 55 60  
 10 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe  
 65 70 75 80  
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly  
 85 90 95  
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala  
 100 105 110  
 15 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln  
 115 120 125  
 Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile  
 130 135 140  
 20 Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg  
 145 150 155 160  
 Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp  
 165 170 175  
 Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly  
 180 185 190  
 25 Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala  
 195 200 205  
 Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met  
 210 215 220  
 30 Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala  
 225 230 235 240  
 Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu  
 245 250 255  
 Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

Met Lys Ser Met Arg Ser Val Leu Leu Leu Phe Pro Leu Ser Leu  
 1 5 10 15  
 Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser  
 20 25 30  
 60 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala  
 35 40 45  
 Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro  
 50 55 60  
 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly  
 65 70 75 80  
 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr  
 85 90 95  
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
 100 105 110  
 70 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
 115 120 125  
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
 130 135 140  
 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
 145 150 155 160

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...259

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe  
1 5 10 15  
Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile  
20 25 30  
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly  
35 40 45  
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His  
50 55 60  
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg  
65 70 75 80  
Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn  
85 90 95  
Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp  
100 105 110  
30 Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser  
115 120 125  
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr  
130 135 140  
Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His  
35 145 150 155 160  
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu  
165 170 175  
Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys  
180 185 190  
40 Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg  
195 200 205  
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr  
210 215 220  
45 Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro  
225 230 235 240  
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu  
245 250 255  
Trp Thr Asn

50 (2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1266 amino acids  
55 (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1266

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu Phe Pro Phe  
1 5 10 15  
Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu Cys Ala Ser  
20 25 30  
75 Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys

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35 40 45  
 Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser  
 50 55 60  
 Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val  
 65 70 75 80  
 Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile  
 85 90 95  
 Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser  
 100 105 110  
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu  
 115 120 125  
 Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser  
 130 135 140  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 145 150 155 160  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 165 170 175  
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu  
 180 185 190  
 Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Arg Leu  
 195 200 205  
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu  
 210 215 220  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 225 230 235 240  
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala  
 245 250 255  
 Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu  
 260 265 270  
 Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser  
 275 280 285  
 Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu  
 290 295 300  
 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser  
 305 310 315 320  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 325 330 335  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 340 345 350  
 Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu  
 355 360 365  
 Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu  
 370 375 380  
 Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu  
 385 390 395 400  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp  
 405 410 415  
 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr  
 420 425 430  
 Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp  
 435 440 445  
 Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn Asp Ile Gln  
 450 455 460  
 Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu Gln Thr Leu  
 465 470 475 480  
 Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser Ser Gly Leu  
 485 490 495  
 Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys Ala Leu Leu  
 500 505 510  
 Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu Tyr His Pro  
 515 520 525  
 Phe Cys Lys Val Met Leu Leu Glu Asn His Ser Ser Gly Lys Thr Thr  
 530 535 540  
 Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys Asn Thr His  
 545 550 555 560  
 Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile Phe Tyr Asp  
 565 570 575  
 Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala Phe Phe Thr  
 580 585 590  
 Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys Asp Arg Asn  
 595 600 605  
 Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn Phe Asn Arg  
 610 615 620  
 Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg Cys Met Ser  
 625 630 635 640

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Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr Thr Asp Asp  
 645 650 655  
 Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala Lys Gln Gln  
 660 665 670  
 5 Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu Ile Tyr Val  
 675 680 685  
 Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu Asn Tyr Leu  
 690 695 700  
 10 Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys Ser Ile Gln  
 705 710 715 720  
 Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro Thr Ile Ala  
 725 730 735  
 Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu Ala Ala Gln  
 740 745 750  
 15 Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile Glu Tyr Leu  
 755 760 765  
 Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val Leu Tyr Tyr  
 770 775 780  
 20 Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp Pro Ala Ala  
 785 790 795 800  
 Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp Asn Ile Asn  
 805 810 815  
 Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu His Asn Leu  
 820 825 830  
 25 Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly Asn Met Ile  
 835 840 845  
 Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp Lys Asp Cys  
 850 855 860  
 30 Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp Glu Ala Tyr  
 865 870 875 880  
 Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val Leu Lys Phe  
 885 890 895  
 Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile Ala Tyr Tyr  
 900 905 910  
 35 Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp Gln Val Ile  
 915 920 925  
 Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu Gln Glu Glu  
 930 935 940  
 40 Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr Gln Ile Trp  
 945 950 955 960  
 Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe Ile Lys Glu  
 965 970 975  
 Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu Ala Thr Ile  
 980 985 990  
 45 Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro Pro Arg Glu  
 995 1000 1005  
 Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr Ile Arg Glu  
 1010 1015 1020  
 50 Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala  
 1025 1030 1035 1040  
 Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr  
 1045 1050 1055  
 Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu  
 1060 1065 1070  
 55 Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg  
 1075 1080 1085  
 Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln  
 1090 1095 1100  
 60 Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys  
 1105 1110 1115 1120  
 Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr  
 1125 1130 1135  
 Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg  
 1140 1145 1150  
 65 Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg  
 1155 1160 1165  
 Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg  
 1170 1175 1180  
 70 Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe  
 1185 1190 1195 1200  
 Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln  
 1205 1210 1215  
 Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser  
 1220 1225 1230  
 75 Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg

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1235 1240 1245  
 Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr  
 1250 1255 1260  
 Asp Glu  
 1265

5  
 1265

(2) INFORMATION FOR SEQ ID NO:516

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1232

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr  
 1 5 10 15  
 30 Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser  
 20 25 30  
 Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu  
 35 35 40 45  
 Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe  
 50 55 60  
 35 Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu  
 65 70 75 80  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 85 90 95  
 40 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr  
 100 105 110  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 115 120 125  
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser  
 130 135 140  
 45 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu  
 145 150 155 160  
 Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser  
 165 170 175  
 50 Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly  
 180 185 190  
 Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln  
 195 200 205  
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu  
 210 215 220  
 55 Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu  
 225 230 235 240  
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu  
 245 250 255  
 60 Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 260 265 270  
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr  
 275 280 285  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 290 295 300  
 65 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg  
 305 310 315 320  
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu  
 325 330 335  
 70 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser  
 340 345 350  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 355 360 365  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 370 375 380  
 75 Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu

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Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala  
 995 1000 1005  
 Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp  
 1010 1015 1020  
 5 Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn  
 1025 1030 1035 1040  
 Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr  
 1045 1050 1055  
 10 Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe  
 1060 1065 1070  
 Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln  
 1075 1080 1085  
 Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp  
 1090 1095 1100  
 15 Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg  
 1105 1110 1115 1120  
 Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu  
 1125 1130 1135  
 20 Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr  
 1140 1145 1150  
 Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp  
 1155 1160 1165  
 Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile  
 1170 1175 1180  
 25 Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr  
 1185 1190 1195 1200  
 Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe  
 1205 1210 1215  
 30 Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu  
 1220 1225 1230

(2) INFORMATION FOR SEQ ID NO:517

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1175 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1175  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser  
 1 5 10 15  
 55 Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 20 25 30  
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 35 40 45  
 Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 50 55 60  
 60 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 65 70 75 80  
 Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 85 90 95  
 65 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 100 105 110  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 115 120 125  
 Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys  
 130 135 140  
 70 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg  
 145 150 155 160  
 Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys  
 165 170 175  
 75 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser  
 180 185 190

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Gly Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu  
 195 200 205  
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu  
 210 215 220  
 5 Glu Arg Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 225 230 235 240  
 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 245 250 255  
 10 Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 260 265 270  
 Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu  
 275 280 285  
 Gly Leu Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn  
 290 295 300  
 15 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu  
 305 310 315 320  
 Leu Tyr Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly  
 325 330 335  
 20 Leu Ala Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys  
 340 345 350  
 Leu Glu Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser  
 355 360 365  
 Gly Asn Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Ala Pro Ile  
 370 375 380  
 25 Leu Glu Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val  
 385 390 395 400  
 Ala Ser Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu  
 405 410 415  
 30 Ile Lys Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser  
 420 425 430  
 Val Glu Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser  
 435 440 445  
 Ser Gly Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr  
 450 455 460  
 35 Gln Lys Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn  
 465 470 475 480  
 Ala Ile Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr  
 485 490 495  
 40 Gln Ala Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala  
 500 505 510  
 Lys Lys Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr  
 515 520 525  
 Leu Asn Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys  
 530 535 540  
 45 Asn Arg Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro  
 545 550 555 560  
 Gln Thr Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr  
 565 570 575  
 50 Gly Ala Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu  
 580 585 590  
 Glu Glu Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His  
 595 600 605  
 Ala Leu Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg  
 610 615 620  
 55 Ser Lys Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala  
 625 630 635 640  
 Leu Pro Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu  
 645 650 655  
 60 Ala Leu Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr  
 660 665 670  
 Thr Ile Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly  
 675 680 685  
 Glu Val Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp  
 690 695 700  
 65 Leu Asp Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln  
 705 710 715 720  
 Lys Asp Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys  
 725 730 735  
 70 Lys Leu His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln  
 740 745 750  
 Asn Gly Asn Met Ile Leu Gln Leu Leu Glu Glu Ile Val Tyr  
 755 760 765  
 Glu Asp Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser  
 770 775 780  
 75 Asp Asp Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn

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785                      790                      795                      800  
 Phe Val Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln  
                                  805                      810                      815  
 5    Ile Ile Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp  
                                  820                      825                      830  
 Arg Asp Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr  
                                  835                      840                      845  
 Leu Glu Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu  
                                  850                      855                      860  
 10   Asp Tyr Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser  
                                  865                      870                      875                      880  
 Val Phe Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg  
                                  885                      890                      895  
 15   Lys Glu Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn  
                                  900                      905                      910  
 Ile Pro Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg  
                                  915                      920                      925  
 Ser Thr Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu  
                                  930                      935                      940  
 20   Tyr Leu Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr  
                                  945                      950                      955                      960  
 Ile His Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile  
                                  965                      970                      975  
 25   Ala Ala Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg  
                                  980                      985                      990  
 Glu Val Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu  
                                  995                      1000                      1005  
 Ala Thr Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr  
                                  1010                      1015                      1020  
 30   Glu Leu Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly  
                                  1025                      1030                      1035                      1040  
 Gln Ile Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile  
                                  1045                      1050                      1055  
 35   His Pro Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala  
                                  1060                      1065                      1070  
 Leu Ile Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu  
                                  1075                      1080                      1085  
 Leu Pro Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile  
                                  1090                      1095                      1100  
 40   Lys Pro Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe  
                                  1105                      1110                      1115                      1120  
 Ala Gln Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile  
                                  1125                      1130                      1135  
 45   Lys Ala Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp  
                                  1140                      1145                      1150  
 Val Ala Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys  
                                  1155                      1160                      1165  
 Gln Glu Val Asn Thr Asp Glu  
                                  1170                      1175  
 50   (2) INFORMATION FOR SEQ ID NO:518  
       (1) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 229 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
 55       (ii) MOLECULE TYPE: protein  
 60       (iii) HYPOTHETICAL: YES  
       (vi) ORIGINAL SOURCE:  
           (A) ORGANISM: Porphyromonas gingivalis  
 65       (vii) FEATURE:  
           (A) NAME/KEY: misc\_feature  
           (B) LOCATION 1...229  
 70       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518  
 75   Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser  
       1                      5                      10                      15  
   Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr  
       20                      25                      30  
   Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro

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35 40 45  
Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro  
50 55 60  
5 Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile  
65 70 75 80  
Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp  
85 90 95  
Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe  
100 105 110  
10 Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg  
115 120 125  
Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro  
130 135 140  
15 Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile  
145 150 155 160  
Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr  
165 170 175  
Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe  
180 185 190  
20 Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr  
195 200 205  
Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr  
210 215 220  
25 Val Ser Gln Gln Lys  
225

(2) INFORMATION FOR SEQ ID NO:519

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 228 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
40 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...228
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser  
1 5 10  
50 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe  
20 25 30  
Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val  
35 40 45  
Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe  
50 55 60  
55 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala  
65 70 75 80  
Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys  
85 90 95  
60 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp  
100 105 110  
Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile  
115 120 125  
Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys  
130 135 140  
65 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg  
145 150 155 160  
Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe  
165 170 175  
70 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu  
180 185 190  
Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala  
195 200 205  
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val  
210 215 220  
75 Ser Gln Gln Lys

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(2) INFORMATION FOR SEQ ID NO:520

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...540

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

```

Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
1      5      10      15
25 Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
    20      25      30
Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
    35      40      45
30 Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
    50      55      60
Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
65      70      75      80
Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
    85      90      95
35 Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
    100      105      110
Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
115      120      125
40 Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
    130      135      140
Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
145      150      155      160
Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
    165      170      175
45 Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
    180      185      190
Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
195      200      205
Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
50      210      215      220
Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
225      230      235      240
Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
    245      250      255
55 Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
    260      265      270
Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
275      280      285
Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
60      290      295      300
Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
305      310      315      320
Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
    325      330      335
65 Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
    340      345      350
Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
355      360      365
70 Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
    370      375      380
Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
385      390      395      400
Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala
    405      410      415
75 Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys
    420      425      430

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420 425 430  
 Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp  
 435 440 445  
 Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu  
 450 455 460  
 Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile  
 465 470 475 480  
 Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln  
 485 490 495  
 Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu  
 500 505 510  
 Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser  
 515 520 525  
 Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:521

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 771 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...771  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile  
 1 5 10 15  
 Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu  
 20 25 30  
 Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Thr Thr  
 35 40 45  
 Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe  
 50 55 60  
 Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp  
 65 70 75 80  
 Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser  
 85 90 95  
 His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu  
 100 105 110  
 Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly  
 115 120 125  
 Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val  
 130 135 140  
 Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr  
 145 150 155 160  
 Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu  
 165 170 175  
 Asn Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe  
 180 185 190  
 Leu Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys  
 195 200 205  
 Tyr Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser  
 210 215 220  
 Arg Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr  
 225 230 235 240  
 Val Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp  
 245 250 255  
 Gly Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser  
 260 265 270  
 Phe Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser  
 275 280 285  
 Phe Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu  
 290 295 300  
 Glu Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala

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305  
 Ile Arg Ser Arg Ala 310  
 325  
 315 320  
 Glu Glu Ala Leu Gly Thr Val  
 330 335  
 5 Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala  
 340 345 350  
 Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly  
 355 360 365  
 Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp  
 370 375 380  
 10 Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro  
 385 390 395 400  
 Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr  
 405 410 415  
 15 Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu  
 420 425 430  
 Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val  
 435 440 445  
 Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr  
 450 455 460  
 20 Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His  
 465 470 475 480  
 Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro  
 485 490 495  
 25 Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr  
 500 505 510  
 Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys  
 515 520 525  
 Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr  
 530 535 540  
 30 Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser  
 545 550 555 560  
 Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn  
 565 570 575  
 Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro  
 580 585 590  
 35 His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe  
 595 600 605  
 Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Asp Pro Thr  
 610 615 620  
 40 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys  
 625 630 635 640  
 Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His  
 645 650 655  
 45 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr  
 660 665 670  
 Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys  
 675 680 685  
 Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val  
 690 695 700  
 50 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile  
 705 710 715 720  
 Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr  
 725 730 735  
 55 Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser  
 740 745 750  
 His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn  
 755 760 765  
 Arg Pro Arg  
 770

(2) INFORMATION FOR SEQ ID NO:522

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc feature  
(B) LOCATION 1...776

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:522

5 Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu  
1 5 10 15  
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn  
20 25 30  
10 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys  
35 40 45  
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu  
50 55 60  
15 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp  
65 70 75 80  
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val  
85 90 95  
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg  
100 105 110  
20 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys  
115 120 125  
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly  
130 135 140  
25 Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala  
145 150 155 160  
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn  
165 170 175  
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu  
180 185 190  
30 Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn  
195 200 205  
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile  
210 215 220  
35 Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser  
225 230 235 240  
Phe Glu Pro Glu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr  
245 250 255  
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe  
260 265 270  
40 Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu  
275 280 285  
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly  
290 295 300  
45 Glu Glu Gly Leu Ala Ser Leu Leu Ala Glu Gly Ser Thr Ala Glu  
305 310 315 320  
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu  
325 330 335  
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly  
340 345 350  
50 Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn  
355 360 365  
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly  
370 375 380  
55 Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp  
385 390 395 400  
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe  
405 410 415  
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile  
420 425 430  
60 Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp  
435 440 445  
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile  
450 455 460  
65 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro  
465 470 475 480  
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn  
485 490 495  
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg  
500 505 510  
70 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser  
515 520 525  
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala  
530 535 540  
75 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly  
545 550 555 560

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Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala  
 565 570 575  
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val  
 580 585 590  
 5 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val  
 595 600 605  
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln  
 610 615 620  
 10 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala  
 625 630 635 640  
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser  
 645 650 655  
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp  
 660 665 670  
 15 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu  
 675 680 685  
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro  
 690 695 700  
 20 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile  
 705 710 715 720  
 Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr  
 725 730 735  
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser  
 740 745 750  
 25 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Ser Lys  
 755 760 765  
 Leu Ile Arg Phe Ala Val Ile Arg  
 770 775  
 30 (2) INFORMATION FOR SEQ ID NO:523  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1158 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1158  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523  
 50 Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala  
 1 5 10 15  
 Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp  
 20 25 30  
 55 Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala  
 35 40 45  
 Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe  
 50 55 60  
 Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Val Leu  
 65 70 75 80  
 60 Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro  
 85 90 95  
 Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val  
 100 105 110  
 65 Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn  
 115 120 125  
 Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala  
 130 135 140  
 Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala  
 145 150 155 160  
 70 Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr  
 165 170 175  
 Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala  
 180 185 190  
 75 Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser  
 195 200 205

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Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala Lys Ala Arg Ser  
 210 215 220  
 Ala Gly Gly Arg Glu Met Ser Leu Ser Ala Asn Gly Ile Leu Ile  
 225 230 235 240  
 5 Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val Ser Asn Ser Tyr  
 245 250 255  
 Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr Pro Met Asn Ser  
 260 265 270  
 10 Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser Met Thr Gly Asp  
 275 280 285  
 Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln Asn Asp Leu Arg  
 290 295 300  
 Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser Asn Leu Pro Val  
 305 310 315 320  
 15 Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu Val Pro Glu Ser  
 325 330 335  
 Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala Ser Leu Val Pro  
 340 345 350  
 20 Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val Ala Pro Pro Lys  
 355 360 365  
 Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala Val Asp Leu Ser  
 370 375 380  
 Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro Asn Gln Asn Leu  
 385 390 395 400  
 25 His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser Thr Gln Ala Leu  
 405 410 415  
 Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg Glu Lys Asn Gly  
 420 425 430  
 30 Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe Asn Glu Phe Ser  
 435 440 445  
 Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe Ala Lys Met Phe  
 450 455 460  
 Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu Thr Phe Pro Met  
 465 470 475 480  
 35 Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn Arg Lys Val Ser  
 485 490 495  
 Val Ala Trp Gln Lys Pro Tyr Leu Gln Thr Glu Phe Leu Leu Thr  
 500 505 510  
 40 Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr Val Thr Asp Asp  
 515 520 525  
 Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val Asn Ile Gly Trp  
 530 535 540  
 Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val Arg Thr Pro Ala  
 545 550 555 560  
 45 Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr Glu Glu Asp Arg  
 565 570 575  
 Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala Ala Asp Asn Gly  
 580 585 590  
 50 Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp Thr Val Lys Arg  
 595 600 605  
 Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro  
 610 615 620  
 His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys  
 625 630 635 640  
 55 Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu Asn Tyr Ala Gly  
 645 650 655  
 His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn  
 660 665 670  
 60 Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala  
 675 680 685  
 Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu  
 690 695 700  
 Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr  
 705 710 715 720  
 65 Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met  
 725 730 735  
 Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met  
 740 745 750  
 70 Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe  
 755 760 765  
 Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser  
 770 775 780  
 Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn  
 785 790 795 800  
 75 Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu



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	65		70		75		80									
	Ser	Gln	Tyr	Thr	Asp	Ala	Met	Leu	Tyr	His	Gln	Lys	Gly	Leu	Asn	Ala
					85					90					95	
5	Ala	Leu	Asn	Leu	Arg	Asp	Thr	Ile	Val	Ala	Ala	Gln	Ala	Trp	Asn	His
				100					105					110		
	Leu	Gly	Thr	Asp	Ser	Arg	Arg	Ile	Gly	Ala	Leu	Ala	Glu	Ala	Ser	Asp
				115				120					125			
	Tyr	His	Tyr	Lys	Ala	Leu	Ser	Leu	Ile	Glu	Ser	Phe	Ser	Gly	Asn	Gln
				130				135				140				
10	Asn	Arg	Pro	Ala	Ile	Lys	Ala	Arg	Ser	Ala	Ala	Leu	Asn	Gly	Ile	Gly
				145				150				155			160	
	Asn	Ile	Asn	Leu	Glu	Leu	Gly	Tyr	His	Asp	Glu	Ala	Glu	Lys	Asn	Phe
				165				170					175			
15	Leu	Lys	Ala	Leu	Gln	Gly	Glu	Lys	Glu	Leu	Asp	Ser	Pro	Leu	Gly	Gln
				180				185					190			
	Ala	Ile	Asn	Tyr	Ala	Asn	Leu	Gly	Arg	Ile	Tyr	Arg	Gln	Arg	Lys	Glu
				195				200					205			
	Tyr	Asp	Lys	Ala	Arg	Thr	Tyr	Phe	Leu	Leu	Ser	Leu	Glu	Gln	Asn	Asn
				210				215					220			
20	Met	Ala	Glu	Asn	Leu	Met	Gly	Ile	Gly	Leu	Cys	Ser	Ile	Asn	Leu	Gly
				225				230				235			240	
	Glu	Val	Asp	Glu	Glu	Lys	Gly	Asp	Tyr	Gln	Lys	Ala	Leu	Gln	Glu	Tyr
				245				250					255			
25	Ala	Thr	Ala	Tyr	Lys	Leu	Met	Glu	Gln	Leu	Ser	Asp	Arg	Trp	His	Trp
				260				265					270			
	Leu	Asn	Ser	Cys	Ile	Pro	Met	Ala	Arg	Ile	Asn	Leu	Lys	Gln	Gly	Asn
				275				280					285			
	Glu	Arg	Leu	Tyr	Gln	His	Phe	Ile	Ser	Leu	Ala	Glu	Gly	Thr	Ala	Lys
				290				295				300				
30	Glu	Ile	Asn	Ser	Thr	Ser	His	Leu	Ile	Glu	Ile	Tyr	Asn	Leu	Gln	Tyr
				305				310				315			320	
	Glu	Asn	Leu	Glu	Arg	Lys	Lys	Glu	Tyr	Lys	Gln	Ala	Leu	Glu	Ala	Phe
				325				330					335			
35	Cys	Leu	Ser	Lys	Thr	Leu	Ser	Asp	Ser	Met	Ser	Ile	Ala	His	Lys	Val
				340				345					350			
	Ser	Ser	Ile	Gln	Glu	Thr	Arg	Phe	Asn	Tyr	Glu	Arg	Asn	Lys	Ser	Gln
				355				360					365			
	Lys	Glu	Leu	Glu	Glu	Ile	Gln	Gln	Val	Ser	Lys	Ala	Lys	Gln	Glu	Lys
				370				375				380				
40	Ser	Lys	Phe	Ile	Leu	Leu	Ser	Thr	Leu	Phe	Ala	Leu	Phe	Ile	Ser	Ile
				385				390				395			400	
	Leu	Leu	Ile	Ser	Val	Leu	Thr	Tyr	Ala	Tyr	Arg	Gln	Gly	Lys	Lys	His
				405				410					415			
45	Asn	Lys	Leu	Ile	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr
				420				425					430			
	Gly	Ile	Thr	His	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu
				435				440					445			
	Asn	Glu	Lys	Met	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr
				450				455				460				
50	Glu	Leu	His	Lys	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu
				465				470				475			480	
	Val	Asn	Gln	Leu	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr
				485				490					495			
55	Pro	Glu	Trp	Arg	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile
				500				505					510			
	Asp	Ser	Phe	Ala	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu
				515				520					525			
	Gln	Pro	Glu	Ser	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu
				530				535				540				
60	Gln	Lys	Ile	Ile	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu
				545				550				555			560	
	Ala	Gly	Gly	Arg	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys
				565				570					575			
65	Asn	Leu	Ile	Ile	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr
				580				585					590			
	Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
				595				600					605			
	Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
				610				615				620				
70	Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
				625				630				635			640	
	Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
				645				650					655			
75	Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
				660				665					670			

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His Ile Ala Pro Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu  
 675 680 685  
 Asn His Arg Phe Glu Asp Glu Arg Pro Thr Ile Leu Val Glu Asp  
 690 695 700  
 5 Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Cys Asp Arg Tyr  
 705 710 715 720  
 Asn Val Leu Ser Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr  
 725 730 735  
 10 Glu His Ile Pro Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met  
 740 745 750  
 Asp Gly Ile Glu Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys  
 755 760 765  
 His Ile Pro Ile Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg  
 770 775 780  
 15 Leu Glu Gly Ile Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe  
 785 790 795 800  
 Ser Pro Glu Glu Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg  
 805 810 815  
 20 Glu Leu Leu Lys Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys  
 820 825 830  
 Pro Glu Glu Glu Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu  
 835 840 845  
 Leu Ala Ala Lys Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp  
 850 855 860  
 25 Phe Ser Ala Gln Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln  
 865 870 875 880  
 Leu Asn Arg Lys Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr  
 885 890 895  
 30 Ile Gln Gln Ile Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu  
 900 905 910  
 Ser Lys Asn Ile Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro  
 915 920 925  
 Ala Tyr Phe Ser Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser  
 930 935 940  
 35 Gln Tyr Arg Gln Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr  
 945 950 955 960  
 Val

40 (2) INFORMATION FOR SEQ ID NO:525  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 556 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 50 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...556  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525  
 60 Met Lys Lys Leu Leu Gln Ala Lys Ala Leu Ile Leu Ala Leu Gly Leu  
 1 5 10 15  
 Phe Gln Leu Pro Ala Ile Ala Gln Thr Gln Met Gln Ala Asp Arg Thr  
 20 25 30  
 65 Asn Gly Gln Phe Ala Thr Glu Glu Met Gln Arg Ala Phe Gln Glu Thr  
 35 40 45  
 Asn Pro Pro Ala Gly Pro Val Arg Ala Ile Ala Glu Tyr Glu Arg Ser  
 50 55 60  
 Ala Ala Val Leu Val Arg Tyr Pro Phe Gly Ile Pro Met Glu Leu Ile  
 65 70 75 80  
 70 Lys Glu Leu Ala Lys Asn Asp Lys Val Ile Thr Ile Val Ala Ser Glu  
 85 90 95  
 Ser Gln Lys Asn Thr Val Ile Thr Gln Tyr Thr Gln Ser Gly Val Asn  
 100 105 110  
 75 Leu Ser Asn Cys Asp Phe Ile Ile Ala Lys Thr Asp Ser Tyr Trp Thr  
 115 120 125

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Arg Asp Tyr Thr Gly Trp Phe Ala Met Tyr Asp Thr Asn Lys Val Gly  
 130 135 140  
 Leu Val Asp Phe Ile Tyr Asn Arg Pro Arg Pro Asn Asp Asp Glu Phe  
 145 150 155 160  
 5 Pro Lys Tyr Glu Ala Gln Tyr Leu Gly Ile Glu Met Phe Gly Met Lys  
 165 170 175  
 Leu Lys Gln Thr Gly Gly Asn Tyr Met Thr Asp Gly Tyr Gly Ser Ala  
 180 185 190  
 10 Val Gln Ser His Ile Ala Tyr Thr Glu Asn Ser Ser Leu Ser Gln Ala  
 195 200 205  
 Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp  
 210 215 220  
 Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp  
 225 230 235 240  
 15 Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp  
 245 250 255  
 Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala  
 260 265 270  
 20 Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu  
 275 280 285  
 Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg  
 290 295 300  
 Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu  
 305 310 315 320  
 25 Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys  
 325 330 335  
 Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg  
 340 345 350  
 30 Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro  
 355 360 365  
 Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val  
 370 375 380  
 Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg  
 385 390 395 400  
 35 Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser  
 405 410 415  
 Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys  
 420 425 430  
 40 Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr  
 435 440 445  
 Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn  
 450 455 460  
 Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala  
 465 470 475 480  
 45 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn  
 485 490 495  
 Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu  
 500 505 510  
 50 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser  
 515 520 525  
 Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu  
 530 535 540  
 Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys  
 545 550 555  
 55 (2) INFORMATION FOR SEQ ID NO:526  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 428 amino acids  
 60 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 65 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...428  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

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Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr
1      5      10      15
Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly
20      25      30
5  Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu
35      40      45
Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn
50      55      60
10 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu
65      70      75      80
Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly
85      90      95
Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp
100      105      110
15 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn
115      120      125
Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp
130      135      140
20 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala
145      150      155      160
Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr
165      170      175
Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu
180      185      190
25 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys
195      200      205
Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu
210      215      220
30 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser
225      230      235      240
Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr
245      250      255
Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His
260      265      270
35 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu
275      280      285
Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val
290      295      300
40 Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val
305      310      315      320
Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp
325      330      335
Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala
340      345      350
45 Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr
355      360      365
Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu
370      375      380
50 Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu
385      390      395      400
Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe
405      410      415
Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln
420      425

```

## (2) INFORMATION FOR SEQ ID NO:527

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (1x) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...310

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:527



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```

Met Arg Lys Thr Ile Ile Phe Cys Leu Leu Leu Ala Leu Phe Gly Cys
1      5      10      15
Ser Trp Ala Gln Glu Arg Val Asp Glu Lys Val Phe Ser Ala Gly Thr
20      25      30
5 Ser Ile Phe Arg Gly Ile Leu Glu Lys Val Lys Ala Pro Leu Met Tyr
35      40      45
Gly Asp Arg Glu Val Trp Gly Met Ala Arg Ala Ser Glu Asp Phe Phe
50      55      60
Phe Ile Leu Pro Val Thr Asp Asp Leu Thr Pro Val Leu Phe Tyr Asn
65      70      75      80
10 Arg Leu Thr Asn Glu Pro Cys Phe Val Ser Asp Gln Gly Ile Thr Glu
85      90      95
Tyr Phe Lys Phe Ala Gln Glu Gly Asp Tyr Ile Glu Val Glu Gly Ser
100      105      110
15 Ser Val Phe Met Ala Asn Leu Leu Tyr Tyr Arg Phe Phe Pro Thr Arg
115      120      125
Ile Thr Ser Tyr Asn Ala Pro Ile Glu Gly Val Val Ser Lys Thr Gly
130      135      140
20 Asn Pro Ala Phe Thr Ile Pro Met Leu Pro Gly Val Ser Asp Cys Ile
145      150      155      160
Glu Ile Ser Asn Asn Arg Lys Val Phe Leu Thr Asn Gln Leu Gly Val
165      170      175
Val Asn Ile Thr Asp Gly Met Glu Pro Pro Ile Ile Ala Gly Val Ser
180      185      190
25 Ala Ser Tyr Gly Ser Ser Val Arg Val Tyr Gly His Val Ser Gln Arg
195      200      205
Trp Asp Ile Ile Gly His Cys Tyr Leu Asp Ile Tyr Pro Thr Asn Cys
210      215      220
Tyr Pro Leu Ser Thr Lys Pro Val Ala Gly Asp Asp Glu Val Phe Val
225      230      235      240
30 Lys Gln Gln Gly Arg Gln Ile Glu Ile Asp Ser Asn Ser Pro Ile Val
245      250      255
Gln Val Val Val Tyr Asp Leu Glu Gly Lys Ser Val Phe Arg Lys Arg
260      265      270
35 Met Thr Glu Asn Ala Tyr Thr Leu Ser Phe Arg Ala Pro Met Leu Gly
275      280      285
Phe Met Thr Ile Met Ile Glu Thr Gln Asn Ser Ile Ile Asn Lys Lys
290      295      300
40 Leu Asn Val Thr Gln Leu
305      310

```

## (2) INFORMATION FOR SEQ ID NO:528

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```

Met Lys Lys Thr Thr Ile Ile Ser Leu Ile Val Phe Gly Ala Phe Phe
1      5      10      15
Ala Ala Val Gly Gln Thr Lys Asp Asn Ser Ser Tyr Lys Pro Phe Ser
20      25      30
65 Lys Glu Asp Ile Ala Gly Gly Val Tyr Ser Leu Pro Thr Gln Asn Arg
35      40      45
Ala Gln Lys Asp Asn Ala Glu Trp Leu Leu Thr Ala Thr Val Ser Thr
50      55      60
70 Asn Gln Ser Ala Asp Thr His Phe Ile Phe Asp Glu Asn Asn Arg Tyr
65      70      75      80
Ile Ala Arg Asp Ile Lys Ala Asn Gly Val Arg Lys Ser Thr Asp Ser
85      90      95
75 Ile Tyr Tyr Asp Ala Asn Gly Arg Ile Ser His Val Asp Leu Tyr Ile
100      105      110

```

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Ser Phe Ser Gly Gly Glu Pro Ala Leu Asp Thr Arg Phe Lys Tyr Thr  
 115 120 125  
 Tyr Asp Asp Glu Gly Lys Met Thr Val Arg Glu Val Phe Met Leu Val  
 130 135 140  
 5 Met Asp Pro Asn Thr Pro Ile Ser Arg Leu Glu Tyr His Tyr Asp Ala  
 145 150 155 160  
 Gln Gly Arg Leu Thr His Trp Ile Ser Phe Ala Phe Gly Ala Glu Ser  
 165 170 175  
 10 Gln Lys Asn Thr Tyr His Tyr Asn Glu Lys Gly Leu Leu Val Ser Glu  
 180 185 190  
 Val Leu Ser Asn Ala Met Gly Thr Thr Tyr Ser Asp Thr Gly Lys Thr  
 195 200 205  
 Glu Tyr Ser Tyr Asp Asp Ala Asp Asn Met Val Lys Ala Glu Tyr Phe  
 210 215 220  
 15 Val Val Gln Gln Gly Lys Ala Trp Gln Val Leu Lys Arg Glu Glu Tyr  
 225 230 235 240  
 Thr Tyr Glu Asp Asn Ile Cys Ile Gln Tyr Leu Ala Ile Asn Gly Thr  
 245 250 255  
 20 Asp Thr Lys Val Tyr Lys Arg Asp Ile Glu Ser Asp Lys Ser Ile Ser  
 260 265 270  
 Ala Asn Val Ile Asp Ile Pro Ser Met Pro Glu Gln Thr Trp Pro Asn  
 275 280 285  
 Met Tyr Gly Phe Asn Ala Lys Arg Leu Lys Glu Thr Tyr Ser Ser Tyr  
 290 295 300  
 25 Glu Gly Asp Val Ala Thr Pro Ile Phe Asp Tyr Ile Tyr Thr Tyr Lys  
 305 310 315 320  
 Ala Leu Thr Ser Met Ala Thr Pro Ser Thr Glu Ala Gln Val Ala Val  
 325 330 335  
 30 Tyr Leu Asn Pro Ser Thr Asp Arg Leu Val Ile Leu Ala Asn Gly Ile  
 340 345 350  
 Thr His Leu Ser Met Tyr Asp Leu Gln Gly Lys Leu Ile Arg Asp Cys  
 355 360 365  
 Ala Leu Ser Gly Asp Lys Val Glu Met Gly Val Gly Ser Leu Thr Lys  
 370 375 380  
 35 Gly Thr Tyr Leu Leu Lys Val Asn Thr Asp Gln Gly Ala Phe Val Arg  
 385 390 395 400  
 Lys Val Val Ile Arg  
 405

40 (2) INFORMATION FOR SEQ ID NO:529

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

45

(ii) MOLECULE TYPE: DNA (genomic)

50

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...2037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

65 GTATGGACT ACAAACTCAC TTCTCGATTG AAGCCCCAGG GCGACCAAGCC GGAAGCCATT 60  
 CGCCAACTCG TACAGGGCAT CAACGAAGGG ATGCCGCTC AGACGCTGCT CGGCGTAACG 120  
 GGTTCCGGCA AAACCTTTTAC GGTGGCTAAC GTGGTGGCGG CGGTCAATCG TCCGACCCCT 180  
 GTCTGTAGTC ACAACAAGAC CTGGGACGCA CAGCTATAGC GAGAGTTCAA AGCCTTCTTC 240  
 CCCGAGATG CCGTGGAGTA TTCTGTCAGC TACTACGACT ACTATCAGCC CGAGGCCCTAC 300  
 CTCCCGTCA CAGACACCTA TATCGAAAAG GACATGGCCA TCAACGCGGA GATCGAAAAA 360  
 CTGCGATTGA GGGCCACGGC TTGCTCCTG TCAGGGGCGA AAGATGTGCT TGTGGTCAGC 420  
 70 TCCGTATCCT GTCTCTACGG TATGGCCAAT CCTGAACTT TTTCCGAAAA GGTGATCAGC 480  
 CTGCACACGG GACAAAGGGC AGACAGGGAT CATTTTATCC GCCTGCTGGT AGAGAGCTAC 540  
 TACACGAACA ATAAAGTAGA GTTCGAGAGC GGCAACTTCC GTGTCAAAGG CGACAGCGTG 600  
 GACATATTCC CCGCCGTAGA AGGTTATGAC GGCCTGGCAT ACAGGGTGGG GTTTTGGGAT 660  
 GGAGAGGTGG AGCGGCTGAG TACCTTCGAT CCGCGAACGG GACGGAATA CGGCTGCTG 720  
 75 TCGSAGCTGA AGATATATCC GSCCAATCTC TTGCTGAACA CTAAGGAGCA GGTGGATCGG 780

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5 GCAGTAGGGA AAATCGATGT GGATCTGGGC GCACAGGTG AITTTCTGAA AGAAATCGGC 840  
 AAACCATATG AAGCCAAACG CTTGTATGAG CCGGTACCGT ATGACTTGGG AATGATCCGT 900  
 GAGTTGGGTT ATTGTTCCGG TATAGAGAAC TATTCGGGCT ACTTCGACGG CCGTGACGGG 960  
 GCGGAACGTC CTTTCTGTCT GTTGGATTAT TTCCCGGAGG ATTTCTGTGT GGTCTAGAGC 1020  
 10 GAAAGCCATG TAACGATACC GCAGATACGT GCCATGTAGS GAGGCGATCG TTCGCGCAAG 1080  
 GAGAATCTGG TCGAATACGG ATTCCGCGCT CCGTCCGCTC TCGACAATCG GCCGCTTCGC 1140  
 TTCGACGAGT TCGAAGCTCT CACCCCGCGG ACCCTTTATA TCASTGCCAC GCCTGCCGAC 1200  
 TATGAGCTGA ACAGAAGCGA AGGCGTGATC GTCGAGCAGC TGATCCGTCC GACCGGACTG 1260  
 CTGGATCCCA TCATCGACGT CAAGCCGACG GCAAAACCAAG TGGACGATCT GATGGAGGAG 1320  
 ATAGCAGCGT GCATCGAAAA GAAAGAGCGC GTACTGGTAA CGACCCCTGAC CAAACGTATG 1380  
 GCAGAGGAGC TTAGCGAATA CCTGCTACGC CACGSTATCA GCACCGGTA CATAACAGC 1440  
 GATGTGGACA CGCTGGAGCG TGTGCTATC ATGGAAGACC TCGCGAAGGG GGTCTACGAT 1500  
 GCACTCATOS GGGTGAATCT GCTCCGCGAA GGATTGSACT TCGCGGAAGT TTCGCTTGTG 1560  
 15 GCTATTCTGG ATGCGGATAA GGAAGGATTC CTGCGCTCGC ATCGTTCTGT CACCGAGACT 1620  
 GCAGGACGTC CCGCCCGGCA CATTCTGGG CGTGTCTAT TCTACGCGGA CAAGATCACC 1680  
 GACAGTATGC AGCTCACCAT GGAAGAGACT GCACGCGGAC GCGCAAGCA ACTGGCCTAC 1740  
 AACGAAGCGC ACGGCATCAC CCCCACACAG ATAGTGAAGA ACAGTGTGCT CATTGGGGGA 1800  
 GAAGGCGATG TGTGCGCTT GCAATCCGAT ACAGAATCCG GTGCGTACAT AGAAGAGAGC 1860  
 20 ATGCTTCCA CCAAGAAGCA AATGCTGGCA GCAGCCAAAG AGCTGGACTT TCTGGAAGCG 1920  
 GCACGACTTC GGGACGAAGC CGCACGATTG GAAAAGAAAC TGGAGCAACT CACAGCC 2037

(2) INFORMATION FOR SEQ ID NO:530

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

ATGGACTACA AACTCACTTC TCGATTCAAG CCCACGCGG ACCAGCCGGA AGCCATTCCG 60  
 CAACTCSTAC AGGGCATCAA CGAAGGGATG CCGCTCAGG CCGTCTCGG CGTAACGGGT 120  
 TCGGGCAAAA CTTTACGGT GGCTAACGTG GTGGCGGCGG TCAATCGTCC GACCTTGTG 180  
 50 CTGAGTCACA ACAAGACCTT GGCAGCACAG CTATACGAG AGTTCAAAGC CTTCTTCCCC 240  
 GAGAATGCGG TGGAGTATTT CGTCAGCTAC TACGACTACT ATCAGCCCGA GGCCTACCTC 300  
 CCGTTCACAG ACACCTATAT CGAAAAGGAC ATGGGCTATCA ACGCGGAGAT CGAAAAACTG 360  
 CGATTGAGGG CCACGGCTTC GCTCCTGTCA GGGCGGAAAG ATGTGCTTGT GGTGAGCTCC 420  
 GTATCCTGTC TCTACGGTAT GGCCAACTCT GAAGCTTTTT CGGAAAAGGT GATCAGCCTG 480  
 55 CACACGGGAC AAAGGGCAGA CAGGGATCAT TTTATCCGCC TGCTGGTAGA GAGCTACTAC 540  
 ACGAACAATA AAGTAGAGTT CGAGAGCGGC AACTTCCGTG TCAAAGGCGA CAGCGTGGAC 600  
 ATATTCCGCG CCGTAGAAGG TTATGACGGC GTGGCATACA GGGTGGAGTT TTGGGATGGA 660  
 GAGGTCGAGC GGCTGAGTAC CTTGATCCG CGAAGCGGAC GGGAAATACGG CCGTCTGTG 720  
 GAGCTGAAGA TATATCCGGC CAATCTCTTC GTGACGACTA AGGAGCAGGT GGATCGGGCA 780  
 60 GTAGGGAAAA TCGATGTGGA TCTGGGCGCA CAGGTCGATT TTCTGAAAGA AATCGGCAAA 840  
 CCATATGAAG CCAACCGCTT GTATGAGCGG GTCACGTATG ACTTGGAAAT CATCCGTGAG 900  
 TTGGGTTATT GTTCCGGTAT AGAGAATAT TCGCGCTACT TCGACGGCGG TGACGCGGGC 960  
 GAACGTCCTT TCTGTCTGTT GGATTATTTC CCGGAGGATT TCCTGTTGGT CATAGACGAA 1020  
 AGCCATGTAA CGATACCGCA GATACGTGCC ATGTACGGAG GCGATCGTTC GCGCAAGGAG 1080  
 65 AATCTGGTCC AATACGGATT CCGCTCGCT CCGCTCTCG ACAATCGGCC GCTTCGCTTC 1140  
 CAGAGTTTCG AAGCTCTCAC CCCCAGGACC CTTTATATCA GTGCCACGCC TGCCGACTAT 1200  
 GAGCTGAACA GAAGCGAAGG CTTGATCGTC GAGCAGCTGA TCCGTCCGAC CGGACTGCTG 1260  
 GATCCCATCA TCGACGTCAA GCGACGCGCA AACCAAGTGG ACGATCTGAT GGAGGAGATA 1320  
 GCACGCTGCA TCGAAAGAA AGAGCGCGTA CTGGTAACGA CGGTGACCAA ACGTATGGCA 1380  
 70 GAGCGAGCTTA GCGAATACCT GCTACGCCAC GGTATCGACA CCGGCTACAT ACACAGCGAT 1440  
 GTGGACACCG TGGAGCGTGT GCGTATCATG GAAGACCTGC GCAAGGGGGT CTACGATGCA 1500  
 CTCATCGGGG TGAATCTGCT CCGCGAAGGA TTGGACTTGC CGGAAGTTTC GCTTGTGGCT 1560  
 ATTCTGGATG CGGATAAGGA AGGATTCCTG CGTTCGCTAC GTTCGCTCAC GCAGACTGCA 1620  
 75 GGACGTGCCG CCGCGCATAT TCATGGGCGT GTCATCTTCT ACGCGGACAA GATCACCGAC 1680  
 AGTATGCAGC TCACCATGGA CGAGACTGCA CGCGACGCG CAAAGCAACT GGCCTACAC 1740

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GAAGCGCACG GCATCACCCC CCAACAGATA GTGAAGAACA GTGCTGCCAT TTGGGGAGAA 1800  
 GGCATGTGT CGGCCTTGCA ATCCGATACA GAATCCGGTG CGTACATAGA AGAGAGCAGC 1860  
 ATGGTGGCTG CCGATCCTTT GGCCGACTAT CTGAGCAAAC CCAAGCTGGA AGCACTCATT 1920  
 GCTTCGACCA AGAAGCAAAT GCTGGCAGCA GCCAAAGAGC TGGACTTTCT GGAAGCGGCA 1980  
 5 CGACTTCGGG ACGAAGCCGC ACGATTGGAA AAGAACTGG AGCAACTCAC AGCC 2034

## (2) INFORMATION FOR SEQ ID NO:531

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...679
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531
- 30 Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln  
 1 5 10 15  
 Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro  
 20 25 30  
 Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val  
 35 40 45  
 Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His  
 50 55 60  
 Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe  
 65 70 75  
 Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln  
 80 85 90 95  
 40 Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met  
 100 105 110  
 Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser  
 115 120 125  
 45 Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys  
 130 135 140  
 Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser  
 145 150 155  
 Leu His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu  
 160 165 170 175  
 50 Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn  
 180 185 190  
 Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly  
 195 200 205  
 55 Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu  
 210 215 220  
 Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu  
 225 230 235 240  
 Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu  
 245 250 255  
 60 Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln  
 260 265 270  
 Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu  
 275 280 285  
 65 Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr  
 290 295 300  
 Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala  
 305 310 315 320  
 Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu  
 325 330 335  
 70 Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met  
 340 345 350  
 Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe  
 355 360 365  
 75 Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe  
 370 375 380

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Glu Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp  
 385 390 395 400  
 Tyr Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg  
 405 410 415  
 5 Pro Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn  
 420 425 430  
 Gln Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys  
 435 440 445  
 10 Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu  
 450 455 460  
 Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser  
 465 470 475 480  
 Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys  
 485 490 495  
 15 Gly Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu  
 500 505 510  
 Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu  
 515 520 525  
 20 Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala  
 530 535 540  
 Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr  
 545 550 555 560  
 Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Ala Lys  
 565 570 575  
 25 Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val  
 580 585 590  
 Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln  
 595 600 605  
 30 Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala  
 610 615 620  
 Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu  
 625 630 635 640  
 Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp  
 645 650 655  
 35 Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys  
 660 665 670  
 Lys Leu Glu Gln Leu Thr Ala  
 675  
 40 (2) INFORMATION FOR SEQ ID NO:532  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 678 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 50 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...678  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532  
 60 Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln Pro  
 1 5 10 15  
 Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro Ala  
 20 25 30  
 65 Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val Ala  
 35 40 45  
 Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn  
 50 55 60  
 Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro  
 65 70 75 80  
 70 Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro  
 85 90 95  
 Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala  
 100 105 110  
 75 Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu  
 115 120 125

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Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys Leu  
 130 135 140  
 Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser Leu  
 145 150 155 160  
 5 His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu Val  
 165 170 175  
 Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn Phe  
 180 185 190  
 10 Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly Tyr  
 195 200 205  
 Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu Arg  
 210 215 220  
 Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu Ser  
 225 230 235 240  
 15 Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu Gln  
 245 250 255  
 Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln Val  
 260 265 270  
 20 Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu Tyr  
 275 280 285  
 Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr Cys  
 290 295 300  
 Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala Gly  
 305 310 315 320  
 25 Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu Leu  
 325 330 335  
 Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met Tyr  
 340 345 350  
 30 Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe Arg  
 355 360 365  
 Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe Glu  
 370 375 380  
 Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp Tyr  
 385 390 395 400  
 35 Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg Pro  
 405 410 415  
 Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn Gln  
 420 425 430  
 40 Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys Glu  
 435 440 445  
 Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu Ser  
 450 455 460  
 Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser Asp  
 465 470 475 480  
 45 Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys Gly  
 485 490 495  
 Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu Asp  
 500 505 510  
 50 Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu Gly  
 515 520 525  
 Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala Ala  
 530 535 540  
 Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr Asp  
 545 550 555 560  
 55 Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys Gln  
 565 570 575  
 Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val Lys  
 580 585 590  
 60 Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln Ser  
 595 600 605  
 Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala Ala  
 610 615 620  
 Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu Ile  
 625 630 635 640  
 65 Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Lys Glu Leu Asp Phe  
 645 650 655  
 Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys Lys  
 660 665 670  
 70 Leu Glu Gln Leu Thr Ala  
 675